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(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (SESTS)

(57) Abstract

Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.

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## SECRETED EXPRESSED SEQUENCE TAGS (SESTS)

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### FIELD OF THE INVENTION

The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

#### BACKGROUND OF THE INVENTION

Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-secreted "chaff", wasting effort and resources in the process.

Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted

proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

#### SUMMARY OF THE INVENTION

The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID 10 NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEO ID NO:17, SEO ID NO:18, SEO ID NO:19, SEO ID NO:20, SEO ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ 15 ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ 20 ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ 25 ID NO:86, SEO ID NO:87, SEO ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEO ID NO:101, SEO ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, 30 SEO ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,

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or a complement of said sequence.

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In other embodiments, the present invention provides an isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:6

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           NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;
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or a complement of said sequence.

In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

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SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEO ID NO:12, SEO ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEO ID NO:32, SEO ID NO:33, SEO ID NO:34, SEO ID NO:35, SEO ID NO:36, SEO ID NO:37, SEO ID NO:38, SEO ID NO:39, SEO ID NO:40, SEO ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEO ID NO:57, SEO ID NO:58, SEO ID NO:59, SEO ID NO:60, SEO ID NO:61, SEO ID NO:62, SEO ID NO:63, SEO ID NO:64, SEO ID NO:65, SEO ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

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or a complement of said sequence.

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In yet other embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

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25 or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described polynucleotides.

#### **DETAILED DESCRIPTION**

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each SEQ ID NO: in the Sequence Listing.

Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

						- (	-,,	
	1	BK8	32		62	DY307	93	DY611
5	2	BV216	DW100	)1	63	DY643	94	EC259
	3	BV274	33	DW831	64	DY656	95	DY711
	4	BV48	34	DW859	65	DY675	96	EC248
	5	DN351	35	DW875	66	DY988	97	EC32
	6	DN381	36	DW888	67	DY992	98	DO703
10	7	DN405	37	DW901	68	DY225	99	DO713
	8	DU651	38	DW902	69	DY236	100	DR294
	9	DU660	39	DW904	70	DY242	101	DYI
	10	DU675	40	DW905	71	DY254	102	DY10
	11	DU684	41	DW906	72	DY914	103	DY106
15	12	DD364	42	DW929	73	DY946	104	DY117
	13	DD379	43	DW981	74	DY955	105	DY148
	14	DD389	44	DX191	75	DY959	106	DY167
	15	DD401	45	DX219	76	DY961	107	DY17
	16	DD413	46	DX245	77	DY981	108	DY 174
20	17	DD426	47	DX256	78	DY357	109	DY175
	18	DD428	48	DX267	79	DY358	110	DY178
	19	DN293	49	DX66	80	DY381	111	DY23
	20	DD454	50	DX81	81	DY413	112	DY27
	21 -	DD472	51	DY780	82	DY414	113	DY41
25	22	DD475	52	DY803	83	DY415	114	DY42
	23	DT306	53	DY809	84	DY431	115	DY8
	24	DW282	54	DY814	<b>8</b> 5	DY.433	116	DY93
	25	DW300	55	DY261	86	DY436	117	EB107
	26	DW303	56	DY264	87	DY543	118	EB113
30	27	DW323	57	DY266	88	DY565	119	EB163
	28	DT258	58	DY271	89	DY585	120	EB25
	29	DW246	59	DY287	90	DY331	121	EB77
	30	DW324	60	DY297	91	DY586	122	EC172
	31	DW333	61	DY306	92	DY696	123	EC302

	124	EC317	158	EJ90	192	EJ224	226	EP378
	125	EC328	159	EM270	193	EJ240	227	EP38
	126	EC341	160	EM278	194	EJ254	228	EO109
	127	EC349	161	EN186	195	EJ258	229	EO120
5	128	ED105	162	EN215	196	EJ265	230	EQ166
	129	ED21	163	EN217	197	EJ280	231	EQ187
	130	ED23	164	EN234	198	EJ285	232	EQ188
	131	ED30	165	EN239	199	EJ307	233	EQ190
	132	ED43	166	EN256	200	EJ38	234	EQ194
10	133	ED54	167	EN260	201	DO235	235	EQ207
	134	EE177	168	EN264	202	DO238	236	EQ208
	135	EE65	169	EN266	203	DO263	237	EQ214
	136	DQ365	170	EN271	204	DO319	238	EQ215
	137	DK393	171	EN274	205	EJ324	239	EQ218
15	138	DK399	172	EN287	206	EN470	240	EQ219
	139	DO1128	173	EN310	207	EN477	241	EQ220
	140	DO1150	174 -	EN342	208	EN539	242	EQ221
	141	DZ34	175	EN363	209	EP451	243	EQ226
	142	DZ42	176	EN423	210	EO10	244	EQ229
20	143	EE116	177	EH106	211	EO14	245	EQ230
	144	EE93	178	EH145	212	EO48	246	EQ231
	145	DJ387	179	EH166	213	EO58	247	EQ233
	146	DJ402	180	EH167	214	EO60	248	EQ237
	147	DN551	181	EH178	215	EO62	249	EQ261
25	148	DN559	182	EH180	216	EO68	250	EQ272
	149	DN603	183	EH186	217	EO89	251	ER104
	150	DN629	184	EH188	218	EO90	252	ER106
	151	DN631	185	EH189	219	EO92	253	ER128
	152	DO11	186	EH190	220	EO97	254	ER134
30	153	DO118	187	EH203	221	EP108	255	ER174
	154	DO15	188	EH206	222	EP165	256	ER201
	155	DO157	189	EH95	223	EP219	257	ER77
	156	DO19	190	EJ148	224	EP234	258	ER80
	157	EJ53	191	EJ179	225	- EP277	259	ER97

	260	ES136 ,	294	ER399	328	FB264	362	FG208
	261	ES306	295	ER408	329	FB38	363	FG265
	262	ES35	296	ER418	330	FB71	364	FG274
	263	ES37	297	ER430	331	FB78	365	FG278
5	264	ES206	298	ER471	332	FC12	366	FG281
	265	ET13	299	ER476	333	FB349	367	FG291
	266	ET22	300	ER493	334	FC136	368	FG294
	267	ET39	301	ER496	335	FC170	369	FG340
	268	ET84	302	ER498	336	FD152	370	FG363
10	269	EF121	303	ER524	337	FE141	371	FG372
	270	EF129	304	EW13	338	FE5	372	FG380
	271	EF45	305	EX25	339	FD131	373	FG401
	272	EF48	306	EX53	340	EC425	374	FG99
	273	EF5	307	EY165	341	EC428	375	FI203
15	274	EF88	308	EY29	342	ED204	376	FE311
	275	EG194	309	EZ35	343	ED205	377	FE315
	276	EG251	310	EZ4	344	ED210	378	FE322
	277	EH12	311	E <b>Z</b> 88	345	ED223	379	FE329
	278	EH213	312	EZ93	346	DI301	380	FE341
20	279	EH22	313	FA8	347	DI303	381	FE366
	280	EH221	314	EV234	348	DI310	382	FE375
	281	EH248	315	EW101	349	DI39	383	FE412
	282	EH29	316	EW109	350	DJ90	384	FE415
	283	EH61	317	· EW150	351	DM290	385	FE442
25	284	EH68	318	EY197	352	DM304	386	FE472
	285	EH78	319	EY206	353	DN618	387	FE557
	286	EH80	320	EY215	354	DN896	388	FE568
	287	ER311	321	EZ209	355	DN904	389	FE619
	288	ER329	322	FA139	356	FG119	390	FE676
30	289	ER343	323	FA171	357	FG126	391	FE682
	290	ER366	324	FA252	358	FG140	392	FF150
	291	ER369	325	FA28	359	FG193	393	FF153
	292	ER381	326	FA316	360	FG197	394	FF168
	293	ER395	327	FA95	361	FG198	395	FF175

	396	FF181	430	FH17	464	FN203	498	FO201
	397	FF46	431	FH170	465	FN228	499	FO209
	398	FF49	432	FH24	466	FN229	500	FO211
	399	FF97	433	FH3	467	FN251	501	FO215
5	400	FG41	434	FH39	468	FN254	502	FO253
	401	FG437	435	FH56	469	FP134	503	FO254
	402	FG441	436	FH6	470	FP14	504	FO261
	403	FG448	437	FH66	471	FP163	505	FO267
	404	FG45	438	FM109	472	FP172	506	FO275
10	405	FG492	439	FM13	473	FP71	507	FO290
	406	FG504	440	FM15	474	FP87	508	FO292
	407	FG565	441	FM150	475	E1118	509	FO316
	408	FG567	442	FM170	476	EI16	510	FO324
	409	FG57	443	FM28	477	EI187	511	FO327
15	410	FG577	444	FM3	478	EI203	512	FO348
	411	FG615	445	FM32	479	EI228	513	FO36
	412	FG625	446	FM36	480	E1231	514	FO38
	413	FG630	447	FM60	481	E1236	515	FO40
	414	FG659	448	FM86	482	EI239	516	FO66
20	415	FG708	449	FM95	483	EI243	517	FO75
	416	FG91	450	FM98	484	E1250	518	FP185
	417	FG884	451	FM99	485	E1255	519	FP193
	418	FG891	452	FN172	486	E1264	520	FP233
	419	FG909	453	FN19	487	EI273	521	FP239
25	420	FG912	454	FN29	488	FO11	522	FP246
	421	FG949	455	FN53	489	FO125	523	FP262
	422	FG952	456	FK199	490	FO128	524	FP268
	423	FG965	457	FK217	491	FO133	525	FP271
	424	FH10	458	FK23	492	FO135	526	FP273
30	425	FH116	459	FK32	493	FO147	527	FQ505
	426	FH123	460	FK59	494	FO152	528	DN647
	427	FH13	461	FK78	495	FO160	529	DN650
	428	FH136	462	FN189	496	FO173	530	DN676
	429	FH149	463	FN191	497	FO182	531	DO94

	532	FR292	566	DN827	600	FY201	634	DU4
	533	FR436	567	DN833	601	FY202	635	DU75
	534	FR451	568	DN834	602	FY243	636	FY386
	535	FR473	569	DN850	603	FY265	637	FY388
5	536	FS10	570	DO913	604	FY316	638	FY398
	537	FS106	571	DO923	605	FY318	639	FY414
	538	FS107	572	DO935	606	FY321	640	GA48
	539	FS143	573	DO938	607	FY354	641	GA63
	540	FS173	574	DO944	608	FY356	642	GA64
10	541	FS28	575	DO949	609	FY421	643	DT382
	542	FS31	576	DO952	610	FY430	644	DT385
	543	FS40	577	DQ12	611	FY455	645	DT388
	544	FV35	578	DT2	612	FY484	646	DT464
	545	FV49	579	DT44	613	FY524	647	DT470
15	546	FV68	580	DT53	614	FY530	648	DT478
	547	FW13	581	DT8	615	FY628	649	DT482
	548	FW64	582	FQ661	616	DQ242	650	DU114
	549	FY127	583	FQ672	617	DQ262	651	DUI18
	550	FY136	584	FQ696	618	DQ276	652	DU123
20	551	FY60	585	FR1087	619	DQ285	653	DU133
	552	FY65	586	FR927	620	DQ304	654	DU156
	553	FY72	587	FR938	621	DQ313	655	DU157
	554	DN1112	588	FR980	622	DQ51	656	FZ5
	555	DN1118	589	FV122	623	DQ54	657	FZ87
25	556	DN1122	590 -	FV131	624	DR628	658	DW181
	557	DN782	591	FV132	625	GU215	659	DW309
	558	DN793	592	FV84	626	FM481	660	DX1
	559	DN795	593	FV85	627	DTI17	661	DX15
	560	DN806	594	FV95	628	DT133	662	DX19
30	561	DN809	595	FX115	629	DT139	663	DX22
	562	DN810	596	FX127	630	DT164	664	DX29
	563	DN814	597	FX154	631	DU160	665	DX3
	564	DN815	598	FY187	632	DU164	666	DX4
	565	DN823	599	FY199	633	DU166	667	FZ428

	668	FZ163	702	FZ209	736	GE89	770	GF151
	669	DY474	703	FZ254	737	DY516	771	GF179
	670	FZ139	704	FZ346	738	DY529	772	GF99
	671	FX76	705	GA82	739	DY530	773	GB261
5	672	FX65	706	GA85	740	DY538'	774	GC499
	673	FX55	707	GA91	741	DY830	775	GD177
	674	DU536	708	DX299	742	DY857	776	GD7
	<b>6</b> 75	FZ534	709	DX304	743	EA17	777	GE300
	676	DU515	710	DX309	744	EA36	778	DX179
10	677	DU475	711	DX316	745	GG73	779	DY757
	678	DU462	712	DX328	746	DU544	780	EC392
	679	DU353	713	DX336	747	DU560	781	EE15
	680	DU341	714	DX354	748	DZ109	782	DU408
	681	DU306	715	DX357	749	EA105	783	DU410
15	682	DU278	716	DX359	750	EA106	784	DU416
	683	DU244	717	DX363	751	EA110	785	DU447
	684	DU238	718	DX364	752	EA123	786	DX111
	685	DU236	719	DY478	753	EA46	787	DX112
	686	DU231	720	DY497	754	EA58	788	DX123
20	687	FZ639	721	DY508	755	EA7	789	DX138
	688	GC456	722	EA89	756	EA82	790	DX146
	689	GG126	723	EA9	757	GE361	791	DX153
	690	GG129	724	EA90	758	FZ510	792	DX157
•	691	GG152	725	GC52	759	GE387	793	EE4
25	692	GG170	726	GC57	760	GE410	794	FZ676
	693	GG182	727	GC585	761	GE463	795	FZ683
	694	GG217	728	GC74	762	GE466	796	GD309
	695	GG440	729	GE28	763	GE468	797	GD358
	696	GG619	730	GE41	764	GE471	798	GG543
30	697	DX279	731	GE51	765	GE524	799	FX516
	698	DX288	732	GE60	766	GE539	800	FX536
	699	DX290	733	GE68	767	GE548	801	FZ1032
	700	DX295	734	GE80	768	GE549	802	FZ1041
	701	DX298	735	GE82	769	GE99	803	FZ1072

	804	FZ781	838	DD12.	872	GP304	906	EM40
	805	GA147	839	DD127	873	GP329	907	EM42
	806	GA284	840	DD177	874	GP338	908	EM58
	807	DY723	841	DD204	875	GP340	909	GF185
5	808	DY737	842	DD207	876	GQ13	910	GF187
	809	DY739	843	DD211	877	GQ18	911	GF196
	810	EC399	844	DD217	878	GQ22	912	GF197
	811	EM254	845	DD504	879	GQ38	913	GF207
	812	FX194	846	DD509	880	GQ40	914	GF209
10	813	FX234	847	DD518	88,1	GQ56	915	GF212
	814	FX281	848	DD537	882	GQ6	916	GF218
	815	FX317	849	DD541	883	DD312	917	GF221
	816	FX353	850	DD71	884	DD352	918	GF222
	817	FX395	851	DH941	885	EK145	919	GF250
15	818	GA293	852	DQ194	886	EK208	920	GF255
	819	GA321	853	DQ204	887	EK223	921	GF256
	820	GA327	854	DQ215	888	EK234	922	GI28
	821	GB160	855	DQ216	889	EK480	923	GI3
	822	GA132	856	EK423	890 -	EK491	924	G130
20	823	GA135 .	857	EK424	891	EK499	925	GI51
	824	GA205	858	EK450	892	EK571	926	G163
	825	GB814	859	EL15	893	EK578	927	GI7
	826	GF87	860	DD285	894	EK581	928	G174
	827	GG687	861	EK598	895	EK591	929	G188
25	828	GG692	862	EK622	896	DD215	930	G19
	829	GG694	863	EK626	897	EK634	931	DY874
	830	GG702	864	EK649	898	EL358	932	DY886
	831	GG705	865	GO653	899	EL360	933	DY900
	832	GP23	866	GP107	900	EL387	934	EM358
30	833	GP56	867	GP123	901	EL391	935	EM381
	834	GP61	868	GP168	902	EM111	936	EM386
	835	GP65	869	GP232	903	EM112	937	EM388
	836	DD115	870	GP274	904	EM12	938	EM396
	837	DD119	871	GP297	905	EM125	939	EM397

	940	EM401	974	GT43	1008	HU212	1042	EY290
	941	EM406	975	GT6	1009	HU141	1043	EY304
	942	EM408	976	HR712	1010	HS555	1044	EY313
	943	EM409	977	HR704	1011	HR95	1045	FK295
5	944	EM423	978	HR693	1012	HR906	1046	FK301
	945	EM424	979	HR628	1013	HR76	1047	FK317
	946	FE196	980	HR605	1014	HR753	1048	FK328
	947	FE204	981	EK341	1015	HR731	1049	FK349
	948	FE205	982	EK390	1016	EN116	1050	FK350
10	949	FE207	983	EN108	1017	EM341	1051	FK354
	950	FE215	984	FK235	1018	FJ283	1052	FK365
	951	FE222	985	GK428	1019	FJ307	1053	FQ105
	952	FE227	986	GT56	1020 ·	FJ70	1054	FQ239
	953	.FE228	987	FQ562	1021	FM176	1055	FQ360
15	954	FE248	988	FQ605	1022	FM197	1056	FQ45
	955	FE263	989	FQ608	1023	FM205	1057	GU353
	956	FE271	990	FQ609	1024	FM208	1058	GX167
	957	GF296	991	FQ612	1025	FM229	1059	GX183
	958	GN38	992	FS49	1026	FQ419	1060	GX208
20	959	GN45	993	FS87	1027	GX48	1061	GX210
	960	GN60	994	GM101	1028	GX5	1062	FM369
	961	GN68	995	GM103	1029	GX92	1063	FM375
	962	GN82	996	GM114	1030	FM289	1064	FM389
	963	GR286	997	GM129	1031	FM290	1065	FM432
25	964	EN10	998	GM153	1032	FM296	1066	FM459
	965	EN37	999	GM158	1033	FM300	1067	FM462
	966	FK127	1000	GM196	1034	FM312	1068	FM479
	967	FK151	1001	GM243	1035	GU512	1069	GX301
	968	GS26	1002	GM259	1036	GU534	1070	GX336
30	969	GS4	1003	GM266	1037	GU608	1071	GX354
	970	EV391	1004	HV38	1038	GX159	1072	GX361
	971	FG535	1005	HV23	1039	GX97	1073	GX403
	972	FG852	1006	HV199	1040	EW304	1074	GX408
	973	GT28	1007	HV181	1041	EY281	1075	GX418

	1076	GU830	1110	GG3	1144	GN97	1178	HE91
	1077	GU925	1111	HA510	1145	HB443	1179	HF289
	1078	GU940	1112	HA422	1146	HC324	1180	HG444
	1079	GX1031	1113	HA382	1147	HC327	1181	HF137
5	1080	GX496	1114	HA360	1148	HC505	1182	HD706
	1081	GX504	1115	HA249	1149	HC724	1183	HG710
•	1082	GX509	1116	HA199	1150	HA1054	1184	HG733
	1083	GX536	1117	HA192	1151	HB1041	1185	HG775
	1084	GX540	1118	GZ568	1152	HB746	1186	H1222
10	1085	GX645	1119	GY520	1153	HB752	1187	HI39
	1086	GX700	1120	GY515	1154	HB975	1188	HH215
	1087	GX730	1121	GY330	1155	HC705	1189	HH357
	1088	GX750	1122	GY307	1156	HA791	1190	HH372
	1089	GX753	1123	HA81	1157	HC1002	1191	HH378
15	1090	GX760	1124	HA73	1158	HC1071	1192	HH390
	1091	GX814	1125	HA29	1159	HC1089	1193	HH396
	1092	GX851	1126	HA24	1160	HC831	1194	HH404
	1093	GX909	1127	HA18	1161	HC986	1195	HH433
	1094	GY102	1128	GZ78	1162	GY72	1196	HI2
20	1095	GY105	1129	GZ70	1163	HG159	1197	HH544
	1096	GY138	1130	GZ7	1164	HG620	1198	HH608
	1097	GY211	1131	GZ496	1165	HD161	1199	HH612
	1098	GX1082	1132	GZ495	1166	HD353	1200	HH625
	1099	GX1108	1133	GZ485	1167	HD378	1201	HH640
25	1100	GX1140	1134	GZ436	1168	HD417	1202	HH648
	1101	GX1165	1135	GZ420	1169	HD427	1203	HH691
	1102	GX576	1136	GZ378	1170	HD434	1204	HJ120
	1103	GX595	1137	GZ37	1171	HD499	1205	HJ140
	1104	GX606	1138	GY558	1172	HD569	1206	HJ181
30	1105	GX619	1139	GG894	1173	HD627	1207	НЈ184
	1106	GG874	1140	GG907	1174	HD648	1208	HJ22
	1107	GG858	1141	GN114	1175	HE111	1209	HJ253
	1108	GG836	1142	GN115	1176	HE142	1210	HJ265
	1109	GG8	1143	GN145	1177	HE178	1211	HJ362

	1212	НJ395	1246	HM372	1280	HO722	1314	HT166
	1213	HJ411	1247	HM380	1281	HO799	1315	HT176
	1214	HJ444	1248	HM422	1282	HO801	1316	HT193
	1215	HJ65	1249	HM444	1283	HO817	1317	HT43
5	1216	НJ674	1250	HM497	1284	HO82	1318	HT81
	1217	НJ705	1251	HM544	1285	HK719	1319	HW149
	1218	HJ81	1252	HM643	1286	HO1077	1320	HW152
	1219	НЈ862	1253	HN72	1287	HO1080	1321	HW190
	1220	НJ949	1254	HN78	1288	HO1087	1322	HW204
10	1221	HK10	1255	HO107	1289	HO1143	1323	HW221
	1222	HK26	1256	HO237	1290	HO1176	1324	HW243
	1223	HK60	1257	HO266	1291	HO1183	1325	HW261
	1224	HJ1037	1258	HO277	1292	HO1216	1326	HW368
	1225	HJ968	1259	HO283	1293	HO1271	1327	HW74
15	1226	НЈ981	1260	HO292	1294	HO1329	1328	HX10
	1227	HJ994	1261	HO294	1295	HO1434	1329	HX102
	1228	НЈ995	1262	HO305	1296	HO1441	1330	HX110
	1229	HK189	1263	HO315	1297	HO1453	1331	HX113
	1230	HK234	1264	HO332	1298	HO854	1332	HX155
20	1231	HK650	1265	HO358	1299	HO868	1333	HX188
	1232	HK658	1266	HO476	1300	HP262	1334	HX29
	1233	HK669	1267	HO481	1301	HQ36	1335	HX50
	1234	HK713	1268	HO502	1302	HQ72	1336	HY13
	1235	HK899	1269	HO54	1303	GM16	1337	HY3
25	1236	HE187	1270	HO60	1304	GM286	1338	HY55
	1237	HK162	1271	HO600	1305	GM295	1339	HY57
	1238	HL25	1272	HO617	1306	GM335	1340	HZ15
	1239	HL380	1273	HO640	1307	GM365	1341	HZ8
	1240	HL73	1274	HO663	1308	HR397	1342	IAl
30	1241	HM50	1275	HO688	1309	HR560	1343	1A21
	1242	HM54	1276	HO692	1310	HR593	1344	1A32
	1243	HM91	1277	HO693	1311	HR598	1345	IA36
	1244	HM236	1278	HO703	1312	HT13	1346	1B2
	1245	HM280	1279	HO717	1313	HT137	1347	IC2

	1348	IC9	1382	IA167	1413	HW786	1447	IE362
	1349	HY229	1383	1A183	1414	HW810	1448	IH32
	1350	HY244	1384	IA188	1415	HW846	1449	11113
	1351	HY344	1385	IA200	1416	HW849	1450	IJ101
5	1352	HY370	1386	IA220	1417	1B15	1451	1J163
	1353	HY374	-1387	IA64	1418	IB19	1452	IJ167
	1354	HY404	1388	IA69	1419	IB22	1453	1F28
	1355	HY419	1389	1A86	1420	1B28	1454	IF376
	1356	HY435	1390	HW936	1421	IB36	1455	1F456
10	1357	HZ103	1391		1422	IB49	1456	IF87
	1358	HZ109	HW10	17	1423	IC103	1457	IJ1201
	1359	HZ111	1392	.·	1424	IC126	1458	IJ1220
	1360	HZ115	HW10	44	1425	IC132	1459	IJ1237
	1361	HZ71	1393		1426	IC142	1460	IJ1240
15	1362	HZ76	HW10	59	1427	IC155	1461	IJ1247
	1363	HZ88	1394	HW430	1428	IC54	1462	IJ1287
	1364	HW115	1395	HW432	1429	IC87	1463	IJ1292
	1365	HW128	1396	HW440	1430	IC92	1464	IJ1299
	1366	HW477	1397	HW456	1431	IE146	1465	IJ583
20.	1367	HW483	1398	HW518	1432	IE147	1466	1J592
	1368	HW491	1399	HW591	1433	IE149	1467	IJ597
	1369	HW499	1400	HW598	1434	IE169	1468	1J629
	1370	HW507	1401	HW627	1435	1Z6	1469	1J638
	1371	HZ116	1402	HW646	1436	JE33	1470	IJ640
25	1372	HZ162	1403	HW649	1437	JE44	1471	1J642
	1373	HZ185	1404	HW693	1438	JE52	1472	1J686
	1374	HZ201	1405	HW695	1439	IE10	1473	IG25
	1375	HZ224	1406	HW697	1440	IE47	1474	IG35
	1376	HZ262	1407	HW711	1441	IE73	1475	IH40
30	1377	IA106	1408	HW715	1442	JA37	1476	IH54
	1378	IA110	1409	HW730	1443	JA78	1477	IJ288
	1379	IA114	1410	HW732	1444	JB12	1478	1J76
	1380	IA153	1411	HW741	1445	JB23	1479	IF292
	1381	IA157	1412	HW750	1446	IE352	1480	IF513

	1481	IF548	1515	1Q58
	1482	IJ1043	1516	15488
	1483	IJ1048	1517	IS564
	1484	131054	1518	IT23
5	1485	111088	1519	IT44
	1486	13777		
	1487	1J887		
	1488	IJ907		
	1489	1J928		
10	1490	1J942		
	1491	ILI		
	1492	IL100		
	1493	IL112		
	1494	IL28		
15	1495	IK11		
	1496	IK14		
	1497	IK20	٠	
	1498	IK203		
	1499	IK209		
20	1500	IK212		
	1501	IK343		
	1502	IK73		-
	1503	IO134		
	1504	IO138		
25	1505	IO151		
	1506	IO202		٠
	1507	IO209		
	1508	IO31		
	1509	IO356		-
30	1510	10420		
	1511	1062		
	1512	IQ15		
	1513	IQ45		

1514 IQ55

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selection "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

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As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplpasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decayalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions, most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

	Stringenc y Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer†	Wash Temperature and Buffer'
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	В	DNA:DNA	<50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	С	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
15	G ·	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	н	DNA:DNA	< 50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	1	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50	T,*; 4xSSC	T,*; 4xSSC
	К	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	<50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
	М	DNA:DNA	≥.50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	0	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	Tp*; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

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<sup>‡</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>†</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\* $T_B$  -  $T_R$ : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature ( $T_m$ ) of the hybrid, where  $T_m$  is determined according to the following equations. For hybrids less than 18 base pairs in length,  $T_m$ (°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length,  $T_m$ (°C) = 81.5 + 16.6( $\log [Na^+]$ ) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The socked polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 12, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

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sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac®kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

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Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

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of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

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## **USES AND BIOLOGICAL ACTIVITY**

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

### Research Uses and Utilities

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as porbes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise antiprotein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligand. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

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Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

# Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

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and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986;
Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner,
K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immunol. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

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A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

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syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA41g fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

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Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

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infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigenpulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

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Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

## 25 Hematopoiesis Regulating Activity

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A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

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example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemo:herapy,either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

### Tissue Growth Activity

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A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-liketissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-liketissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

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plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, <u>Epidermal Wound Healing</u>, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

# 15 Activin/Inhibin Activity

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A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

# Chemotactic/Chemokinetic Activity

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A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

# Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### 15 Receptor/Ligand Activity

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A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusioninjury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

# 20 <u>Tumor Inhibition Activity</u>

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

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# Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

# **ADMINISTRATION AND DOSING**

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A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

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can directly signal T cells. Alternatively antibodies able to bind surface immunolgobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

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The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

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which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about  $0.01~\mu g$  to about 100~mg (preferably about 0.1~ng to about 10~mg, more preferably about  $0.1~\mu g$  to about 1~mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, et al., FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

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For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

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Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses(including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorbtion of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

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The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

# Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
	Human	Placenta	26yrs., 1 specimen
AC			Fetal ES cells
AD	Murine	Embryo	-
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
ΑI	Human	Blood	Adult PBMC/TH1or2
ΑJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
ΑT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
ΑZ	Human	Colon	Caco-2 Adenocarcinoma
В	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM		Muscle	N/A
	Human		
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C			PeripheralBloodMononuclearCell
	Human	Blood	
CA	Murine	Embryo	Fetal ES cell embryoid bodies
СВ	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	SalivaryGland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU.	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	PeripheralBloodMononuclearCell
DA			·
	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

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DL ·	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DÜ	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	
		Testes	26yrs., 1 specimen
EQ ER	Human		10-61 yrs., pool of 11
ES	Human	Brain Placenta	19-23wks., M/F pool of 5
ET	Human		26yrs., 1 specimen
EU	Human	Testes	10-61 yrs., pool of 11
EV	Human	Kidney	Adult Kidney
_	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FH Human Brain 19-23wks., M/F pool of 5 FI Human Small Intest Adult Small Intestine FI Human Lung CA Adult Lung CA FK Human Kidney Adult Kidney FM Human Brain N/A FN Human Brain 19-23wks., M/F pool of 5 FO Human Brain N/A FP Human Placenta 26yrs., 1 specimen FQ Human Testes 10-61yrs., pool of 11 FR Human Placenta 26yrs., 1 specimen FS Human Testes 10-61yrs., pool of 11 FT Chicken Fetal Lung Fetal Lung FU Chicken Fetal Lung Fetal St. 23 Limb Bud FV Human Testes Adult NCCIT TeratoCA FW Human Frain 19-23wks., M/F pool of 5 FY Human Placenta 26yrs., 1 specimen FZ Human Placenta 26yrs., 1 specimen FZ Human Placenta 26yrs., 1 specimen FZ Human Placenta 26yrs., 1 specimen GG Human Blood PeripheralBloodMononuclearCell GB Human Placenta 26yrs., 1 specimen GC Human Fetals 10-61yrs., pool of 11 GB Human Placenta 26yrs., 1 specimen GC Human Fetals 10-61yrs., pool of 11 GB Human Placenta 26yrs., 1 specimen GC Human Fetals 10-61yrs., pool of 11 GB Human Placenta 26yrs., 1 specimen GC Human Fetals 10-61yrs., pool of 11 GB Human Placenta 26yrs., 1 specimen GC Human Fetals Kidney2 Fetal Kidney GH Human Brain N/A GF Human Placenta 26yrs., 1 specimen GG Human Fetal Kidney2 Fetal Kidney GH Human Placenta 26yrs., 1 specimen GH Human	EC	T T	Di.	NT/A
FI Human Lung CA Adult Lung CA FK Human Kidney Adult Kidney FM Human Brain N/A FN Human Brain 19-23wks., M/F pool of 5 FO Human Brain N/A FP Human Brain 19-23wks., M/F pool of 5 FO Human Placenta 26yrs., 1 specimen FQ Human Testes 10-61yrs., pool of 11 FR Human Placenta 26yrs., 1 specimen FS Human Testes 10-61yrs., pool of 11 FT Chicken Fetal Lung Fetal Lung FU Chicken Limb Bud Fetal St. 23 Limb Bud FV Human Testes Adult NCCIT TeratoCA FW Human Testes Adult NCCIT TeratoCA FW Human Brain 19-23wks., M/F pool of 5 FY Human Placenta 26yrs., 1 specimen FZ Human Placenta 26yrs., 1 specimen G Human Blood PeripheralBloodMononuclearCell GA Human Testes 10-61yrs., pool of 11 GB Human Placenta 26yrs., 1 specimen GC Human Fetal Kidney PeripheralBloodMononuclearCell GB Human Placenta 26yrs., 1 specimen GC Human Placenta 26yrs.	FG	Human	Brain	N/A
FJ Human Kidney Adult Kidney FM Human Kidney Adult Kidney FM Human Brain N/A FN Human Brain 19-23wks., M/F pool of 5 FO Human Brain N/A FP Human Placenta 26yrs., 1 specimen FQ Human Placenta 26yrs., 1 specimen FR Human Placenta 26yrs., 1 specimen FR Human Placenta 26yrs., 1 specimen FS Human Testes 10-61yrs., pool of 11 FT Chicken Fetal Lung Fetal Lung FU Chicken Limb Bud Fetal St. 23 Limb Bud FV Human Testes Adult NCCIT TeratoCA FW Human Testes Adult NCCIT TeratoCA FW Human Placenta 26yrs., 1 specimen FY Human Placenta 26y				<del></del>
FK Human Kidney Adult Kidney FM Human Brain N/A FN Human Brain 19-23wks., M/F pool of 5 FO Human Brain N/A FP Human Placenta 26yrs., 1 specimen FQ Human Placenta 26yrs., 1 specimen FR Human Placenta 26yrs., 1 specimen FS Human Testes 10-61yrs., pool of 11 FT Chicken Fetal Lung Fetal Lung FU Chicken Limb Bud Fetal St. 23 Limb Bud FV Human Testes Adult NCCIT TeratoCA FW Human Testes Adult NCCIT TeratoCA FW Human Brain 19-23wks., M/F pool of 5 FY Human Placenta 26yrs., 1 specimen FZ Human Placenta 26yrs., 1 specimen FZ Human Placenta 26yrs., 1 specimen GG Human Blood PeripheralBloodMononuclearCell GA Human Testes 10-61yrs., pool of 11 GB Human Placenta 26yrs., 1 specimen GC Human Placenta 26yrs., 1 specimen GC Human Festes 10-61yrs., pool of 11 GD Human Placenta 26yrs., 1 specimen GG Human Festes 10-61yrs., pool of 5 FF Human Placenta 26yrs., 1 specimen GC Human Festes 10-61yrs., pool of 11 GD Human Placenta 26yrs., 1 specimen GG Human Fetal Kidney2 Fetal Kidney GH Human Blood PeripheralBloodMononuclearCell GN Human Fetal Kidney2 Fetal Kidney GH Human Fetal Kidney2 Fetal Kidney GN Human Adrenal Gland Adult Adrenal Gland GP Human Pancreas Adult HPC-3 Ductal AdenoCA GR Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Brain I9-23wks., M/F pool of 5				
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GK Human Fetal Kidney2 Fetal Kidney GL Murine Lymph Node Adult Lymph Node GM Human Uterus N/A GN Human Blood PeripheralBloodMononuclearCell GO Human Adrenal Gland Adult Adrenal Gland GP Human Ovary PA-1 Teratocarcinoma GQ Human Pineal Gland N/A GR Human Pancreas Adult HPC-3 Ductal AdenoCA GS Human Retina 16-75yrs., pool of 76 GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5		Human	Retinoblastoma	
GL Murine Lymph Node Adult Lymph Node GM Human Uterus N/A GN Human Blood PeripheralBloodMononuclearCell GO Human Adrenal Gland Adult Adrenal Gland GP Human Ovary PA-1 Teratocarcinoma GQ Human Pineal Gland N/A GR Human Pancreas Adult HPC-3 Ductal AdenoCA GS Human Retina 16-75yrs., pool of 76 GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 5		Murine	•	•
GM Human Uterus N/A GN Human Blood PeripheralBloodMononuclearCell GO Human Adrenal Gland Adult Adrenal Gland GP Human Ovary PA-1 Teratocarcinoma GQ Human Pineal Gland N/A GR Human Pancreas Adult HPC-3 Ductal AdenoCA GS Human Retina 16-75yrs., pool of 76 GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5	GK	Human	Fetal Kidney2	· ·
GN Human Blood PeripheralBloodMononuclearCell GO Human Adrenal Gland Adult Adrenal Gland GP Human Ovary PA-1 Teratocarcinoma GQ Human Pineal Gland N/A GR Human Pancreas Adult HPC-3 Ductal AdenoCA GS Human Retina 16-75yrs., pool of 76 GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5		Murine	Lymph Node	
GO Human Adrenal Gland Adult Adrenal Gland GP Human Ovary PA-1 Teratocarcinoma GQ Human Pineal Gland N/A GR Human Pancreas Adult HPC-3 Ductal AdenoCA GS Human Retina 16-75yrs., pool of 76 GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5		Human	Uterus	
GP Human Ovary PA-1 Teratocarcinoma GQ Human Pineal Gland N/A GR Human Pancreas Adult HPC-3 Ductal AdenoCA GS Human Retina 16-75yrs., pool of 76 GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5			Blood	<u> -</u>
GQ Human Pineal Gland N/A GR Human Pancreas Adult HPC-3 Ductal AdenoCA GS Human Retina 16-75yrs., pool of 76 GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5	GO	Human	Adrenal Gland	Adult Adrenal Gland
GR Human Pancreas Adult HPC-3 Ductal AdenoCA GS Human Retina 16-75yrs., pool of 76 GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5	GP	Human	Ovary	PA-1 Teratocarcinoma
GS Human Retina 16-75yrs., pool of 76 GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5	_	Human	Pineal Gland	
GT Human Brain N/A GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5	GR	Human	Pancreas	
GU Human Fetal Kidney2 Fetal Kidney GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5	GS	Human	Retina	16-75yrs., pool of 76
GV Rat Retina Newborn Retina GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61yrs., pool of 11 GZ Human Brain 19-23wks., M/F pool of 5	GT	Human	Brain	N/A
GW Chicken Limb Bud Fetal St.26 Limb Bud GX Human Brain N/A GY Human Testes 10-61 yrs., pool of 11 GZ Human Brain 19-23 wks., M/F pool of 5	GU	Human	Fetal Kidney2	Fetal Kidney
GX Human Brain N/A GY Human Testes 10-61 yrs., pool of 11 GZ Human Brain 19-23 wks., M/F pool of 5	GV	Rat	Retina	Newborn Retina
GY Human Testes 10-61 yrs., pool of 11 GZ Human Brain 19-23 wks., M/F pool of 5	GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GZ Human Brain 19-23wks., M/F pool of 5	GX	Human	Brain	N/A
GZ Human Brain 19-23wks., M/F pool of 5	GY	Human	Testes	10-61 yrs., pool of 11
	GZ	Human	Brain	
	Н	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC ·	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61 yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
			Fetal Kidney
HG	Human	Fetal Kidney2	•
HH	Human	Brain	N/A
HI	Human	Testes	10-61 yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
НО	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61 yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID		Muscle	N/A
	Human		
IE T	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61yrs., pool of 11
IH	Human	Muscle	N/A
П	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
			• • • • • • • • • • • • • • • • • • •
IP IO	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
rt	Human	Brain Thalamu	Adult Brain Thalamus

### SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth
  McCoy, John
  LaVallie, Edward
  Racie, Lisa
  Merberg, David
  Treacy, Maurice
  Spaulding, Vikki
- Agostino, Michael
  (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1519
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: Massachusetts
  - (E) COUNTRY: U.S.A
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy Disk
  - (B) COMPUTER: IBM PC Compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Brown, Scott A.
  - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 498-8224
  - (B) TELEFAX: (617) 876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 400 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAGATGTTG	AGGTGGCTGC	TGACCTTGGG	TCTCATCTCC	TTGATTTTCT	TTATCTTCTT	60
CATTGCCGTC	CTCTCTAGGC	TGTCTTTGGC	GAGGAGGCC	CCTGCGGAAT	CGTGGTCTAT	120
ATCCCCGATA	CATATTCTGC	CTCACTGGTC	TACCTTGTTC	TCCTGCACCC	TGGTTGTCAG	180
CACCCTCCAT	CACTTCTCC	TOCACAGGAG	CCTTCCAATA	CTCTCCTCCA	CCCCCATAGG	240

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GTCTCCGCAT GTAGTAAGGT GGGAACCTTC GCCTGCGGTA GGGCCGGCGT TGTTGGGCCT GGCCTTCGGG AGCACTCTCC GATCCCTCGT TCTTTTCCCC ACTCTCACTA TTCTGGTAAT TTTGCTGGTA ATTGCGTGGA GGAGAACAGG TAGACTCGAG	300 360 400
(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 165 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
GAATTAGTTG CCAGCACTTT AAAAATTGGT ATAGTTCACA TAAATATTCT GAATTCAGGC TTTTGGAAAA GTTGTGGACC CAAGAATACT AGGCCCGCAT TTTCTTACGT CAACATTCTT TCCAGGATGA TGAATGGACT GTTCTCTTTG GCCCCCTATC TCGAG	60 120 165
(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 299 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
GAATTCTAGA CCTTCCTCTC CTACTCCCTT CCTTAGGCTC CTGAACTCGT TTGCTCCTAA ATCTTGTTAA TTCTTTTTCT CTGGATTTTG GTTTCTTTTG GCTTTCCCCT TTCTCTGTCT CCAACACTCT TTCCCCATGT CTTTCTGGCT GTCTCTATGT TCCTCTTCTC TTATCCTCAA CTTTCTGCC ATTCGGCCT CCTCCCCACC TCCCACGCCC CAGCCCCTCC CTCCTTGGTC TCCTTTTCGA TATGCCAAAC CAATTTTGGG TCGAGTGCAT TCCCTCGAG	60 120 180 240 299
(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 241 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
GCGATTGAAT TCTAGACCTG CCTGGATTGC CTTCTGTTGT GGTAGACAAA TCACCATTAA ATGACTAAGT TTCACTGTTT TATGTGTTAAA TGATCCTTAA TAACAAAAAG TTTTAAAGTC TTAATTTCGT AAGATTATGT AAAGGTTAAG AAAGAAATTT TAAGTGAAAA TGATAAAACC AAGCAAATGT TTATTAGTTC AATTGTTTTT CTTTTTATCT TGCAGCAACG CACATCTCGA G	120 180
(2) INFORMATION FOR SEQ ID NO:5:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

T AGGAAATGAC	TTTATTGTGG	TTGAATTAGT	TAAAGGGTAC	60
T GGGAAATGGT	GCTAACCTCA	TCAAAGGAAG	CTCAAATAAA	120
G GCACAACGTG	ATGATATCAA	GGGACACCAG	CAACCTCCAC	180
A AATCACAACG	CAAATCACCG	CCGGAGCCAG	GAACTTAGAC	240
T AGGAGGAGTA	GCTAAAGAAA	CATACAAATC	CTTACCAAAA	300
G CTTTCAAGGC	TGCCTGGCAT	CAGTTGATTT	AAATGGACGG	360
				368
	TT GGGAAATGGT TG GCACAACGTG AA AATCACAACG AT AGGAGGAGTA	TT GGGAAATGGT GCTAACCTCA TG GCACAACGTG ATGATATCAA AA AATCACAACG CAAATCACCG AT AGGAGGAGTA GCTAAAGAAA	TT GGGAAATGGT GCTAACCTCA TCAAAGGAAG TG GCACAACGTG ATGATATCAA GGGACACCAG AA AATCACAACG CAAATCACCG CCGGAGCCAG AT AGGAGGAGTA GCTAAAGAAA CATACAAATC	T AGGAAATGAC TTTATTGTGG TTGAATTAGT TAAAGGGTAC TT GGGAAATGGT GCTAACCTCA TCAAAGGAAG CTCAAATAAA TG GCACAACGTG ATGATATCACA GGGACACCAG CAACCTCCAC AA AATCACAACG CAAATCACCG CCGGAGCCAG GAACTTAGAC AT AGGAGGAGTA GCTAAAAGAAA CATACAAATC CTTACCAAAA GG CTTTCAAGGC TGCCTGGCAT CAGTTGATTT AAATGGACGG

- (2) INFORMATION FOR SEQ ID NO:6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 430 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGGCC	TTCATGGCCT	ATTAAAATTA	AAAATGCTAA	GGATCTGGCC	CCACAGGCCC	60
CAAAGCTTTC	ACAGAGCTCC	TCTTAGACAT	GAAGATGCCC	ATTGGCCTCC	TAGGTCCCAG	120
GAGGTGTGGG	CAGGACTGCC	CTTCCTCCGT	TCTCATTGCG	GGGCTCCTGA	AGGGGGTATC	180
TGAAAGTATG	TAAATCTGAT	GGGAGGTCTG	ATCCTCCTTT	TGCTAGCCCC	TGAACTCTGT	240
GGTGGAGTCT	GGCTGATGGC	CAGGGCCATG	TCCTAGAGGG	GACTCCCCTG	CAGGAGGCGG	300
GCTCTAAAGG	GAGTGGTGTC	CCTTTAGGCC	AGGGTTCACA	GTCGGGGTGG	TCTGGAGACT	360
GCAGGACTCA	GGGCCTGGGG	GTGGCATCAG	TCTGGCCAGG	CCCTGCGTCA	CTTGCACCCA	420
CTGTCTCGAG						430

- (2) INFORMATION FOR SEQ ID NO:7:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 391 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGTGGCTCA TGCCTGT	AAT CCCGGCACTT	GGGTAGGCCA	GGGCAGCAGG	ATCGCTTGAG	60
CCCGGGAGTT CGAGACA					120
AAAAATTGCC AGGTGTG	GTC GTGTGTGCCT	GTGAGGCTGA	GGTGGGAGGC	TCGCTTGAGC	180
CCAGGGGTCA AGGCTGC	AGT GAGCCATGAC	TGCACGCCAC	TGCACTCCAG	CGTGGGTGAC	240
AGAGTGAGAT ACTGTAT					300
ATGTTATTTA GAAATAT	GGA GATAAATAAA	AATAACTGAA	AGTAGGTCGT	TGCTTCTGAG	360
GAGAGAAATT GGGAGTT	GGC AAGGTCTCGA	G			391

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:

  (A) LENGTH: 351 base pairs

  (B) TYPE: nucleic acid

  (C) STRANDEDNESS: double

  (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTTTTGGAG	CTGCTAAAAT	GCCGGATTAC	CTCGGTGCCG	ATCAGCGGAA	GACCAAAGAG	60
GATGAGAAGG	ACGACAAGCC	CATCCGAGCT	CTGGATGAGG	GGGATATTGC	CTTGTTGAAA	120
ACTTATGGTC	AGAGCACTTA	CTCTAGGCAG	ATCAAGCAAG	TTGAAGATGA	CATTCAGCAA	180
CTTCTCAAGA	AAATTAATGA	GCTCACTGGT	ATTAAAGAAT	CTGACACTGG	CCTGGCCCCA	240
CCAGCACTCT	GGGATTTGGC	TGCAGATAAG	CAGACACTCC	AGAGTGAACA	GCCTTTACAG	300
GTTGCCAGGT	GTACAAAGAT	AATCAATGCT	GATTCGGAGG	ACCCACTCGA	G	351

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 354 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTGATGTGTC	ACCCCAAGTG	CTCCACGTGC	TTGCCAGCCA	CCTGCGGCTT	GCCTGCTGAA	60
TATGCCACAC	ACTTCACCGA	GGCCTTCTGC	CGTGACAAAA	TGAACTCCCC	AGGTCTCCAG	120
ACCAAGGAGC	CCAGCAGCAG	CTTGCACCTG	GAAGGGTGGA	TGAAGGTGCC	CAGGAATAAC	. 180
AAACGAGGAC	AGCAAGGCTG	GGACAGGAAG	TACATTGTCC	TGGAGGGATC	AAAAGTCCTC	240
ATTTATGACA	ATGAAGCCAG	AGAAGCTGGA	CAGAGGCCGG	TGGAAGAATT	TGAGCTGTGC	300
CTTCCCGACG	GGGATGTATC	TATTCATGGT	GCCGTTGGTG	CTTCCAAACT	CGAG	354

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 432 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCC	TTCATGGNCT	AGGAGGAGGA	AGAGGAGTAC	GAGGATGACG	AGGGAGGAGG	60
GGGAAGACGA	GGAGGAGGAG	GAGGCTGCGG	CAGAGGCTGC	CGCGGGGGCC	AAACATGACG	120
ATGCCCACGC	CGAGATGCCT	GATGACGCCA	AGAAGTAAGG	GGGGCAGAGA	TGGATGAAGA	180
GAAAGCCCAC	GAAGAAAAA	GCCTGGTTTT	GTTTTTCCCA	GAATATCGAT	GGACTTAAAA	240
AGGCTCAGGT	TTTTGACCAA	AATACAATGT	GAATTTATTC	TGACATTCCT	AAAATAGATT	300
AAATTAAAGC	AATTAGATCC	TGGCCAGCTC	GATTCAAATT	TGACTTTCAT	TTTGAACATA	360
TATATATATA	CAAAAGGTGT	TAAAGAAAAC	TGAATTAAAC	CCAAAATTAT	GTTTTCATGG	420
TCTCTCCTCG	AG					432

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 687 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTATTTTACA	TGCCCACCAG	CATTGTATGG	GGCTTCTCAC	TTGTCCACAT	GCTTGCCTGT	60
GTCATATTTG	ACTTAAAGCT	TATTTTGACG	GGAAACCAAT	TTGTCCTTTT	TTTGGAAAGG	120
GATGGCACCA	CAGATGTGAC	GCGGACAATG	CATTTTGGGA	CCCCTACAGC	CTACGAGAAG	180
GAATGCTTCA	CATATGTCCT	CAAGGGCCAC	ATAGCTGTGA	GTGCAGCCGT	TTTCCCGACT	240
GGAACCAAAG	GTCACCTTCT	TGACTCCTTT	GCCCGTTCAG	CTTTATGGGA	TTCAGGCCTA	300
GATTACTTGC	ACGGGACTGG	ACATGGTGTT	GGGTCTTTTT	TGAATGTCCA	TGAAGGTCCT	360
TGCGGCATCA	GTTACAAAC	ATTCTCTGAT	GAGCCCTTGG	AGGCAGGCAT	GATTGTCACT	420
GATGAGCCCG	GGTACTATGA	AGATGGGGCT	TTTGGAATTC	GCATTGAGAA	TGTTGTCCTT	480
GTGGTTCCTG	TGAAGACCAA	GTATAATTTT	AATAACCGGG	GAAGCCTGAC	CTTTGAACCT	540
CTAACATTGG	TTCCAATTCA	GACCAAAATG	ATAGATGTGG	ATTCTCTTAC	AGACAAAGAG	600
TGCGACTGGC	TCAACAATTA	CCACCTGACC	TGCAGGGATG	TGATTGGGAA	GGAATTGCAG	660
AAACAGGGCC	GCCAGGAAGC	TCTCGAG				687

- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 420 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTCGGCC	TTCATGGCCT	AGTCGGTGGG	TGCCTGTAGT	CCCAGCTACT	TGGGAGGCTG	60
AGGGAGGAGA	ACTGCTTGAA	CCCGGGAGGC	AGAGGTTGCA	GTGAGCCGAG	ATTGTGCCAC	120
TGTACTCCAG	CCTGGGCCAC	AAAGCAAGAA	TCTGTCTCAA	ааааааааа	AAGAAAAGAA	180
AAGAATAAAT	TTCTTTTCCC	CTTGAAGAAG	TTGATTTAGG	CACAGACTCT	GGACTCTGGA	240
TTTCCCACAA	TGTCTTATCT	AGTCAACTCA	AGTATCTGGA	CTACAATTTT	CTTGAAAGCA	300
AAGCCCATAT	ATTAATAATC	TTTACTTGTA	TATAAATATT	CAATAAATCA	TTAAGTAAAT	360
GTGTAGAAGA	ATTTTATGCT	CAATAAGATC	CACCCGATCA	TGCATTTGAA	AATTCTCGAG	420

- (2) INFORMATION FOR SEQ ID NO:13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 379 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

60	CATTTTGGGG	GTCAACATCC	CTGCTTTTCT	AGCACATACT	TTCATGGCCT	GAATTCGGCC
120	CCAGTTGTCC					
180		TTATATATAT				
240		ACCCTAACTT				

•	
ACATACCACA GGTTCTGGAA TTCTCATCTT CGAACCTAGA GAAATAGGTG CTATAAACAG	300
GGAATTAAGC AAAATGCTGG ATGCTATAGA TCTTTTAATT GTCTTAATTT TTTTTCTATT	360
ATTAAACAAC AGGCTCGAG	379
1	
(2) INFORMATION FOR SEQ ID NO:14:	
(i) SEQUENCE CHARACTERISTICS:	

- - (A) LENGTH: 528 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTCATGGCC	TACGGAAAGT	CAGCATGGAT	AACAGACTGA	TGGAACTCTT	TCCTGCCAAT	60
AAGCAAAGTG	TTGAACACTT	CACAAAATAT	TTTACTGAGG	CAGGCTTGAA	AGAGCTTTCA	120
GAATATGTTC	GGAATCAGCA	AACCATCGGA	GCTCGTAAGG	AGCTCCAGAA	AGAACTTCAA	180
GAACAGATGT	CCCGTGGTGA	TCCATTTAAG	GATATAATTT	TATATGTCTA	GGAGGAGATG	240
AAAAAAAACA	ACATCCCAGA	GCCAGTTGTC	ATCGGAATAG	TCTGGTCAAG	TGTAATGAGC	300
ACTGTGGAAT	GGAACAAAAA	AGAGGAGCTT	GTAGCAGAGC	AAGCCATCAA	GCACTTGAAG	360
CAATACAGCC	CTCTACTTGC	TGCCTTTACT	ACTCAAGGTC	AGTCTGAGCT	GACTCTGTTA	420
CTGAAGATTC	AGGAGTATTG	CTATGACAAC	ATTCATTTCA	TGAAAGCCTT	CCAGAAAATA	480
GTGGTGCTTT	TTTATAAAGC	TGAAGTCCTG	AGCGAGGATG	CCCTCGAG		528

- (2) INFORMATION FOR SEQ ID NO:15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 466 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCC	TTCATGGCCT	AGCCCAGGCC	ACGCTACACT	CTGCCCACAC	TGGTGAGCAG	60
GAGGTCTTCC	CACGCCCTGT	CATTAGGCTG	CATTTACTCT	TGCTAAATAA	AAGTGGGAGT	120
GGGGCGTGCG	CGTTATCCAT	GTATTGCCTT	TCAGCTCTAG	ATCCCCCTCC	CCTGCCTGCT	180
CTGCAGTCGT	GGGTGGGGCC	CGTGCGCCGT	TTCTCCTTGG	TAGCGTGCAC	GGTGTTGAAC	240
TGGGACACTG	GGGAGAAAGG	GGCTTTCATG	TCGTTTCCTT	CCTGCTCCTG	CTGCACAGCT	300
GCCAGGAGTG	CTCTGCCTGG	AGTCTGCAGA	CCTCAGAGAG	GTCCCAGCAC	TGGCTGTGGC	360
CTTTCAGGTG	TAGGCAGGTG	GGCTCTGCTT	CCCGATTCCC	TGTGAGCGCC	CACCCTCTCG	420
AAAGAATTTT	CTGCTTGCCC	TGTGACTGTG	CAGACTCTGG	CTCGAG		466

- (2) INFORMATION FOR SEQ ID NO:16:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 288 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCC	TTCATGGCCT	AGCGTGATCC	TGGAACGTGC	TCTAGTTCGA	GAGAGTGAGG	60
GCTTTGAGGA	GCATGTACCA	TCTGATAACT	CTTGAAGATA	CAGAGAGAAA	TCCATCTTTT	120
CCCAGGTCTC	CTTCACTGAA	AACAAAAATC	TACTTACATA	CACTGTCACC	TTAGCATCAG	180
AGTCGGATTA	ATGAACTGCG	GAACAAGAGG	TTGTGAGAAT	CTAAGATGGA	ACCTTTCTTT	240
CTTTCTTTCT	TTTTTTTTAA	ATTTTGTATT	TTCCATCCAA	CACTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:17:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCC	TTCATGGCCT	AGGGCTCTGC	TTATAAACTT	CAAAGTTACA	CTGAAGGATA	60
CGGTAAAAAC	ACCAGTTTAG	TAACCATTTT	TATGATTTGG	AATACCATGA	TGGGAACATC	120
TATACTAAGC	ATTCCTTGGG	GCATAAAACA	GGCTGGATTT	ACTACTGGAA	TGTGTGTCAT	180
CATACTGATG	GGCCTTTTAA	CACTTTATTG	CTGCTACAGA	GTAGTGAAAT	CACGGACTAT	240
GATGTTTTCA	TTGGATACCA	CTACCTGGGA	ATATCCAGAT	GTCTGCAGAC	ATTATTTCGG	300
CTCCTTTGGG	CAGTGGTCGA	GTCTCCTCTT	CTCCTTGGTG	TCTCTCATTG	GAGCAATGAT	360
AGTTTATTGG	GTGCTTATGT	CAAATTTTCT	TTTTAATACT	GGAAAGTTTA	TTTTTAATTT	420
TATTCATCAC	ATTAATGACA	CAGACACTAT	ACTGAGTACC	AATAATAGCA	ACCCTGGTCT	480
CGAG						484

- (2) INFORMATION FOR SEQ ID NO:18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTGGCCT TCATGGCCTA GGA	GATATAC CTAATGCTAG	ATGATGAGTT	AGTGGGTGCA	60
GCGCACCAGC GTGGCACATG TAT	ACATATG TAACTAACCT	GCACAATGTG	CACATGTACC	120
CTAAAACTTA AAGTATATAT AAA	AAAAAAA GACNTCGCTA	GTGAGCACGC	TGTATACGAC	180
ATCGCTAATG AGGACACCAT ACA	AGGCATC GCTAACGATG	ACGCTGTACA	CAACATCACT	240
AATGATGACA CCGTATAAGA CAT	CGCTAAT TATGACGCTG	TATACGACAT	CGCTAATGAC	300
ACCGTACGAG GCACGCTAAC AAG	GATGCTG TACACAACAT	CGCTAATGAG	GACAGTGTAC	360
AAGCCATCGC TAATGAGGAC ACT	GTATATG ACATTGCTAA	CGAGGACACT	GTACAAGGCA	420
TTGCTAACGA GGACGCTGTA CAC	AACATCG CTAATGACAC	CATATAAGAC	ATCACCAATG	480
AGGATGCTGT ATATGACATC GCT	TAATAACA CCGCTCGAG			519

- (2) INFORMATION FOR SEQ ID NO:19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 342 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCAGCTCTCA	TCCTCGTCTC	CCCAACACCA	TAACGTCCTC	ATCCCGCCTC	CAACCCACAC	60
CAGGCCGAAG	CCCTCAGAGA	GTGTTTTCAT	CAGGAACCAC	TCTCGAACCT	GAAGGTTGAC	120
TTTAGCGTTT	AGCAACCCAG	GGCGGTGTGT	GTGTTTCCCG	TTTTGTTTTC	TGAGTGGTAG	180
CAGTGATCAC	CGTAATTCCA	TGTAGCCATG	TGCTAGCAGA	ACCCCTGTGT	CCTCACCGTG	240
GCCCGTGTGA	CCCCAGCCGA	CGAGTGCCCG	GCGGAGTCCC	CGCTGCCTTC	CCATGGTCCA	300
GTGAGCTGCC	AGGGCATCAC	ATGACTCTCA	GCTGGGCTCG	AG		342

- (2) INFORMATION FOR SEQ ID NO:20:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 580 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCGGCC	TTCATGGCCT	AGAGCAGCTC	TGAGGTAGAA	ATTACAACGA	TGAAAAGAGC	60
ACAACGTACA	AAACCAAGAA	AGAGTCTGTT	GTGTGAAGGG	TCATTCGATG	AAGAAGCTTC	120
TGCACAGTCC	TTTCAGGAAG	TGTTAAGTCA	ATGGAGAACC	${\tt GGAAATCATG}$	ATGACAACAA	180
GAAACAGAAT	TTACATGCAG	CAGTAAAAGA	CTCATTGGAA	GAATGCGAAG	TACAGACTAA	240
TCTGAAAATT	TGGAGAGAAC	CACTTAATAT	TGAACTTAAA	GAAGACATTC	TATCCTATAT	300
GGAAAAATTA	TGGCTTAAAA	AACACAGGAG	AACTCCACAA	GAGCAACTTT	TTAAAATGCT	360
ACCAGATACG	TTCCCACATC	CACATGAAAC	CACTGGTGAT	GCACAGTGTT	CTCAAAATGA	420
AAACGATGAA	GATAGTGATG	GTGAGGAGAC	CAAAGTACAA	CACACAGCTC	TTTTATTGCC	480
AGTAGAAACA	TTAAACATAG	AGAGACCTGA	ACCATCTCTA	AAGATAGTCG	AACTGGATGA	540
TACTTATGAA	GAGGAATTTG	AAGAAGCAGA	ACATCTCGAG			580

- (2) INFORMATION FOR SEQ ID NO:21:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 301 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAATTCGGCC	TTCATGGCCT	AGAAAGATCT	AATTATCATG	GACCTGCGAC	AGTTTCTTAT	60
GTGCCTGTCC	CTGTGCACAG	CCTTTGCCTT	GAGCAAACCC	ACAGAAAAGA	AGGACCGTGT	120
ACATCATGAG	CCTCAGCTCA	GTGACAAGGT	TCACAATGAT	GCTCAGAGTT	TTGATTATGA	180
CCATGATGCC	TTCTTGGGTG	CTGAAGAAGC	AAAGACCTTT	GATCAGTTGA	CACCAGAAGA	240
GAGCAAGGAA	AGGTTTGGAA	AGATTGTAAG	TAAAATAGAT	GGCGACAAGG	ATCGGCTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:22:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 332 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAATTCGGCC TTCATGGCCT	AAAAAAAGGA	TGGTGTGTTG	AGACCAGAAG	CAGCAGCAGT	60
CCTCGACATC AACTACAACT	TTCCTTCGCA	CAGTGCATAC	CCTCTGATAT	ACTGAACCCA	120
ACGCCTATCC TCCAGCCCCC	TAAGAACTAG	AGAGGGAGCC	TCACAACATT	CCAATTTAAT	180
CCTTCAGAAA ATTCATTACT	CTTCAAAGTT	GTCTGTGGTT	TTGTGACAAC	GATATGACTA	240
GGTGCAAAAT GGCTTGCAAC	TAATTAACAA	ACATAGAAGC	ATCCAACAAA	CATATACGTG	300
CACAATCTGA GGATTTAGGG	ATGAAGCTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:23:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 239 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

1	GAATTCGGCC	TTCATGGCCT	ACCAGCCTGG	GCGACAGAGC	AAGACTCAGT	CTCAAAACAA	60
	AACAAAACAA	AACAAAAAGA	GAAGGCTATT	ATTAACATTC	GAGATAATGT	GCCAGACTGC	120
	TTCCATGTAT	TTTCATTATT	CTGTCCCAAA	TCTGGTGAAG	TGGGTATCTG	CACAGCTTTC	180
	TCTAGATTGA	ACAACTAGTA	AGGGGGCTGG	CCCTGGAGAA	AGTTACCTCC	TGCCTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:24:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 238 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATTCGGCC	TTCATGGCCT	ACTTTTATAT	TGTTATTTTT	GTAAAGCATC	TTTTCTTCAA	60
TTCTTGTTGG	CATTCTGGGC	CAAAATATTT	CAGGTTGGTT	CGGTGTGGAG	TTAAGAAAAG	120
CAGGCGTTTT	AGTGGAGAAA	TGGGGAACAG	CATCAAGAAA	GGCTTTTTTC	CTTTTTTCTT	180
TTTTTTTTGG	AGACAGAGTC	TTGCCCTGTC	ACCCAGGCTG	GAGTGCAATG	GTCTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:25:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 231 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACTGAACAAA ATATTTTCAA AGACATTTGT CATTCCTTAA AGCCAAGATT TTAAAGACTA ATGTCCTTCC TGAGGGTTAC TTTACTATAC TGTGTATGGT GTATAGCCAC AGAAAGTCAG TCTGATAAAT TTTCAATGTG TAAGTGTGAT GCATTCAACC CAGATCTCGA G	120 180 231
(2) INFORMATION FOR SEQ ID NO:26:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 307 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
GAATTCGGCC TTCATGGCCT ACACAGAGTA TATTTATAGC TATCTCAGGG TCCTTGTCCA ATTGTCTGTG TCATTCTTC ATCTGCTTCT TCTGCTTCTG TTTACTCTTC ATTTTGGACC TATTTCCCT TATTTGGTGC TTTGCATACA ATTTGTTGGG ACTGGATCTT TGCTAGTCCT TTAAATGTTT TTAAGCTTTG TTTTGGGATG CAGTTAGGTG ACTCAGAAAC AATCAGAAAC AATTTGATCC TTTTATGTCT CTTAAGCTTT GTTATAGGCA GGACCAGAGC TCTCGAG	60 120 180 240 300 307
(2) INFORMATION FOR SEQ ID NO:27:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 253 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
GAATTCGGCC TTCATGGCCT ACAATAATAG CCTCCCACCT GGTCTTCCTT CTTCAGTCTC TTCAGTCTTT CCCCAAAGCTC TTGAATCCTA CATGAACCCA TGCCTCGGTC AAAATATTAC AGGCTGCAGC CAATCTTCAA GTGGCATACA GGCCAAACAT CCATTTATAA TATGGTTGGA ATTCCTAACA CATTTATCA TAGATCTAAT GCCATACAAT AGGTGGAGGT TAGATCCTCA CGCAACTCTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:28:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 254 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
GAATTCGGCC TTCATGGCCT ACAGAGAACT TGTGTTCCGG TTTATTGAAG TTCAGACACT TCTCCTCGCT CCATTCTGTC CACATTTGTG TGAGCACATC TGGACACTCC TGGGAAAGCC TGACTCAATT ATGAATGCTT CATGGCCTGT GGCAGGTCCT GTTAATGAAG TTTTAATACA CTCCTCACAG TATCTTATGG AAGTAACACA TGACCTTAGA CTACGACTCA AGAACTATAT GATGCCAGCT CGAG	60 120 180 240 254

- (2) INFORMATION FOR SEQ ID NO:29:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 211 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCGGCC	TTCATGGCCT	ACGAGAAGGA	GTGGAAGAGT	AAGCAGACTA	GGAAAATACA	60
GTACAACCAT	CAGGCAGCAT	TACAGACCCA	CTTAAGGTTT	GTGGCCATGT	GTGGTTGTGT	120
GGTTTTTTTT	CTGGCCATGC	TCAGTTACAT	AGGGGCAAGT	GCAAAAAAA	CCCCAGAGTT	180
TGTTTTAACT	AGAGCTCTGG	TTTTGCCAAA	С			211

- (2) INFORMATION FOR SEQ ID NO:30:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 521 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATTCGGCC	TTCATGGCCT	AGGATCAGGT	TCGTCCTTTA	GTGTTGTGTA	TGGTTATCAT	60
TTGTTTTGAG	GTTAGTTTGA	TTAGTCATTG	TTGGGTGGTG	ATTAGTCGGT	TGTTGATGAG	120
ATATTTGGAG	GTGGGGATCA	ATATAGGGGG	AAATAGAATG	ATCAGTACTG	CGGCGGGTAG	180
GCCTAGGATT	GTGGGGGCAA	TGAATGAAGC	GAACAGATTT	TCGTTCATTT	TGGTTCTCAG	240
GGTTTGTTAT	AATTTTTTAT	TTTTATGGGC	TTTGGTGAGG	GAAGTAGGTG	GTGGAGCACA	300
GGCACTGCAG	GTCAATGGAG	GTGGAGTACA	GGGACTACAG	GTCAATGGAG	GTGGAGCACA	360
GGGACTAAAG	GTCAATGGAG	GTGGGGCACA	GGGACTACAC	GTCAGTGGAG	GTGGAGTCAC	420
AGGGACTACA	GGTCACTGGA	GGTGGAGCAC	AGAGACTACA	GGTCAGTGGA	GGTGGGGCAC	480
AGAGACTACA	GGTCAGTGGA	GGTGGAGCAC	AGAGACCACA	G		521

- (2) INFORMATION FOR SEQ ID NO:31:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 238 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAATTCGGCC	TTCATGGCCT	AAAATTTCCT	CTAAGTACTG	ATTTAGCTGC	ATTGTATAAG	60
TATATGCTTC	CATTTTCATT	CATTTCCAAA	TATTTTCTAA	TTTCCTTTGC	TTTTTTTAA	120
TCAGGAATTC	GGGCCTTGCT	GTGTTGCCCA	GGCTGGAGAG	CAGTGCCACT	ATCACAGCTC	180
астатаааст	CAAACTCCTG	GGCTCAAGCA	ACCCTCCCAC	CTCCCAACTC	CCCTCGAC	238

- (2) INFORMATION FOR SEQ ID NO:32:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
GGTTTCTTAA AAAAAAAAA AAAAGGAATT TGATCCAGAG CAATTTTCT CAATTAAAAT TTGTGATTAC ATTCTGAGT TTCCATGGCA GAGTTGTGAG TGGGGCTGTG ATATAATTTA ACTTCTCCTA AATTGCTGAC ACCGATAACC CTATAAATTA ACAGATGGCG GAGGGAAATC TCCTGGCTTC TTCCTGGCTA GTTTTTTTA ATGGTCTGAT TTTTGTAATA GGGGTTTTGA GTCCCAGCCG ACTCGAG	60 120 180 240 257
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 251 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
GAATTCGGCC TTCATGGCCT AAAGACTTAC GTTATATTTT CATATACTCC TTCCCACTCT TAGTGTGTTG TCAATATACA TTTTGTTTTA CATGTAAAAA CACCACAGTA TATTGTTCTT AATTTTGCTT TTAATAGTAA ACTGTCTTAT AACAAATTAT GAAAATGGAA AAAAACATGT CTTTCTTATT TGCCCTCATA TTTATCCATT TAGGCACTCT TCCTTTTTCC CTTTCATTCC AGGTTCTCGA G  (2) INFORMATION FOR SEQ ID NO:34:	60 120 180 240 251
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 245 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
GAATTCGGCC TTCATGGCCT ACTAACATT ATGAAAATTA TTTGTAAATA AAATAAGAGG CATTGAGATT AAAATTGGAG ATAAAGTTGC TGATGTGTTG TTTTCCTGAA GTATTTTTTTTCTTAATTCT GATCTTTGTT TCCCAATACA ATCACACTCA CACCCTTGCA GTTCAGTTTC CTGACGACTC TCTAGTGTGC CAGATCTGTG TTTCTATGTC AGTGATCTGT TCCCCATCTC TCGAG	60 120 180 240 245
(2) INFORMATION FOR SEQ ID NO:35:	
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 383 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAATTCGCTT	CATGGCCTAC	CGAGAAATGG	GTGTGATTGC	TGCCATGAGA	GATGGTTTTG	60
GTTTCATCAA	GTGTGTGGAT	CGTGATGTTC	GTATGTTCTT	CCACTTCAGT	GAAATTCTGG	120
ATGGGAACCA	GCTCCATATT	GCAGATGAAG	TAGAGTTTAC	TGTGGTTCCT	GATATGCTCT	180
CTGCTCAAAG	AAATCATGCT	ATTAGGATTA	AAAAACTTCC	CAAGGGCACG	GTTTCATTTC	240
ATTCCCATTC	AGATCACCGT	TTTCTGGGCA	CGGTAGAAAA	AGAAGCCACT	TTTTCCAATC	300
CTAAAACCAC	TAGCCCAAAT	AAAGGCAAAG	AGAAGGAGGC	TGAGGATGGC	ATTATTGCTT	360
ATGATGACTG	TGGGGGTCTC	GAG				383

- (2) INFORMATION FOR SEQ ID NO:36:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 133 base pairs
    - (B) T"PE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCC	TTCATGGCCT	ACTGCCGCTC	CTGGTGCTGC	TTGTGTGCTC	GTTTGGTGCG	60
GACCTGGTAC	CTCTTTTGTG	AAGCGGCAGC	TGAGGAGACT	CCGGCGCTCG	CCATGGCCGA	120
CGAAAAGCTC	GAG					133

- (2) INFORMATION FOR SEQ ID NO:37:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 276 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCGGCC	TTCATGGCCT	AAGGTAGTCT	AGGCTCATCT	TCATGAGGGA	ACTGAGGTCT	60
TGGGGGGTGG	GGGTTACCCA	AATAGGTTCA	CAGAAGAACC	AGAAATAAAA	CCTGCCTTTC	120
TAGACTGTAA	GTCTTGTGAT	TGTCATCTAA	ATGGTTGTCT	CTATACAGCA	ACTCATCTCT	180
AGAACTGAAA	ATAAGTTTAA	ATCCCTCCTC	CATCCCCAAT	AATTCAAGCT	GCATTTCAGA	240
GAAAACCAGG	ACTTTGGAAT	CAGACAGCAA	CTCGAG	•		276

- (2) INFORMATION FOR SEQ ID NO:38:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 336 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTATCAAGGA CACATCATGA CCTGAAAACG CCCCTGCCAC GAGGAAAGAA	ICTTAGAGTA GGAGTTGGAA C ICTACTCACT CAGTTTCCCT A CAGATGTTCC GGCTACATTT A GTCAACAAAC AATCACTAAA A ACTACAGGGT AGAACCCAGT C GAAAATTACA AGGGAACAGA C IION FOR SEQ ID NO:39:	AAGCTCTCT ACCCAGGCTG ATCAGTGAGG ATGGAAGGTG	CTCCAGATCG AGTGTAATGG AATTGACTGA	GATTCAACCG GGATAAACCA TGTGGACAGC	60 120 180 240 300 336
	EQUENCE CHARACTERISTIC:  (A) LENGTH: 385 base (B) TYPE: nucleic aci (C) STRANDEDNESS: do. (D) TOPOLOGY: linear	pairs id			
,,	MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION:	SEQ ID NO:3	39:		
GCAGGATGTT TAGGAAGGTC TGAGGGGGTT TGGTGATCTA TGGACGGTGC	TTCATGGCCT AGTCGGAGAA G GATATGGTGT TTGCGTCATT C CTGGGAGAGA AGGGAAAGAA C CGGAAGGTTTG ATGAAATCCT G GGCATTGAGA TTCCTGCAGA G AACCGAGCTG GGAAGCCTGT C CCCCGCCCCCA CTCGA	CATCCGCAAG CATCAAGATT GGAGGCCAGT GAAGGTCTTC	GCATCTGATG ATCAGCAAAA GATGGGATCA CTTGCTCAGA	TCCATGAAGT TCGAGAATCA TGGTGGCTCG AGATGATGAT	60 120 180 240 300 360 385
	TION FOR SEQ ID NO:40:  SEQUENCE CHARACTERISTIC  (A) LENGTH: 245 base (B) TYPE: nucleic ac: (C) STRANDEDNESS: dou (D) TOPOLOGY: linear	pairs id			
, (ii)	MOLECULE TYPE: cDNA	-			
(xi)	SEQUENCE DESCRIPTION:	SEQ ID NO:	40:		
GGTTTTCTTA AAATGAGTGA	TTGCTAAAAA AAAAAAAAAA C TCTATAAAATA CTGATTAAAA A ATACAGGCAA AATGCCTTAC A TATGATGACA ATTATGATGA 1	AAAAAAGTAC ATTTTACTTT	ACTGTCTGCC ACATTTACTA	TTATAAGCTA AGCACCCAGA	60 120 180 240 245
(2) INFORMA	TION FOR SEQ ID NO:41:				
(i)	SEQUENCE CHARACTERISTIC  (A) LENGTH: 247 base  (B) TYPE: nucleic ac  (C) STRANDEDNESS: do  (D) TOPOLOGY: linear	pairs id uble			
(ii)	MOLECULE TYPE: cDNA				
(xi)	SEQUENCE DESCRIPTION:	SEQ ID NO:	41:		

60 120

GAATTCGGCC TTCATGGCCT AAATAAAGAT GATTTTTGTG CTTAGCAGTT TAAGGTATAT GGCTGCATAT GCAAAACTCT TTCCCAATTC AGTCGCTACT TTTACTTCTG CCCTTTCTAT

CCATCGTCTT CATTTTGTGT GTACAGTGCT GTGTGTAAGC TTATCAGTGT GTTTTTTAT

TTGTATCAGT CATGAAAGTC CTGTTAGGTA TCCAGAGTTC TATTTATCTA GCTGTACAGA

180

TCTCGAG	47			
(2) INFORMATION FOR SEQ ID NO:42:				
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 106 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear				
(ii) MOLECULE TYPE: cDNA				
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:				
GOATATOGTA ACTOAGAACC ATTITCHEST TOTAGE STORY	60 .06			
(2) INFORMATION FOR SEQ ID NO:43:				
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 237 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear				
(ii) MOLECULE TYPE: cDNA				
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:				
TTAGATGATA AGCGATTTTT ACCTTTTTT TTTTTTCAAA GCAACTTGAT CCTGTAAGTT TTGGCATCTT AAGTGGAAAT GTTCATGCAG TTTTGCTGGA TCTTCGCTAT GGCAGTAAAA	60 120 180 237			
(2) INFORMATION FOR SEQ ID NO:44:				
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 476 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>				
(ii) MOLECULE TYPE: cDNA				
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:				
AATGGAGGAC ACATATTTGG GGAGTTTTGA GAGGATGTGT ATGTGTGTG	60 120 180 240 300 360 420 476			

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 358 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45: GAATTCGGCC TTCATGGCCT AGGCAAACTC TGCTGGACTT AACTTCATCA ATGTAGTGGG 60 CTCTGTTTGT GGGGCCCAGG CTTTGATGAG TGGTTCAAAC CCCATGCTGG GCTGTAACAC 120 TGGTGCCATA ACTCCTGCAG GAATAAACCT GAGCGGCCTT CTACCCTCAG GAGGTCTGCT 180 ACCAAATGCA CTGCCCAGTG CAATGCAGGC AGCTTCTCAA GCAGGTGTTC CATTTGGTTT 240 AAAAAATACT TCAAGTCTCA GGCCCTTAAA TCTACTCCAG CTTCCAGGTG GTTCACTTAT 300 TTTTAACACT CTGCAGCAGC AGCAACAGCA GCTCTCCCAG TTTACACCAC AACTCGAG 358 (2) INFORMATION FOR SEQ ID NO:46: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 353 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46: GAATTCGGCC TTCATGGCCT AATCATTTTG ACTTTCAGTG CTTTCAATGA CCAGTGGCCT 60 CCAGGGATAA AGCAACTGCT TGGTTTGCAG GGCGTCCTCT GCGCTGCTGA GCCATCAGCC 120 TCCAATACGC CAATGCCCAT AGATGCTAGT TACAGCCCTG CTTCCTCCTA CATAGGGTTC 240 TGTCATCACT GAGTCTCACC ATTTCCCTCT CCCCAGTGTC TTTATTATGT GACACACACA 300 CACGGCACTA TGTTTAAAAA AGCGTGCTCA CTGGCAACCT CTTGGCGTTG TGTGTTCATT 353 CTGTGTTTTG TATTGGTGGT ATCTTGGGGT CGACCGAAAG AGTCAACCTC GAG (2) INFORMATION FOR SEQ ID NO:47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 456 base pairs (B). TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
- GAATTCGGCC TCATGGCCT AGGGAGCTAC CAGATGCTGA AGAAAGGGCC CTGGCAGACT 60
  GGGTTCAAAC TCAGCCATTG TCAGCTTGGT AACCTTGAC AAGTGTCTTC CCCTCTGTGA 120
  GCCTCAGTTT TCTCAATAGT AAGAGGGGAT AACACACTTA CCTCTCATAG CTGTGGACAT 180
  GCAGAGGCTG GGCTGTGTTT AATTGATTCA GGAAATTCAC CTGTAAGAGA AAAATCGGG 240
  CCGTCCATTGG GGCTTGTGTT AATTGATTCA GGAAATTCAC CAGAGGCCCC CTAGATGCAA 300
  CGTCCTTTGG GTGTCTGGCA GTGGGCACAA AGATGACCA AACAGTGCCC CACCCTCACC 360
  CCGTCAACCG TCAGTGCAGC AGTGGGCTGG GTGCTTGCGT CCCACCAGTGA GGAAGGCAGA 420
  AGGGGTCCCT GCCCTCAAAG GAGGACGATA CTCGAG 456
- (2) INFORMATION FOR SEQ ID NO:48:

WO 98/45437 PCT/US98/06956\_

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCGGCC	TTCATGGCCT	AGCTGCCCCG	CAGCACTTAC	CGGAGCGACC	ATGAGGGTGA	60
CGATTTGAAG	CACACACAGG	CTTCCCGCCA	CCTCCTTTAA	ACCGCCGCTG	GCTTGCCAGG	120
GACAGACGGC	GCGGTTGGCT	CCCCAAAATT	CCGACTGATA	CGCGCCTCGG	CGAGCGAAAG	180
CAAACGCGGG	ATACTCTCGC	GTTCCTGATT	GGCTGCAGTT	GGAATTGATC	ACACCTTTTC	240
AGTTGTACTT	CAATCCTGAA	TTAATCTTTA	AACACTTTCA	AATATGGAGA	TTAATCACCA	300
ACTTCTTATT	TTTTGGGCCA	GTTGGATTCA	TTATTTTTA	TAACATGATT	TTTCTATATC	360
GTTACTGTCG	AATGCTAGAA	GAAGGCTCTT	TCCGAGGTCG	GACAGCAGAC	TTTGTATTTA	420
TGTTCCTTTT	TGGTGGATTC	TTAATGACCC	TTTTTGGTCT	GTTTGTGAGC	TTAGTTTTCT	480
TGGGCCAGGC	CTTTACAATA	ATGCTCGAG				509

- (2) INFORMATION FOR SEQ ID NO:49:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 467 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAATTCGGCC T	TCATGGCCT	AAAGCAAGTG	ATTTTCTTTT	TTTTAAAGAC	AGGGTCTCAC	60
TTGGTCACCC A	GGCTGGAGT	ACAGTGACAT	CATCACGGCT	CACTGCAACC	TTCGCCTCTT	120
GGGCTCAAGT G						180
GTGTACCACC A	CGCCTGGCA	GAGACCGGGT	TTTGCCGTTG	CCCAAGCTGA	TCTCGAACTC	240
CTGAGCTCAA G	CGATCTGCC	CGTCTCAGCC	TCCCCTAAGC	AAGCATTTTT	AAGTTTCTAT	300
GCTGTTTAAT T						360
TTATGATATT G						420
CATATCTTTT T						467

- (2) INFORMATION FOR SEQ ID NO:50:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 168 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GAATTCGGCC	TTCATGGCAG	AGTGGAAGGG	GTTGTAAATA	TTAGGAGAGA	GATAATTCTT	60
AGTGCATTTC	TCTGAGGATG	AAGCATGAGA	TGAATCCATG	GCACGAATGG	AACAGCTGGG	120
GAAAGCAGGT	CAGAATGGAT	ATGGATATAA	ATACTGTGAG	TTCTCGAG		168

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
GAAGTAAATT ATTACGATTT CCTTAGGTGG TTAATAAATT ACCATTATTT TCTCTATTTT ACAGATCACG AAATGATAAGG TAACTTACCG AAAGTTACAT TATTTAAGTT AATCAAATGT TTATTGATTG CCAGACTTTT TTCTAGGCTT AAGCAAAATGT TGGAAAATAC TTCTCTGAGC TTCCAAAAAAT GTTATTCTA CTTGTCAGTG CTGCAGGAGT CTCTCGAG	60 120 180 228
(2) INFORMATION FOR SEQ ID NO:52:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 247 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
GCAGAGTCAA TAGATACTTT AAATTGAAGT AAAGAATTAA AAAAGGAAGT GGATAGTTTG GGTATTAGTT TAGCTAGAAA TACAAAAGAAA CTTGACTTCT AGGGCAGTAC AAATTCAAGC CTTCCACAAA CAAACAGTTG AGAGTATGTT TATCTTCTTA AAATGTGTGG GTGCCTTCCC ACCACTTCAC CTGCTCCTCA CTGGTGCTTT GTCCCCTCCC TACTACCATT CCTGTCCCGG TCTCGAG	60 120 180 240 247
(2) INFORMATION FOR SEQ ID NO:53:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 235 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
GGCCAAAACA AAGCTTATAA AGGTTCCTGC TCCCAACGTA ATTACCTCCA ATCGGCATTT AAAGACATCC GCATTGCTTA CAGCACATCC TAGCCTCATG CTTGCCCAAG GATGGACTCG AAATGAACTA TTTCCAGAGC GACTTATTCA GGCATTCTGT GGAGCCTCCG TTGCCCTGTC CATCACCGGA GCTTTTGTAA TTGCAGCTAT GCCCATTGGCC TCCGGCAACC TCGAG	60 120 180 235
(2) INFORMATION FOR SEQ ID NO:54:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 231 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
109	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAATTCGCCT	TCGTGGCCTA	AAAAGAAAAA	ATCTAAGGTA	GATTGTGCCT	TTTGTGCCTT	60
TCCTCTGCTC	AAGACCTTTC	AGTGGCTTCC	CACTTCACTC	AGTAAAAGGC	AAAAAGTCCT	120
TTTAATAACC	TACAAGGCAT	TATGTTACCC	ACATTGTCCC	TGCTCCCCTA	CATTGTACTC	180
				TCACTGGCTG		231

- (2) INFORMATION FOR SEQ ID NO:55:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 330 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GAATTCGGCC	TTCATGGCCT	AGAAATATTT	TCCTACAAGA	GTACTGAATT	TCAGGAAATG	60
GGATAGAGCT	TCTAACCAGT	GTATTCCGTC	AAGTAAGATA	ATAACAGCTG	ACCTGCCAAC	120
AGCATTACAG	GGAGATTCTT	TGCTCAGCTA	ACACATTTCT	GTTTTTCAAA	ATTGATGCTT	180
AATTGTAGCT	GTTATTCTAA	TTTGTGACAT	GGAACTAACT	CATGCTTCAA	TCCTTGATAG	240
AGCAAAACTC						300
CTGCTTTGCC	ACAGAAAATG	GAGACTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:56:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 230 base pairs.
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GAATTCTAGA	CCTGCCTCGA	GATCTGAACT	ATAATCTTTT	CCATTCTATC	TAGCTCCCAT	60
					ACTAGGGTTC	120
					CACGGAACAT	180
				CTCCCTCGAG		230

- (2) INFORMATION FOR SEQ ID NO:57:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 416 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAATTCGGCC	TTCATGGCCT	AAAGGGAAAG	TGGGAATATA	CACAATGCAN	ACACTAGCCA	60
					GCTTCAGAAA	
					CTCTGGAGGG	

GGAAGAGGAT CAACCTTCTC TCATACCGCA CAGCAAGGGA ACCAAAGTAA TATAAATCAC TCTTAAAAAT GTCATGTTAC TTTAAGAATA AGCCATACTG CTGGCACCTA GAATATTTTT GTGGGTCCCC ATCTCTGGCT TTTCTTGTTC AAATGGCCCC CAGGCTAAGA GGCAGCTGCT CACATCCCTG CAACAAACAT GTTCTTTCCT TTCTGCATAG CCTTCCATTT CTCGAG	240 300 360 416
(2) INFORMATION FOR SEQ ID NO:58:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 289 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
GAATTCGGCT TCATGGCCTA CTAGACCTGC TCAGTCGTTC CTAATGAATA AAAATCAAGT GCCAAAGCTT CAGCCCCAGA TAACTATGAT TCCTCCTAGT GCACAACCAC CACGCACTCA AACACCACCT CTGGGACAGA CACCTCAGCT TGGTCTCAAA ACTAATCCAC CACTTATCCA GCAAAAGCCT GCCAAGACCA GCAAAAAGCC ACCACCGTCA AAGGAAGAAC TCCTTAAACT AACTGAAACT GTTGTGACTG AATATCTAAA TAGTGGAAAG TCACTCGAG	60 120 180 240 289
(2) INFORMATION FOR SEQ ID NO:59:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 382 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	-
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
GAATTCGGCC TTCATGGCCT AATTTGAGGC CTGGGTGGAA CTGACAGGTG GAGTTTGAAG GCACATCTGC TAGCTCACAT AGGAAACAGA ATCTCCCAGG GAAAAGACAT AGGACCTCTG ACTCTAACTG AGGTTCTGGA TTATTATGAG AGATTTTCAG AAATGGTCTA ATCGTGTTGG CTTGCTCCAT ACCATAGATT TTAAGAGACA GTAGAGCTTC TGCGATGAGA TTCCCCCATA AAATAATTAT GGATCTGCAC TGGCAAGCTG GTCTTGGCTC CAAAGACCAA GAGTTGGTTT GTGGTGCTGA TCCTGAACCC TTGCGATGCA ACTGTCTGGT AGTAAAATGG CTTTGTATGG TAAGAAAAGCT TTAATCCTCG AG	60 120 180 240 300 360 382
(2) INFORMATION FOR SEQ ID NO:60:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 196 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
AAAAAAAAAC CAAACCCTAT TATTTCATTG ACAGATTGTC TTAGAGTTGA TAGCATTTAA TAATTGAGTA AGTACAGTCC TTCCTTGTTC CCAACGTGCC CTATTTTTTC TTTCTTCTCT ACTTTTGCAT ATGCATTTTC CCTCTTTCTT GTTTCTTGGT GAATTCCTAA ACCTTTTTTT	60 120 180

- (2) INFORMATION FOR SEQ ID NO:61:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 281 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAATTCGGCC	TTCATGGCCT	AACCACATTT	TTCTAATTAG	TGTTCTAGAC	TGGCTAGATA	60
AATCAACAAT	GAATCAACAG	TCTTTAAGCA	CATATACAGG	TATGATAACT	CTGTAGTTAA	120
CTCAAATCCT	TGTGCTATGT	ATTATTTTGC	TGCGTAACTC	AGAATTCAGG	AAGCTACCCA	180
CCCAATCAGT	CTTTAGCTGT	TTTATTTCAG	TAACAAGTTT	ATGCAGAACC	TTCCATATCT	240
CTCATAAAAC	CAGAGCATTC	ATAGAACCAG	AAACTCTCGA	G		281

- (2) INFORMATION FOR SEQ ID NO:62:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 400 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAATTCGGCC	TTCATGGCCT	AAAAGATTTG	AGCATTTCAA	AATTTTAAAC	ATAAAAGCAT	60
AAACGTAGAT	AAAATGAAGG	TGTACTATGA	TATCTTCAGT	TTTATCAGAA	ATGATGTAAA	120
AATTACAACC	TCTTTAAAAA	GTAGTGTTAA	TCATTAAGTT	AGAAAATATA	TAGCTGGGCA	180
TGGTGGCAGA	TGCCTGTAAT	CCCAGCTACA	TGGGAAGGTG	AGGTGGGAGA	ATCGCTTGAA	240
CCCAGGCAGT	GGAGGATGCA	GTGAGCCAAG	ATCATGCCAC	TGCACCCCAG	CCTGGGTGAC	300
AGAACAAGAC	TCCATNTCAA	GGAAAAAAAA	AAAGAAAAAT	ATATATATGA	ACTTCAGAAT	360
CTGAGGTCAT	ATATAGACAG	GTCTTCCCCC	CGTCCTCGAG			400

- (2) INFORMATION FOR SEQ ID NO:63:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 297 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GAAACCATAG	TGGCAGATTT	GTAGCAAAAA	GAATCTTTGT	AACCTTCCCT	TTAGATGTCC	60
TGTGTTATGG	CTTGGTTTTT	CTCAAAGATC	ATAGATTGCA	GTGTTTATCT	CAACTCAGTA	120
TTTCCTTTGA	AAATTGAACT	TTTCTCTATA	TTTTCCTTTC	CCCCATGCAA	ACTTTTTGAT	180
TGTTTTTCTG	AAATCATAAT	TCATTTGACT	TACCAGTTAA	TATTGATACA	GGTCTTGCAT	240
GTTATGAAGT	GCATTGTGTA	CATTATCTTG	TTTAATTTTC	ACAACACTCT	TCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:64:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGTCGCAGAA	GAGTGTCAGA	ACAATCAGTT	AAAGAAGCTC	AAAGAAATCT	GTGAGAAAGA	60
AAAGAAAGAA	TTAAAGAAGA	AAATGGATAA	AAAGAGGCAG	GAGAAGATAA	CAGAAGCTAA	120
ATCCAAAGAC	AAAAGTCAGA	TGGAAGAGGA	GAAGACAGAG	ATGATCCGGT	CATATATCCA	180
GGAAGTGGTG	CAGTATATCA	AGAGGCTAGA	AGAAGCGCAA	AGTAAACGGC	AAGAAAAACT	240
	CACAAGGAAA					300
TTCCTCCTCA	TTCTTGTCGG	AAACTTGCCA	TGAGGATCCC	TCTGTTTCCC	CCAAACTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:65:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GAATTCGGCC T	TCATGGCCT	ACTGGGGGAA	GAAGGCTGCT	TTATGTTTAT	TTTTCAAGAC	60
ТТТАААААТА Т	TTTTTGGTT	GTATTGCACT	AGGAAATCTC	TCCCACCTCT	CCCTTTTCTC	120
TTTCTTTCCC T						180
AGGGCTGAGG A						240
CCTGGCGGTG G						300
TGTCAAGGAA A	AAGGGGTAG	GAAGGAAGGT	GGAGGGATTG	ATCTAGTACC	AGGGAGAATA	360
TTCCACTGAA C						393

- (2) INFORMATION FOR SEQ ID NO:66:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GAATTCGGCC	TTCATGGCCT	AATTTGTTAT	TGCTAGAAAA	TACACAGTTT	TGAGATTTTT	60
GGGCATAATT	GGCCTTAGTG	TGTCACTTCT	GCATTAAAAT	ATAGGTTAAT	AATCAGATGA	120
AAGCAGCCAA						180
TTTGTATTTT						240
ACTCCTTCTC						300
TCCTTCTCCC						335

- (2) INFORMATION FOR SEQ ID NO:67:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67: GGTGACATAT TTATTGCTTC TGTTTTCCAA CTACATCACT TCAACTAGAA GTAAAGCTAT 120 GATTTTCCTG ACTTCACATA GGAGGCAAAT TTAGAGAAAG TTGTAAAGAT TTCTATGTTT TGGGTTTTT TTTTCCCTTT TTTTTTTAA GAGTATAAGG TTTACACAAT CATTCTCATA 180 ATGTGACGCA AGCCAGCAAG GCCAAAAATG CTAGAGAAAA TAACGGGATC TCGAG 235 (2) INFORMATION FOR SEQ ID NO:68: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68: GAATTCGGCC TTCATGGCCT ACCACAATCT GTTTGCTTTT CCTCTTTAGA TTCCAAAAAT AACACCCCAA AGGCTACCTT TTCAAATATT CTACAACATC TGCAAAAATC TTTAGTACTC 120 TGTCCTTGGA GTCAGTCAAG AAATTCCACC CCAGAAGTGT AAAAACCAAT CAATAATATA 180 240 TGACACTGAT TTTCTCTAAA TTATTATTTT TCTTATGGTT GAGTCTCCTG CCAACTTTAT GTTTCCCAAT CGGCTCG 257 (2) INFORMATION FOR SEQ ID NO:69: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 261 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69: GAATTCGGCC TTCATGGCCT AGCTGGGCAT GGTGATGCAC GCCTGTAATT CTAGCTACTC 60 AGGTGGGGGG TTAAAGGTGA GGCAAGGTCA GCGGTGAAGT GCAGCTCAGA GGGAGGGGTC 120 AAACATAAAC CAGAACTTAT AGGTCTAGAG GTAAAATGGG ATTCATGGGG GGCAGAGGTC 180 AAAGGTGAAG CAGAAGTCAG GGGTGAAGGA AGGTCTGCAA AGTTAAAGGT GCGGTTTCCA 240 261 GAGTCAGAAG GGGTGCTCGA G (2) INFORMATION FOR SEQ ID NO:70: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 279 base pairs

  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AACAGGTTTT TAAGTAGGGA TTAAAATAAA	TTCATGGCCT AGATTGAATT TTTA AAAATTAGCA AATATTAAGA ACAT TTTAAATTCA ACAAAAATAA ACAC TATATTTTTG CCAAAAGAAG TGTA GATATAAATAA TATTAGAAAC TGGC	ACGAGT AAAAGTCAGT ATTTTA AACTCCTATA AGTTCA AAGAGTTAAC	TTATTTTAGA 120 ATACATTTAT 180
(2) INFORMA	ATION FOR SEQ ID NO:71:		
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 255 base pai  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:71:	
ATAAATGAAA AAATTTCTAG	TTCATGGCCT AGTTACATTT ATAA GGGTCATTGG CCAATTGTTT GGAG TGATTTATTG TGACTTTCAT GCAT CATAGCCTTA CGAGAAGAAA ATAT TCGAG	GGAAAA AATACACCAT TTGGAT GATTTTAAAG	GTTCTAAAAT 120 ATTTTATATA 180
(2) INFORMA	ATION FOR SEQ ID NO:72:		
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 138 base paid  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	•	
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:72:	
	TCTAGACCTG CCTCGAGATC GTCT TTTGCACACT CATCTCATTC TATG CACTCGAG		
(2) INFORM	ATION FOR SEQ ID NO:73:		
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 208 base pa  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
( <b>xi</b> )	SEQUENCE DESCRIPTION: SEQ	) ID NO:73:	

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PCT/US98/06956 WO 98/45437

(1) INFORMATION FOR SEQ ID NO:74:  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 268 base pairs (B) TYPE: nucleic acid (C) STRANDEDINESS: double (D) TOPOLOGY: linear  (11) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:  GAATTCOGCC TYCATGGCCT ACATGANACT GYTAGTCACT TCATTTCTGT TYCTTCCCTG TYCCAACAGC CCATCTTCGT GGGAAGAACC AAGCTTTAGG CYTGGCTCTG AACAGCCACA 120 AAGTGACTCTG GCTAAGGTCC TGCCAATTTCG CYCAAGCTCAGG GAGACCAGG GTATGAGGT GATACCAGGT CCCTGTCCCC ACTCCACCTG TGGATTTAGC CYCAGGTG GAACCCAGGT GAACCCAGGT CAACCCAGGT CCCGTTCCCC ACTCCACCTG TGGATTTAGC 268  (2) INFORMATION FOR SEQ ID NO:75:  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDINESS: double (D) TOPOLOGY: linear  (11) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:  GAATTCOGCC TYCATGGCT ACGTGAACAA GACCTCCCCA AACCTTCAGG TAGTCAACCA GCCCGACAAGG CCCCACCAC GACACACTCT GAACGTCAGT GACCAGGT GAGCCACTGG GGGCGGGAGAG TCCAACACG CCCCAAGAAG GGACATCCTA GACCAAGAACCT AACACAAGGAT TTTGACATCA ATGAGACTTT GCCCTGGATG ATTGTGCTTT TCCTGCTGCT GGGTGCTTGTG GTGATTGTGT GTGATGTATC GACCAAGAACCT GAACACCAAG GACACTTG GAACTTCTG GAACTCCTA GACCAAGAACCT GACCAAGAGATTT GCCCTGGATG ATTGTGCTTT TCCTGCTGCT GAACACCAAG GACACCACG GACACTGG GACACCAGG GACACAGG GACACCAGG GACACCAGG GACACCAGG GACACCAGG GACACCAGG GACACCAG			
(A) LENGTH: 268 base pairs (B) TYPE: nucleic acid (C) STRANDENNES: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:  GAATTCGGCC TCATGGCCT ACATGAAACT GYTAGTCACT TCATTCTGT TCCTCCTG TTGCAACAGC CCATCTTGGT GGGAAGAACC AAGCTTTAGG CTTGGCTGT AACAGCACAG AAGTGACTTG GCTAAGGTCC TCCATTTGC GCCAAGGAACCA AAGCTTAAGG CAAGCACAGG GCAGTTCAGA GTATGGGGT AACACCAGGT CCCTGTCCCC ACTCCACCTG TGGATTTACC CTGGATTGG CAAGCCCCAT TACTCGAG  (2) INFORMATION FOR SEQ ID NO:75:  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:  GAATTCGGCC TTCATGGCCT ACGTGAACAA GACCCTCCCA AACCTCTAGG TAGTCAACCA CCAGCAAGGA CCCCACACA GACCATCCT GAAGTGGTG CCCTCAAGG AGGCCACTCG GGGGGAGAAGA TCCAGCAGC CCCACACAG GGACACTCT GAAGACATCAT GGGGGAGAAGA TCCAGCAGC CCCACACAG GGACACTCT GAAGACATCAT GGGGGAGAAGA TCCAGCAGCC CCCACACAG GGACACTCT GAAGACATCAT GGGGGTGATGTG GTGTCATGTT CCCGGGAAAAG CTCGAG (2) INFORMATION FOR SEQ ID NO:76:  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTCGA AAATACACTG TACTCACAGA GTGCTCATTAC AGGGAGAAGA TCTCATCTCTTT TCTCAGGAGA TATCTCAGG TAGTCAATCAC AGGGAGAAGA TCTCATCTTT TCTCAGGAGA TATCTTCATCT TCTAGTCTTACACACA ATGAGAATAATA GCAGTGCTTA TCAAAGAACACACACTCTATTAAAA GCATTCACACT AAAATAATAATA GCAGTGCTTA TCAAAGAACACACACACCTATTAAAAA GCATTCACACT AAAATAATAATA GCAGTGCTTA TCAAAGAACACACACACCTATTAAAAA GCAATCACACT GAAAATTAATA GCAGTGCTTA TCAAAGAACACACACACACACACACACACACACACACACA	(2) INFO	RMATION FOR SEQ ID NO:74:	
GAATTCGGCC TTCATGGCCT ACATGAAACT GTTAGTCACT TCATTTCTT TTCTTCCCTG TTGCAACAGC CCATCTTCGT GGGAAGAACC AAGGTTTAGG CTTGGCTGT AAAGGCACAC AAGTGACTTG GCTGAGGTCC TGCATTTCG CTCATGCTCA GCAGGGGGA AAAGCACACA GCAGTTCAGA GTATGGGGTC AAACCCAGGT CCCTGTCCCC ACTCCACCTG TGGATTTACC CTGGATTGGG CAAGCCCCAT TACTCGAG  (2) INFORMATION FOR SEO ID NO:75:  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (11) MOLECULE TYPE: CDNA (x1) SEQUENCE DESCRIPTION: SEQ ID NO:75:  GAATTCGGCC TTCATGGCCT ACGTGAACAA GACCCTCCCA AACCTTCAGG TAGTCAACCA CCAGCAAGGC CCCACACAA GACACTCT GAAGCTGCTG GGGCACAAGA TCCAGACATCAT GAACAACAT TTGACATCAA ATAGGACTT GCCCTGGATT TATGGCTT TCCTGCTGCT ACACAAGACT TTTGACATCAA ATAGGACTTT GCCCTGGATG ATATGGCTT TCCTGCTGCT GGGCGTGTGTG GTGATTGTGG TGTGCAGTTT GCCCTGGATG ATATGGCTT TCCTGCTGCT GGTGCTTGTG GTGATTGTGG TGTGCAGTTT GCCTGGATG ATATGGCTT TCCTGCTGCT (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (11) MOLECULE TYPE: cDNA (x1) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTGA AAATACACTG TTACTATCTT AATCTCAAGA GTUTCATTAC AGTGAGAACT TTTACAAGTA ATAGACTG TTACTATCTT AATCTCAAGA GTUTCATTAC AGTGAGAACT TCTATTAAAA GCATACCAGT TAAACAAGACA TCATTTACAACAACAACATCTT TCAAGAACACT TTTACATCTT TCAAGAACA (x1) SEQUENCE DESCRIPTION: SEQ ID NO:76:	( i	(A) LENGTH: 268 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
GAATTCGGCC TTCATGGCCT ACATGAAACT GTTAGTCACT TCATTTCTOT TTCTTCCCTG TTGCAACAGC CCATCTTCT GGGAAGAACC AAGCTTTAGG CTTGGCTCTG AACAGCCACA 120 AAGTGACTTG GCTGAGGTCC TGCCATTTCC CTCATGCTCA GCAGGGGGGA GCAGACCAGG GCAGTTCAGA GTATGGGGTC AAACCCAGGT CCCTGTCCCC ACTCCACCTG TGGATTTACC CTGGATTGGG CAAGCCCCAT TACTCGAG  (2) INFORMATION FOR SEO ID NO:75:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:  GAATTCGGCC TTCATGGCCT ACGTGAACAA GACCCTCCCA AACCTTCAGG TAGTCAACCA CCAGCAAGGC CCCACCACA GACCATCCT GAAGCTGCTG CCGTCCATGG AGGCACTGG GGGGGAAGAG TCCAGCACGC CCATCAAGGG CCCCAAGAGG GGACATCCTA GACAGAACCT ACACAAGCAT TTTGACATCA ATGAGCATT GCCCTGGATG ATTGTGCTTT TCCTGCTGCT GGTGCTTGTG GTGATTGTGG TGTGCAGTAT CCCGGGAAAG CTCGAG (2) INFORMATION FOR SEQ ID NO:76:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCCCGA AAATACACTG TACCTAAGA GTGTCATTAC AGTGAGGAATC TCAGAATCTT TCAAGGACA TTCTTTTAGTTC CAAGTTCCAG  GAATTCTAGA CCTGCCCCGA AAATACACTG TACCTAATATA AACTCAAGA GTGTCATTAC AGTGAGAATCT TCATAGAAGCA TTCTTTTTAGTTC CAAGTTCCAG 180  GAATTCTAGA CCTGCCCCGA AAATACACTG TACCTAATATA AACCTCAAGA GTGTCATTAC AGTGAGAATCT TCATAGGAGCA TTCTTTTTCTT CTTTTTAGTTC CAAGTTCCAG 180  GAATTCTAGAATCTT TCAAGGAGCA TTCTTTTTCTT CTTTTTAGTTC CAAGTTCCAG 180  GAATTCTAGAATCTT TCAAGGAGCA TTCTTTTTCTT CTTTTTAGTTC CAAGTTCCAG 180  GAATTCTAGAATCTT TCAAGGAGCA TTCTTTTCTT CTTTTTAGTTC CAAGTTCCAG 180  GAATTCTAGAATCTT TCAAGGAGCA TTCTTTTCTT CTTTTTAGTTC CAAGTTCCAG 180  GAATTCTAGAATCTT TCAAGGAGCA TTCTTTTCTT CTTTTTAGTTC CAAGTTCCAG 180  GAATTCTAGAATCTT TCAAGGAGCA TTCTTTTTCTT CTTTTTAGTTC CAAGTTCCAG 180  GAATTCTAGAATCTT TCAAGGAGCA TTCTTTTCTT CTTTTTAGTTC CAAGTTCCAG 180	()	i) MOLECULE TYPE: cDNA	
TTGCAACAGC CCATCTTCGT GGGAAGAACC ARGCTTTAGG CTTGGCTCTA ARCRGCACAG AAGTGACTTG GCTGAGGTC TGCCATTTCG CTCATGGCTCA GCAGGGGGA GCAGACCCAGG GCAGTTCAGA GTATGGGGTC AAACCCAGGT CCCTGTCCCC ACTCCACCTG TGGATTTACC CTGGATTGGG CAAGCCCCAT TACTCGAG  (2) INFORMATION FOR SEQ ID NO:75:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TTPE: nucleic acid (C) STRANDEDMESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:  GAATTCGGCC TTCATGGCCT ACGTGAACAA GACCCTCCCA AACCTTCAGG TAGTCAACCA CCAGCAAGGC CCCCACCACA GACACACTCT GAAGCTGCTG GGGGGAGAAGT TCCAGCACGC CCATCAAGGG CCCCACACAGG GACACTCTG AACGACACAT CTGACACACA TCCTGAGAGGACT TCTGCCTGGT ACGTGAATAG CTCGAGAGGC CCCCACACAG CCCCACACAGG GACACACTTT TCCTGCTGCT GGTGCTTGTG GTGATTGTGG TGTGCAGTAT CCGGGAAAAG CTCGAG  (2) INFORMATION FOR SEQ ID NO:76:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TTPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTACTAT AATCTCAAGA GTGTCATTAC AGGTGAGAATCT TCAGGAAGCT TTACTACTAT AATCTCAAGA GTGTCAATAC AGGTGAGAATCT TCAGGAAGCT TTACTACTATT AATCTCAAGA GTGTCAATAC AGGTGAGAATCT TCAGGAAGCT TTACTACTATT AATCTCAAGA GTGTCAATAC AGGTGAGAATCT TCAGGAAGCT TTACTACTATT TAAAGAACA CCGAAAAATCTT TCAGGAAGCT TTCATACTAT TAATCTCAAGA GTGTCAATAC 120 180 180 180 180 180 180 180 180 180 18	O	:i) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 286 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:  GAATTCGGCC TTCATGGCCT ACGTGAACAA GACCCTCCCA AACCTTCAGG TAGTCAACCA CCAGCAAGGC CCCCACCACA GACACTCCT GAAGCTGCTC CCGTCCATGA GAGCCACTGG GGGCGGAAGAG TCCAGCACGC CCATCAAGGG CCCCCAAGAGG GGACACTCTA GACAGAACCT ACACAAGCAT TTTGACATCA ATGAGCATTT GCCCTGGATG ATTGTGCTTT TCCTGCTGCT GGTGCTTGTG GTGATTCTGG TGTGCAGTAT CCGGGAAAAG CTCGAG  (2) INFORMATION FOR SEQ ID NO:76:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTATCTT AATCTCAAGA GTGTCATTAC AGTGAGAATCT TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA 120 CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT	TTGCAACA AAGTGACT GCAGTTCA	GC CCATCTTCGT GGGAAGAACC AAGCTTTAGG CTTGGCTCTG AACAGCCACA TG GCTGAGGTCC TGCCATTTCG CTCATGCTCA GCAGGGGGCA GCAGACCAGG GA GTATGGGGTC AAACCCAGGT CCCTGTCCCC ACTCCACCTG TGGATTTACC	120 180 240
(A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDMESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:  GAATTCGGCC TTCATGGCCT ACGTGAACAA GACCCTCCCA AACCTTCAGG TAGTCAACCA CCAGCAAGGC CCCCACCACA GACACACTCT GAAGCTGCTG CCGTCCATGG AGGCCACTGG GGGCGAGAAG TCCAGCACCC CCATCAAGGG CCCCAAGAAG GACACTCTA GACAGACCT GGTGCTTGTG GTGATTGTGCTACA ATGAGATTT GCCCTGGATG ATTGTGCTTT TCCTGCTGCT GGTGCTTGTG GTGATTGTGG TGTGCAGTAT CCGGGAAAAG CTCGAG  (2) INFORMATION FOR SEQ ID NO:76:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDMESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTACTAT AATCTCAAGA GTGTCATTAC AGTGAGAATCT TCATTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA 120 CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT	(2) INFO	RMATION FOR SEQ ID NO:75:	
GAATTCGGCC TTCATGGCCT ACGTGAACAA GACCCTCCCA AACCTTCAGG TAGTCAACCA CCAGCAAGGC CCCCACCAC GACACATCCT GAAGCTGCTG CCGTCCATGG AGGCCACTGG GGGCGAGAAG TCCAGCACGC CCATCAAGGG CCCCAAGAG GGACATCCTA GACAGAACCT ACACAAGCAT TTTGACATCA ATGAGCATTT GCCCTGGATG ATTGTGCTTT TCCTGCTGCT GTGGTTGTG GTGATTGTGG TGTGCAGTAT CCGGGAAAAG CTCGAG  (2) INFORMATION FOR SEQ ID NO:76:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTATCTT AATCTCAAGA GTGTCATTAC AGTGAGAATC TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAGGAACA 120 CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT		<ul><li>(A) LENGTH: 286 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
GAATTCGGCC TTCATGGCCT ACGTGAACAA GACCCTCCCA AACCTTCAGG TAGTCAACCA CCAGCAAGGC CCCCACCAC GACACATCCT GAAGCTGCTG CCGTCCATGG AGGCCACTGG GGGCGAGAAG TCCAGCACGC CCATCAAGGG CCCCAACAGG GGACATCCTA GACACAACCT 180 ACACAAGCAT TTTGACATCA ATGAGCATTT GCCCTGGATG ATTGTGCTTT TCCTGCTGCT 240 GGTGCTTGTG GTGATTGTGG TGTGCAGTAT CCGGGAAAAG CTCGAG 286  (2) INFORMATION FOR SEQ ID NO:76:  (i) SEQUENCE CHARACTERISTICS:	(	ii) MOLECULE TYPE: cDNA	
CCAGCAAGGC CCCCACCAC GACACATCCT GAAGCTGCTG CCGTCCATG AGGCCACTGG GGCGAGAAG TCCAGCACGC CCATCAAGGG CCCCAAGAGG GGACATCCTA GACAGAACCT ACACAAGCAT TTTGACATCA ATGAGCATTT GCCCTGGATG ATTGTGCTTT TCCTGCTGCT GGTGCTTGTG GTGATTGTGG TGTGCAGTAT CCGGGAAAAG CTCGAG  (2) INFORMATION FOR SEQ ID NO:76:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTATCTT AATCTCAAGA GTGTCATTAC AGTGAGAATCT TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA 120 CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT	(	xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 199 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTATCTT AATCTCAAGA GTGTCATTAC 60 AGTGAGAATC TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA 120 CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT	CCAGCAAG GGGCGAGA ACACAAGC	GC CCCCACCACA GACACATCCT GAAGCTGCTG CCGTCCATGG AGGCCACTGG  AG TCCAGCACGC CCATCAAGGG CCCCAAGAGG GGACATCCTA GACAGAACCT  AT TTTGACATCA ATGAGCATTT GCCCTGGATG ATTGTGCTTT TCCTGCTGCT	120 180 240
(A) LENGTH: 199 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTATCTT AATCTCAAGA GTGTCATTAC 60 AGTGAGAATC TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA 120 CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT	(2) INFO	RMATION FOR SEQ ID NO:76:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTATCTT AATCTCAAGA GTGTCATTAC 60 AGTGAGAATC TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA 120 CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT		<ul><li>(A) LENGTH: 199 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
GAATTCTAGA CCTGCCTCGA AAATACACTG TTACTATCTT AATCTCAAGA GTGTCATTAC 60 AGTGAGAATC TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA 120 CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT	(	ii) MOLECULE TYPE: cDNA	•
AGTGAGAATC TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA 120 CTGAAATCTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT	(	xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
	AGTGAGA CTGAAAT	ATC TCATTTAAAA GCATACCAGT GAAATTAATA GCAGTGCTTA TCAAAGAACA CTG TGAGAATCTT TCTAGGAGCA TTCTTTTCTT CTTTTAGTTC CAAGTTCCAG	120 180

- (2) INFORMATION FOR SEQ ID NO:77:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GATTGAATTC TAGACCTGCC	TCGAGTTCCA	CGTCCATGGC	CATCCTGAGC	ATGCTGCAGG	60
ACATGAATTT CATCAACAAC	TACAAAATTG	ACTGCCCGAC	CCTGGCCCGG	TTCTGTTTGA	120
TGGTGAAGAA GGGCTACCGG	GATCCCCCCT	ACCACAACTG,	GATGCACGCC	TTTTCTGTCT	180
CCCACTTCTG CTACCTGCTC	TATAAGAACC	TGGAGCTCAC	CAACTACCTC	GAG	233

- (2) INFORMATION FOR SEQ ID NO:78:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 276 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GAATTCGGCC	TTCATGGCCT	AAGAATAGAG	AAAACGTTTT	CAGCAGGCTT	CACAGAGAAA	60
CCAAACAATA	TTTAGAATAT	GACAGCATAT	GAAGAGTCTG	CTACTCTCCC	AGTGACCCAT	120
ACTTTCTCTT	CCATCTCTGC	TGGTTCTCTC	TACTACCGAT	TCTTTCTTGC	TGTTCTCCTT	180
CTCCATCACC	GTGACTTCTA	TTGCCTTACT	CTAATGTCTT	GTCTTCTGTG	TTACCCTTCT	240
GTGTGTTTTG	CATTCAGAAC	TCCCCCTCCG	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:79:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 273 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAATTCGGCC	TTCATGGCCT	<b>ААААААА</b> АА	AAAAATCCCT	GGCTGAGAAC	TATTGGATTA	60
GGGCCTCCNG	TACCTATCTT	TGAGGGGGAA	AGGATGCTAC	CATCAACTTT	TCTGAATGCC	120
AGGAATGCCT	TTTAGTATAG	TTATTTCACT	TACTATTTTA	TAGCATATTT	TAATTGTATA	180
GTAAGCATTG	TGTCTGTTTT	ATGGTAAGGA	AACTAAAATT	GAGAGATTAG	GCTGCTCGTG	240
GTGGCTTATA.	CCTTGTAATC	CCAAGCACTC	GAG			273

- (2) INFORMATION FOR SEQ ID NO:80:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 284 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GAATTCGGCC TTCATGGCCT AGCGAAATGA CGAAATCTAG CCCTTTGAAA ATAACATTGT	60
TTTTAGAAGA GGACAAATCC TTAAAAGTAA CATCAGACCC AAAGGTTGAG CAGAAAATTG	120
AAGTGATACG TGAAATTGAG ATGAGTGTGG ATGATGATGA TATCAATAGT TCGAAAGTAA	180
TTAATGACCT CTTCAGTGAT GTCCTAGAGG AAGGTGAACT AGATATGGAG AAGAGCCAAG	240
AGGAGATGGA TCAAGCATTA GCAGAAAGCA GCGAAGGGCT CGAG	284
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
(2) INFORMATION FOR SEQ ID NO:81:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 284 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
(AI) DEGEMEN PROCESSION DAY IN NO. VI.	
GGGAACTGGA GGAAAACCAT CACAAGATGG AGTGCCAGCA AAAACTGATC AAGGAGCTGG	60
AGGGCCAGAG GGAAACCCAG AGAGTGGCTT TGACCCACCT TACGCTGGAC CTAGAAGAAA	120
GGAGCCAGGA GCTGCAGGCA CAAAGCAGCC AGATCCATGA CCTGGAGAGC CACAGCACCG	180
TTCTGGCAAG AGAGCTGCAG GAGAGGGACC AGGAGGTGAA GTCTCAGCGA GAACAGATCG	240
AGGAGCTGCA GAGGCAGAAA GAGCATCTGA CTCAGGATCT CGAG	284
(2) INFORMATION FOR SEQ ID NO:82:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 311 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) 10100001. 1211001	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
GAATTCGGCC TTCATGGCCT ACTGTGTTGA CTTGGTGGCT TGCTTGATAA GAAGGTTTTA	60
TGAAGCACAG CAGATATCTC AGCTGCTAAT CCTGTAAGCC CTTTACCCAT TCTCGCTTTT	120
CTCTGCTCTT GCCACATCAT GAATAGATTG GTATACTATT GTGGGATACT TCTAGTTTTA	180
GCACATGATA TAGGTTATGG TTAATGTTCC TTTCCATCTT CCTGGTTACT GATAATGTTC	240
CTTTTCTGTA GATGGGTCTA TTCGATGGAA GAGTTTCAGC TTTGTTCGTG TTATTTCCCT	300
GGGACCTCGA G	311
(2) INFORMATION FOR SEQ ID NO:83:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 329 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
•	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
GAATTAATCG TAAGAGAACC TCAGCATTGT GCACGATAAG AGAATGTGTC AGTATTTCAG	60
GGTTCTACAT TTTATCTGTA AAATGTGACT TTTTTTTTTT	120
ATGTTGCTTT GTACCTGGTG TCTTTTATTA AGAATTTACT CCCCCCATTT CTCACAGAGA	180
ATABCACTCC CGACTCATTC TCACAATATA ATAGAAATGT TAGCAACCAG ATTCATGTAA	240

GGACTAAGTG GTCCTCATGA ATTGCATTAA GACTCTGTAC TGCTCATATT ACACTCCATC	300 329
(2) INFORMATION FOR SEQ ID NO:84:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
GAATTCGGCC TTCATGGCCT AGAAAGACAT CATTTAAGTN CTTTTAACAT TTAGTTTGTG GTCATAAGTT GACCTTTATG TGCTTTCTGA ATTGGAACTT AAAATAATCT TTAATTCATT ATTTTTTCTA CTTCTAGGCC AGTTTTGAGT TTAATATTTA TAAAAGGTTA GATAGTTATA GATAGGATTA TTTTGCAGTT TTGAAACAAC ATACAAATTG TTATAGATTT CAGAGTAGGG CTAATCACAG GAAAGACAAA AGTCAGAATG CTTNAGGTAA GCCCCTTCTC ATTATATAAG ATCAAGCTCG AG	60 120 180 240 300 312
(2) INFORMATION FOR SEQ ID NO:85:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
GAATTCGGCC TTCATGGCCT AAAAACTTTC AACTTAGAAA AACTAGCAAG GGATTGTTCA CCCTTACCCC AGTGGTTGGT GCTAGAGAAA AAATGGAGGA TGTCTGTTCC ACGCAGACCC TGGTGGTTTA AAACACACAT ATAGATGGCT CTGGGACCAT CAAAATAGCA GCACAAAGA GCCACTCCAC CAGCCTCCCC TCCACTCCCC CAGGCCCCAC ACAGCAGAAG GCTCCAGCCA CTTTTTGGAA GCCTGTAGCC TGGCTCCATC TTGCCCTGTG CCACAAATGC CCATGGCCCT CGAG	60 120 180 240 300 304
(2) INFORMATION FOR SEQ ID NO:86:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
GAATTTTGAA CACTAAAGCT TTGGATACAC AAATTTATAA CATCTTATTT ATAAATCAGT GGTGTACAGA AAGCAGAGAT CCCATAATCA AGCATGGCAA ACATGTTGAA GAATATGCTT ACAATGATTT CTGCTATAGA TTTCATAATG GGGATTCAGA GAAGTAGAGT TATGGTGCTG GTTCACTGCA TTGATTGGAT CAGGCGCTGG AAACTCTCCC TGATAGATTT TATTCTCACC TGTTGGGCAA TTTCCAGAAT ATTCTGCTGT AATTTTACAT GTGGGCTCGA G	60 120 180 240 291

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

4	GAATTCGGCC	TTCATGGCCT	AGCTAGAAAA	ааааааааа	AAGCCCTTTT	CAGTTTGTGC	60
			ATTGATGCAG				120
			GAATGACAAA				180
			TAATTGCCAA				240
	TGTTTCACAA	AGCTTAGACC	TTTACCTTCC	AGCCACCCCA	CAGTGCTTGA	TATTTCAGAG	300
	TCAGTCATTG	GTTATACATG	TGTAGTTCCA	AAGCACATAA	GCTAGAAGAA	GAAATATTTC	360
	TAGGAGCACT	ACCATCTGTT	TTCAACATGA	AATGCCACAC	ACATAGAACT	CCAACATCTC	420
,	GAG						423

- (2) INFORMATION FOR SEQ ID NO:88:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 172 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GCGATTGAAT TCTAGACCTG	CCTCGAGCTT	GGGGGGATTA	CAGTTCAACA	AGAGATTCAG	60
GCAGAGACAA ATATTCCAAA					
CTTTGAGTCA ACCCATATGA					172

- (2) INFORMATION FOR SEQ ID NO:89:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 260 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

- (2) INFORMATION FOR SEQ ID NO:90:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 250 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90: GAATTCGGCC TTCATGGCCT AAACTAAGAT AAAAATAAAC AGATAGGAGA GCTGAATTCC ATTTCAAGTC CTCATGTATA TGCTTACAAA GTTCCAAATT AAGCTTGGGA CTGGTTCTTA 120 CATGGCAGGT AATCCAAACC TTTTCTATTT ACTGAAGATT TTCAGCTCTC TTACAGAAAT 240 ACACAGGCTA CCATTAAAAT TGTAGGGATA AATTTTAAAT TGAATTTGAA AATAAGAGCA 250 AGTACTCGAG (2) INFORMATION FOR SEQ ID NO:91: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91: GAATTGAAAC ACAGAGTTGT TCTGCTGATA GTTTTGGGGA TACGTCCATC TTTTTAAGGG ATTGCTTTCA TCTAATTCTG GCAGGACCTC ACCAAAAGAT CCAGCCTCAT ACCTACATCA 120 GACAAAATAT CGCCGTTGTT CCTTCTGTAC TAAAGTATTG TGTTTTGCTT TGGAAACACC 180 CACTCACTTT GCAATAGCCG TGCAAGATGA ATGCAGATTA CACTGATCTT ATGTGTTACA 240 260 AAATTGGAGA AAGTCTCGAG (2) INFORMATION FOR SEQ ID NO:92: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 354 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92: GAATTCGGCC TTCATGGCCT AATTTCATCT TTTTTTCCTG GTGCTGCATA AACATATATT 60 AAATGTTGTT ACTGATCCCT AGTACTGTTG ATTTGTGACC CTTCTCCTGA GGGAGACTAA 120 AGCTGCTTGA GCTAAAGGCT TTTGAGACAT CCCATACGGT TCCCTGAACA AAGTTTTCTC 180 TCCTGACCTC AGTTCTCTTG ATGACCTTGG CAAGTGGGCC CGACTAGTTG GACACTAATG 240 AGGCATCGTA ACATGCCGGC CCCATCCTGT CCATTCTGTT CTCTTTGCCA TCTAGCATTC 300 354 AGTGTTGTGT CTTCCTAGTG GGCATGAAGA CGGCTTTAAA ACCATCCACT CGAG (2) INFORMATION FOR SEQ ID NO:93: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 493 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double

on the second se

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCT	GAAAATG	CAAAACATGA	AGAAAGTGAT	TGAGGCAATT	CGAGTGGAGC	TGGTTCAGTA	60
			GCCAGGAGCA				120
GGA	CTACACA	GAAAGTCTGC	TCCAGCTCCA	CGATGCTGAG	ATTGTGCGGT	TAAAAAACTA	180
CTA	TGAAGTT	CACAAGGAAC	TCTTTGAAGG	TGTCCAGAAG	TGGGAAGAAA	CCTGGAGGCT	240
TTT	CTTAGAG	TTTGAGAGAA	AAGCTTCAGA	TCCAAATCGA	TTTACAAACC	GAGGAGGAAA	300
TCT	TCTAAAA	GAAGAAAAAC	AACGAGCCAA	GCTCCAGAAA	ATGTTGCCCA	AGCTGGAAGA	360
AGA	GTTGAAG	GCACGAATTG	AATTGTGGGA	ACAGGAACAT	TCAAAGGCAT	TTATGGTGAA	420
TGG	GCAGAAA	TTCATGGAGT	ATGTGGCAGA	ACAATGGGAG	ATGCATCGAT	TGGAGAAAGA	480
GAG.	ACTCCTC	GAG					493

- (2) INFORMATION FOR SEQ ID NO:94:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 293 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GAATTCGGCC TTCATGO	SCCT ACACACGGCC	AAATTTGAGG	GCATTCTCAC	ATGTGTTCTT	60
CTCTCAAAAC CACTGGG	GGTT GACAGATCCA	GGAGGCTAAA	AAAAAGTGAC	CTCTATAATT	120
CTTTAAAGGT GCTATTT	TTTA GAANATTGTA	TAATTTATTC	ACAGTATATC	TAAAACAGAA	180
TTAAGGACAA TTAAAA	TATC TTATGTGACA	GCCTTTATGT	CTAGTCACAT	TTGATGAAAT	240
AAAAAACTTC TGAATCT	IGAA TAGAAGTTCT	ACTGTNTCAG	GATTGAACTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:95:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GAATTCGGCC TTCATGGCCT	AAAAAGACAG	GAAAATAAGT	CTCTTTGTAT	CCTTATTAAT	60
CATTTGAAAT TATGCTATAA	TATTTTTTAA	AACTCACCTG	TTTGGTTCTG	GGTGAAGCAG	120
TTCCTGAAGG AGTGTTTTGT					180
GTAAGTTTGG GAAATAGTGG	GTTAGACAAA	GTTGAGTTAC	TGTTGGCCTT	TCAGACCTTT	240
GATACGCTAA TGTGCATTTT	AAATCTCCAA	GAAGCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:96:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 279 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAATTCTCCA	GCCTGGGTGA	CAGAGTAAGA	CTCCATCTCA	AAAACAAAAA	AACCCAACAG	60
GATAAAATTT	AATAGGAGTA	AATATAAAGT	TCTACGTTTT	GATTTTAAAA	ATCTAGGTAC	120
TGTATAGTGT	GTATTAGTTG	GGGTTCCTTT	TTTGAAACTT	AATCTTGCCT	ATAAAACACA	180
AAAGAGTTTA	AGATGATATT	GAGACTCCTC	CTGTCCTCAT	TCCTTTTCCT	TCCTAATAGC	240
TCACTCCTCA	ACCTCTTACC	TCACCCACAA	CAACTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:97:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GAAT	TCGGCC	TTCATGGCCT	AGGATACCTT	CATTTCAAGG	AGCCTCTTTA	CAGTAACTGG	60
GCTA	AACATT	TTGTTGTCGT	CCGTCGGCCT	TATGTCTTCA	TCTATAACAG	TGACAAAGAC	120
CCTC	TGGAGC	GTGGAATCAT	TAACCTGTCC	ACAGCACAGG	TGGAGTACAG	TGAGGACCAG	- 180
CAGO	CCATGG	TGAAGACACC	AAACACCTTT	GCTGTCTGCA	CAAAGCACCG	TGGGGTCCTT	240
TTGC	AGGCCC	TCAATGACAA	AGACATGAAC	GACTGGTTGT	ATGCCTTCAA	CCCACTTCTA	300
GCTC	GAG						307

- (2) INFORMATION FOR SEQ ID NO:98:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 292 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAGCTGTGTC	AGCATCGATC	AGGGGTCTGT	AGACAAAAAT	TCCCAAAGAT	TTGAGACTTT	60
ATTGGGGGAA	ACAGATCACT	GGCGGGGAAT	AAGCCACAGG	CCAAAGGAGG	AAATGCTGGG	120
ACCAGAAGTC	CCGCTTGCCG	CCTTTTGCTA	AAAGTTCCGC	ACGCCTGCTC	GGCGTGGGCG	180
CAAGCATAGT	GTCGTCGGGG	CTCTGCGACG	TCTGATTGGC	TCTCTGCAGT	GCACCGTCGA	240
GGTAGAAGGC	TCAGCTCCTA	GTCGCTCCCA	AATTACTTTG	TTGGTGCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:99:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 397 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
    - (b) TOPOLOGI: Timear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCGGCC TTCATGGCCT AGCTTGAGGA ATGACCCAAC TCTCTCTGGA AAGTCACTTT

GCCTCTCTGT	TCTGGTTCTC	TCATTTTATA	AAGTGCCTTC	TTCCTTTCTG	CATTTATAAG	120
TAAACATGAG	AAAAATCTGA	AAAGACTTCT	TCAGGATGTT	TAAGGAAACA	AATGTTGCTT	180
TCCTTGGGTT	GGGTCGTTTC	ATAAGAGTGA	TGTTTGCCAT	AAAACTGGAG	CCTCATAGAC	240
GATCCTGCAG	GGAGGAAGCT	TTCCTTGGTC	ACCTGACTCA	TGTGTTTATA	TATAGTATAG	300
AGGAGAGGTA	TTCCAAAAGA	CCCGTCGCTT	TTCCTGTGTC	CCACAGCTGC	CTGTAGAGTT	360
GTGGCACCAT	AAACTTTAGC	AGCTGGAAAT	CCTCGAG			397

- (2) INFORMATION FOR SEQ ID NO:100:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAATTCGGCC	AAAGAGGCCT	ATTAATTTAA	TAAAGCCATA	TCATACCTCT	CTTTAACATT	60
GTTAAAAGGA	AACTGTGTGT	GTGTATTTGT	GTTAATGTTA	ANTTCTCTTC	ATTTTTGTGC	120
TTGGGGGGCT	GTTTATTTGA	GGATGGTCGG	GGGGCGGGTG	GGTCAGACCC	ATCCATCCCC	180
CATGGAAGAC	CAGACCCATC	CATCCCCCAT	GGAAGACCAT	TCCCGTGTGT	TCAGACTGGC	240
AGGGTACTTC	CATAGACAGG	AACATTCTGG	ATGCTCTGAT	GCTGAACACT	ACCAGAATCG	300
GCCATGGATT	TGCTTTGAGC	AAACACCCCG	CAGTCAGGAC	TTACTCCTGG	AAAAAGGACA	360
TCTTCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:101:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 340 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GAAAAAAATA	GACAAAACTA	TGATGTAAAA	ATGCTTAAAA	ACAATTATTC	CTCTCTGCTA	60
ATTTTAATGC	AAAATAAATG	ATGCTAGCAT	TTAATATGTT	TATATGATCT	TGTTTTTAGG	120
ATTGAAATTT	TAATACAATG	GCCTTTTGTA	ACTATTTTTA	CTATTATAGC	TCAGGTGTTT	180
GAATTCTCTC	TACCCCACCT	ATCACCCCTA	TCCCCTAACA	AAGAGTCTGG	CTTCATAAAT	240
ACTGTTGAAT	GAAAATTGGT	TCTCTAAATG	GTTAACAAGA	TGAATCCACA	TAAATCATAA	300
TTCAGTACTG	AGGAACCGAA	TTTATACCCA	GCGTCTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:102:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AGTGTTCTGG AAATAGCTGG GAGGCCTGTG TGTTTAGGAG CGCCTTAAAC AGTAGGATAT	120
AAGGGCAGAG AAGTAGCTGG GAACTGAGAA GAACTTTGGC TGTTATTCTA GTAAGACTGA	180
AAATTTCAGG TGGGATTTGA ACAGAGATGT GTGGTGATCT GACTTGGTTC ATTCTGCTGT	240
GCTGAAGAGA CTGGAGGTGC GGGGCAAGTA TGGAAGCATG GAGACCATTA ATTTATGGGG GCAATGGTAG AGGGAAGAGA AACAATGCTA TTAACTGGAG TAGGAGCACA CAGAGAACAA	300 360
GCACTCGAG	370
(2) INFORMATION FOR SEQ ID NO:103:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 270 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear,	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	
GCGATTGAAT TCTAGACCTG CCTTGAGATC ACCGAGTGCT TCATCTCTGA CAGTTCCTCT	60
GACCAGATGA CCACAGGCAC CAACGAGAAC GCCGACAGCA TGACATCCAT GAGCACACCC	120
TCAGAGCCTG GCATCTGCCG CTTTACCGCC TCACCACCCA AGCCCCAGGA TGCGGACCGG	180
GGCAAAAACG TGGCTGTGCC CATCCCTCAC CGGGCCAACA AGAGTGAGTG CTCAGACCAC	240
CTCCCAGGCA GTGCCCCCC GACTCTCGAG	270
(2) INFORMATION FOR SEQ ID NO:104:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 286 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) Toronodi. Iinedi	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
GAATTCGCCT TCATGGCCTA ATATGCTTAT GAATATGATG TTGATGGACA GCTCCAAACA	60
GTTTACCTCA ATGAAAAGAT AATGTGGCGG TACAACTACG ATCTGAATGG AAACCTCCAT	120 180
TTACTGAACC CAAGTAACAG TGCGCGTCTG ACACCCCTTC GCTATGACCT GCGAGACAGA ATCACTCGAC TGGGTGATGT TCAATATCGG TTGGATGAAG ATGGTTTCCT ACGTCAAAGG	240
GGCACGGAAA TCTTTGAATA TAGCTCCAAG GGGCTTCTAA CTCGAG	286
(2) INFORMATION FOR SEQ ID NO:105:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 291 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) TOPOLOGI: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
•	
GAATTCGGCC TTCATGGCCT ACTTAAATCT TAGATGCTAA TGGGAGAAAC TGATTTTTTA	60
AAAAACAGGG AAACTAATTA ACATTTTATC AGATATGCTA TGAAGTAAAC AGTTGAAGAC	120
TGACAGTCCA GTGGATACCG AGGAGTTCCT TTAGATACCC TGGTGAGGTA AGGACACAGG CAAGGGGAGA GCTGAGACCT GAATATGAGG AGAAGCCAGG CGAGCACACA ATAGGGCAGA	180 240
TABLESON ALMOS TO THE PROPERTY ALL THE PROPERTY ALL AND CONTRACTOR ALMOST ALMOS	

AAGGAGCAGT AGGTCAAAGC CTGAGGCAGG AGAGAGCTTG ACTGACTCGA G 291 (2) INFORMATION FOR SEQ ID NO:106: (i) SEOUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106: GAATTCGGCC TTCATGGCCT AGAAATGGTT CTGAAAGCGA CAGTAGAGAG ATGCAGTTGT 60 GATGATTTCA ACAACCTGGA TGTTTTCTTT CTCCTCTTTG CTTCCATTCA TCTCTGTTGG CTGCTGTTGA TGGAGTCAGA CAGTAAACAC GTGGCTTGGA TAACACCCAT CATCCTATGA 180 AGAATATAGG GAGTACTTGT TCTCTGTTGA TTCAACTTTT ATGTCTCCAG TAACATTGCG 240 CTTATGAAGG TACCTGTATT TGTATGGACT CTGAATAAAG AAGAATTCAT TTGTTTAGCA AGTATTAGTT CAGCAACCAC TGAGAAACAA GCACTCGAG 339 (2) INFORMATION FOR SEQ ID NO:107: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 439 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107: GAATTCGGCC TTCATGGCCT ACATCATGTC AAAGAGTACT ACATACAGTT TGGAATCTCC TAAAGACCCG GTACTACCAG CTCGTTTCTT CACTCAACCT GACAAGAATT TCAGTAACAC 120 CAAAAATTAT CTGCCTCCTG AAATGAAATC ATTTTTCACT CCTGGAAAAC CTAAAACAAC 240 CAATGTTCTA GGAGCTGTTA ACAAGCCACT TTCATCAGCA GGCAAGCAAT CTCAGACCAA ATCATCACGA ATGGAAACTG TAAGCAATGC AAGCAGCAGC TCAAATCCAA GCTCTCCTGG 300 AAGAATAAAG GGGAGGCTTG ATAGTTCTGA AATGGATCAC AGTGAAAATG AAGATTACAC 420 AATGTCTTCA CCTTTGCCGG GGAAAAAAG TGACAAGAGA GACGACTCTG ATCTTGTAAG 439 GTCTGAATCG GAGCTCGAG (2) INFORMATION FOR SEQ ID NO:108: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 298 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108: GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TCGAGAGGCA GGTCTAGAAT TCCAAATGTA AAATTTACTA AGGCTTTTCA TGTGGAAGTA GAATGCATAT ATCTTTCTTG 120 ATATAACAAA TGAATTTGGT TGTAGCTAAC GTGTTGTACT AGTAAAGGTC CACCTGCTAA 180 240 ACTITITCTT TITTGTTGAG GTATAGACAG TAGAGTGATA CCGATACATG AGGAAAATGA GAACTGGAAT GCAGGCCAAA AGCTGGTCCT TTCCAGATGA ATGTAACCAA GACTCGAG 298

- (2) INFORMATION FOR SEQ ID NO:109:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 355 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GAATTCGGCC	TTCATGGCCT	ACACTCTCAA	ATATGTGGCC	TTTAACGGGA	CCAAAGTAGG	60
AAAGCAGATA	GTGGAAAACT	TCTCTCCCAA	TCAGACCAAG	TTCACGGTGC	AAAGAACGGA	120
CCCCGTGTCA	CGCTACCGCT	TTACCCTCAG	CGCCAGGACG	CAGGTGGGCT	CTGGGGAAGC	180
CGTCACAGAG	GAGTCACCAG	CACCCCGAA	TGAAGCTTAC	ACCAACAACC	AAGCAGACAT	240
CGCCACCCAG	GGCTGGTTCA	TTGGGCTTAT	GTGCGCCATC	GCCCTCCTGG	TGCTGATCCT	300
GCTCATCGTC	TGTTTCATCA	AGAGGAGTCG	CGGCGGCAAG	TACCCAATAC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:110:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GAAAAAACTG GGTCAAAGAA TTACGGAAAA TGTTGGGAAA TGAAATCTGT TTATGTATAG	60
TTGGTAATAA AATAGACTTG GAAAAGGAGA GACATGTTTC CATTCAAGAA GCAGAGTCGT	120
ATGCAGAATC TGTGGGAGCA AAACATTATC ATACTTCAGC CAAACAGAAC AAAGGAATTG	180
AGGAACTCTT TCTTGACCTT TGTAAAAGGA TGATAGAAAC AGCACAAGTG GATGAGAGAG	240
CAAAAGGCAA TGGCTCTAGT CAGCCGGGAA CTGCAAGGCG AGGTGTACAG ATTATTGATG	300
ATGAACCTCA AGCCCAGACC AGTGGTGGAG GGTGCTGTTC TTCTGGATAA CTGTTCACGC	360
CTAAGAAATT AAAAGACAGA ACAAAACTGT GGATCATTGC CCTCGAG	407

- (2) INFORMATION FOR SEQ ID NO:111:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCGGCC	TTCATGGCCT	AAAAGAAAGT	ACATTAAAGC	AACTTGCATC	TCAAAACAAT	60
ACATTTCTCT						120
ATGGGTAAAG	TTGTCTAAAT	ATGGGATTCC	TTAGAATCCA	TCCTCCTTCC	CAAGCATTTC	180
CCCATGTTTC	CTTCCACCCC	CAAATTCTTA	CCCCATTTCA	GGCAGAGCTG	AGCAAACATA	240
AGCCTTCTCT	_					300
CAGAAAAGGT						360
TGGAGAGAAT						395

WO 98/45437

	PCT/US98/06956	
(2) INFORMATION FOR SEQ ID NO:112:		
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 301 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:		
GAATTCTAGA AACTACAGTA GTGGGACACA TAACATAGAA GTAATCGTCC TGGAAGAAGT AAGAGTGTTC ACCACATATT TTCTGTTCAA GAGAATAATC TGATCCCCTG GCATCATTA TTCTCCGTAC TGATCACTAC ATCATGGCCC TGTGCTGATT GTGCTGAGCC AGCTCACCAT TCTCATTATT TTTAGATATC AGAGCTTAAA GAACCTTCAG GGTTTATAAA TCTGACCTCA TTTTCTCTTC G	ATCTCAGTTT 12 GGGTCCTTTT 18 GAGGATACCC 24	0
(2) INFORMATION FOR SEQ ID NO:113:		
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 268 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:		
GAATTCGGCC TTCATGGCCT AAGCATGCTG TCTTGTGATG GTGATTTCAT CATGGGATTA TTAACGGCAT CCATTTTCTT GGGCGTCAAG TTGTTGCAGG TGCGATGCAG CAGCAAGAAA AACTCATCCA ACAAGAGAGG GCACTGCTAA ATGGAAGAGA AGCTGTGCCC TTCAGATGAA ATATTGCCAA GCCTTCATGC AAGTTCAGCC CATAACAGCA GTCTCGAG	TGTCCACCAT 12 ACTTTACAGA 18	0
(2) INFORMATION FOR SEQ ID NO:114:		
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 260 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	·	
(ii) MOLECULE TYPE: cDNA		
(xi) SPONENCE DESCRIPTION: SEO ID NO:114:		

GAATTCGGCC	TTCATGGCCT	ACCCGCATCC	CAGCTCTATT	ATAAAAAATA	AAGAAGAAGA	60
TAATTCATTT	CCTTAAGCTG	CCCTTACACT	ATTAGTCAGG	AATGTTTGTG	TTCACTTCCA	120
CTACATACCT	TACGATCTCT	TTTGCTTTGC	TTTTTTTCAG	TCAAGTCTCT	ATTTATGAGG	180
TGGACAAGCA	AGATTGTCGC	AAATTTTGCA	CTACTGGCAT	CGATGGAGCC	ATGACAATTT	240
GGGATTTCAA	GACCCTCGAG					260

- (2) INFORMATION FOR SEQ ID NO:115:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 259 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC	TTCATGGCCT	AAACATTTTC	TGAAAAACGT	GATAGAAAGA	AGGAGGAGCT	60
GTTTCTAGGA	GGGAAATAAA	TAATTTGGCA	GGAGACTTTT	TGAACTAGAT	ATCTATTGAA	120
TAACAAAGTG	ACAATGTTCC	CCATCCTCTC	ATTTCCATTC	CCAATTTTAC	TTCTCGTCCC	180
AATTCAAATC	ATTCTTACTT	ATGATCGGCG	CTATGTCAGT	GCCTCTCAGC	TGGTCTTCCC	240
AGACCCAGTC	ACCCTCGAG					259

- (2) INFORMATION FOR SEQ ID NO:116:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 238 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

AATTACATTT ATGCAACO	AA GCTATCAAAA GGACTGGCTG	60
CAAAATCGTC AATAGAGI	AT TATTGGAAAA GATTGTTTTC	120
AATGAGAAAA CAAATGTA	AT GATGCTTTCT GTCATGATTT	180
AGGAAATTGG AAAAATAA	AT GAAAAAGAAA AACTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:117:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 279 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCGGCC	AAAGAGGCCT	ACCCTAGACC	TGTTTTCTGT	TCTCTACTCT	TGAAATGCTA	60
ATGACCTTCA	TGACCAGAGT	CCGCTATTGC	AGTTTGTGGT	TGACAGGCAT	CTCTCACTCA	120
CTGTGCTGCA	ACTCAACTCT	TTATCTTCAA	CCAAACAGGG	CCTCCCCGCA	GCTTTCCCAC	180
TGCCACTCAG	TGGCACTCCA	TCCAGGGTTT	CCAAAGTGTA	AGACCCCGGA	ATTTATCTTT	240
GACACTTCCA	TCTCCCTCCA	CCCCTCATCC	AATTCATCA			279

- (2) INFORMATION FOR SEQ ID NO:118:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 656 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCGGCC	AAAGAGGCCT	AGTTATAATG	ATGGAAGAAG	TGGAAAAACT	TTGTGATCGG	60
CTTGAACTGG	CAAGCTTACA	GTGCTTGAAT	GAAACACTCA	CATCATGCAC	AAAAGAATAG	120
GAAAGGCTGC	TTTGGAAAAA	CAGATAGAAG	AAATAAATGA	GCAAATCAGA	AAAGAGAAAG	180
AGGAAGCTGA	GGCTCGTATG	CGACAAGCAT	CTAAGAACAC	AGAGAAATCA	ACTGGTGGAG	240
GTGGAAATGG	AAGTAAAAAT	TGGTCAGAAG	ATGATCTACA	ATTACTAATT	AAAGCTGTGA	300
ATCTGTTCCC	TGCTGGAACA	AATTCAAGAT	GGGAAGTTAT	TGCTAATTAC	ATGAACATAC	360
ATTCTTCCTC	TGGAGTCAAA	AGAACTGCCA	AAGATGTTNT	TGGCAAAGCA	AAGAGTCTCC	420
AAAAACTTGA	CCCTCATCAA	ANAGATGACA	AAATATAAA	GGCATTTGAT	AAGTTCAANA	480
AAGAACATGG	AGTGGTACCT	CAAGCAGACA	ACGCAACGCC	TTCAGAACGA	TTTGAAGGTC	540
CATATACAGA	CTTCACCCCT	TGGACAACAG	AAGAACAGAA	GCTTTTGGAA	CAAGNTTTGA	600
AAACATACCC	AGTAAATACA	CCTGAAAGNT	GGGAAAANAT	AGCAGAAAGT	CTCGAG	656

### (2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 523 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GAATTCGGCC	AAAGAGGCCT	AGAGACAAAT	AGGTGATACT	GAATTTTATA	CTGTTTTCTA	60
CTTTTCCATT	AAAACATTGG	CACCTCAATG	ATAAAGAAAT	TTAAGGTATA	AAATTAAATG	120
TAAAAATTAA	TTTCAGCTTC	ATTTCGTATT	TCGAANCAAT	CTANACTGTT	GTGATGAGTG	180
TATGTCTGAA	CCTGTAATTC	TTAAAANACT	TCTTAATCTT	CTAGAAGAAA	AATCTCCGAA	240
GAGCTCTCTC	TAGAAGTCCA	AAATGGCTAG	CCATTATGCT	TCTTTGAAAG	GACATGATAA	300
TGGGACCAGG	ATGGTTTTTT	GGAGTACCAA	GCAAGGGGAA	TGGAGCACTT	TAAGGGCGCC	360
TGTTAGTAAC	ATGAATTGGA	AATCTGTGTC	GAGTACCTCT	GATCTAAACG	GTAAAACAAG	420
CTGCCTGGAG	AGCAGCTGTA	CCTAACAATA	CTGTAATGTA	CATTAACATT	ACAGCCTCTC	480
AATTTCAGGC	AGGTGTAACA	GTTCCTTTCC	ACCAGATCTC	GAG		523

## (2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCGGCC AAAGAGGCCT AATTCTTCC TGTGATATGA GAATTTCTTT TCTTTCAGCA 60 GCTTTACCTG CATTTGGCTT TGGCTTTTGC AATCGGCCCC TCATTCTCGA G 111

- (2) INFORMATION FOR SEQ ID NO:121:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCGGCC AAA	AGAGGCCT AACCGCGGCC	GCTACTTCGG	CCTCTTTGGA	AAAAAAAAG	60
TGAAAGAAAA NAT	CACAATA CAGGGAAAAG	TGAGCTAAAA	ATCCCGGCAT	TAAAAAGCCC	120
TTGATGTGGT CCT	GAATCGG CTATTTCTAT	CTGTTCCCTG	AGCCTAACCT	CAGCGCTGGC	180
CTCTCTAAAC CTC	CTTTTCAG TCCTCTCATT	TTGAAAACAG	GGCCCATTAC	ACATTCTCTG	240
AAAGCTTGCT GAG	GTGATTTA ACCACATAGT	CTAGGGGAGG	CACTCATCAA	ACATAAGGCC	300
TCTCTTTTTG ATT	TTTTATCC TATAGTGGTA	TCTATCTAGA	GGCTGGTGAA	GACAGTGTGG	360
TGGAAGGAAA GTG	GGGAAGGA TACACTGAAA	TAGGACATAG	ACGTAGAGGG	GAGTCGATGG	420
TCATCTGGCT TGA	ATAGGGAA AGTTAGAGAG	CTCTCCTGAA	CCACAGTTAC	AGAGCTTGGG	480
ATTATAACAC ACA	ACAGCCCC AGAGAAAACA	CTTTGTTTAC	CATATTTCCT	CTTCTGCTGG	540
GGCTCTGGCA CCT	TTAATTGG TCAAAAGGCA	GCACTCGAG			579

- (2) INFORMATION FOR SEQ ID NO:122:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 257 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GAATTCTAGG	AATGGGTCGG	GAAGTTGAGA	ATCTTATATT	AGAAAATACA	CAACTGTTGG	60
AAACCAAAAA	TGCTTTGAAC	ATAGTGAAGA	ATGATTTGAT	AGCAAAAGTG	GATGAACTGA	120
CCTGTGAGAA	AGATGTGCTG	CAAGGGGAAT	TGGAGGCTGT	GAAGCAAGCC	AAACTGAAAC	180
TAGAGGAAAA	GAACAGAGAA	TTGGAGGAAG	AGCTTAGGAA	AGCTCGGGCA	GAAGCTGAAG	240
ATGCAAGGCA	ACTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:123:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 421 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCCTGT	AACTCGGAAA	AGATATCAGA	GGAATGTTCG	TGGCATCAGA	GAGAAAGATG	60
AGAGCTCACC	AGGTGCTCAC	CTTCCTCCTG	CTCTTTCGTG	ATCACCTCGG	TGGCCTCTGA	120
AAACGCCAGC	ACATCCCGAG	GCTGTGGGCT	GGACCTCCTC	CCTCAGTACG	TGTCCCTGTG	180
CGACCTGGAC	GCCATCTGGG	GCATTGTGGT	GGAGGCGGTG	GCCGGGGCGG	GCGCCCTGAT	240
CACACTGCTC	CTGATGCTCA	TCCTCCTGGT	GCGGCTGCCC	TTCATCAAGG	AGAAGGAGAA	300
GAAGAGCCCT	GTGGGCCTCC	ACTTTCTGTT	CCTCCTGGGG	ACCCTGGGCC	TCTTTGGGCT	360
GACGTTTGCC	TTCATCATCC	AGGAGGACGA	GACCATCTGC	TCTGTCCGCC	GGTCACTCGA	420
G						421

- (2) INFORMATION FOR SEQ ID NO:124:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 123 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTCTAGA	CCTGCCTCGA	GAAAATGAAA	GTCTTTTCTC	AAAAAACTTC	TTCCCAGGTC	60
TGTGAAGCAG	CACAGTGGCC	CCTTCTGGCT	CTCACCTTGT	ACCTCGTCCT	TGTTTGCCTC	120
GAG						123

- (2) INFORMATION FOR SEQ ID NO:125:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 303 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCGGCC TTCATGGCCT	AAGATGGCGT	CTCACAAATC	ATATGCCAAT	TACTGAAATT	60
GGAGGTGAAA ATATTCTAGA	TTTATTGTGG	GATATATA	TTTTATGGTG	TATGGCTCCC	120
AACACCACAT GCCACTGAAC	TATATAAAAC	TTTATGTCAG	AACACTTACT	TGTGTCATAT	180
GTAACCCTCT TGCAAATAAT	ATTCCCTTAC	TACAGATCTG	TCCCACTGTT	CTCAGAAAAT	240
AAAACATGGG AACGTTGGAA	TGTCTCCTTG	CTATAAGATA	TTGAATTCTA	GACCTGCCTC	300
GAG					303

- (2) INFORMATION FOR SEQ ID NO:126:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 508 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCGGCC	TTCATCCCCT	ATCABCACAA	ACCTAACTTA	CAAAAGCAGC	TGGTTGAAGC	60
						120
AATGAATACG						
TGTTAAAAAA	CTACAAGAAG	AGATTGAGAA	AATTAGGCCA	GGCTTTGAGG	AGCAAATTIT	180
ATATCTGCAA	AAGCAATTAG	ACGCTACCAC	TGATGAAAAG	AAGGAAACAG	TTACTCAACT	240
CCAAAATATC	ATTGAGGCTA	ATTCTCAGCA	TTACCAAAAA	AATATTAATA	GTTTGCAGGA	300
AGAGCTTTTA	CAGTTGAAAG	CTATACACCA	AGAAGAGGTG	AAAGAGTTGA	TGTGCCAGAT	360
TGAAGCATCA	GCTAAGGAAC	ATGAAGCAGA	GATAAATAAG	TTGAACGAGC	TAAAAGAGAA	420
CTTAGTAAAA	CAATGTGAGG	CAAGTGAAAA	GAACATCCAG	AAGAAATATG	AATGTGAGTT	480
AGAAAATTTA	AGGAAAGCCA	CCCTCGAG				508

- (2) INFORMATION FOR SEQ ID NO:127:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 713 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAATTCGGCC TTCATGGCCT	AGCGGCAGTC	CAGATCACGG	TTACTGTGAC	CTGACTGGAG	60
AAAAATTATG TGTCTGCAAT	GATAGTTGGC	AAGGTCCTGA	TTGTTCTTTG	AATGTTCCCT	120
CTACTGAGTC TTACTGGATT	CTGCCAAACG	TTAAACCCTT	CAGTCCTTCT	GTAGGTCGGG	180
CTTCACATAA AGCAGTTTTA	CACGGGAAAT	TTATGTGGGT	GATTGGTGGA	TATACTTTTA	240
ACTACAGTTC TTTTCAAATG	GTCCTAAATT	ACAATTTAGA	AAGCAGTATA	TGGAATGTAG	300
GAACTCCATC AAGGGGACCT	CTCCAGAGAT	ATGGACACTC	TCTTGCTTTA	TATCAGGAAA	360
ACATCTTTAT GTATGGAGGC	GCCCCAAGGC	CCGACCCCTC	CCCCAAAGGG	GCAGTCCCCT	420
TCTTGCAGGT CTCAGCTTGC	GGGGTGGGGG	GAGTCATGCC	CAGGGGAGGA	GACTTTTTAT	480
CTGGAGGGGA GAGAAGGATT	CTAGGGGTGT	GGAGTTGGAG	AAAGAGGCTT	CCTTGAGCCA	540
CCCTTCCCAC CCCAGCCCTT	GNTGGTCCCT	AGGCCAAGCC	ACCAAGTGAA	ACCTTCCAGG	600
ATACTAGCCC GCCAGCTGTG	GGCCCCAGAA	AGCCAGCCTG	CCTTTTAGCA	CTTGGATACA	660
CACAGACCCA CGGAGCTCTC	TGTGTTTGGC	CTCTCACACA	CACACAACTC	GAG	713

# (2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 277 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GAATTCGGCC AAAGA	GGCCT AAGAGATTCA	GGACCTGCAG	AGTCGCCAGA	AGCATGAAAT	60
TGAATCTTTG TATAC	TAAAC TGGGCAAGGT	TCCCCCTGCT	GTCATTATTC	CCCCAGCTGC	120
TCCTCTGTCG GGGAG	AAGAA GGAGACCCAC	TAAAAGCAAA	GGCAGCAAGT	CTAGTCGCAG	180
CAGCTCATTG GGCAA	TAAAA GCCCACAGCT	TTCAGGCAAC	CTGTCTGGTC	AGAGTGGAAC	240
TTCAGTCTTA CACCC	CCAAC AGACCTCCAC	AGTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:129:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 670 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GAATTCGGCC	TTCATGGCCT	AAGGCTACCG	ATATTGGAGA	AGCTAACTAT	GGGTTTTACC	60
ACACGTAACA	GCTTTTTGGT	GAAATCAGTT	GTTATACTAA	TAAGCTTTCC	TCTAATTGAT	120
TTGAGTTTTG	GTTTTTGTGT	TTGTATTTGC	GGGTTTTGTC	TCTTTTGTTT	TCTTGTTTTT	180
AGTAAATTGG	TTTTTCTTCA	ATGTATTTTC	TTAAAGTAGT	CTAGCTTTAC	CCAGTTTCCT	240
TGGCAAATTG	AAATTTAGGC	CATGAAGGCC	GAATTCGGCC	TTCATGGCCT	ACTCAGCCTC	300
CCCAAGTAGC	TGGGACTACA	GGCGTGTGCC	ACTATTCTCA	GCTGATTTTT	GTATTTTTAG	360
TGGAGACGGG	TTTTTGCCAT	GTTAGTTGGC	CAGGATGGTC	TCTCTCTCGA	CGTCGTGATC	420
CGCCCGCCTC	GGCCTCCCAA	ATTGCTGTGA	TGACAGGCGT	GAGCCACCCC	GCNTGGCNTG	480
TCCTACCTCT	TTTTTAAGAC	CTCTTCCTGT	AAGCACTGGA	TAATCTACTT	CTAGTAATGT	540
GAAACTGACT	ATATNTTGAA	TTCATATGTT	TTCAATCAAC	CTGTTGCAGT	TTATATTTCA	600
CACCCTGCTC	CCTTTTGACA	GTTTAAGTAC	AGATAGTCTC	AGCAGTTCTG	GAGACCATGT	660
AAAGCTCGAG						670

# (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 462 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

			TCTATTTACC			60
GACATGCTGT	TAATATTTAG	AAATATTTCT	CCAACATTCA	GAGTGCCTGG	GTACCACACA	120
TGGATGCGAC	TAAGATTCTT	AAGTCTGGTT	TCTAAGAGCT	TCTTCAATGT	CTCCAACTAT	180
CTTTTCAGGC	TCATGTTTGA	GACCTTCCTT	TCAAGAATAA	TTTGCTTGTG	ATCTGGTTCA	240
AGCTGAACAG	AGATTTTCAG	ATGACTCCCA	AACTATCTGC	AACACATCAG	CCCTATTAAC	300
TCTTCTCAGA	ATGCTCATAC	AGAAGCCATG	CCAGTGCACA	AAAGCCACTT	CTGACACCTG	360
GCCCTGTCTG	ACTCATGGAT	TTCTTCCAGG	ATTGCTCTTT	CTATCTGCTT	TAAACCTCCT	420
TGTCAATTGA	CTTTCCTTGG	CTCCCAACCC	ACTTTACTCG	AG		462

## (2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 535 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GAATTCGGCC TTCGTGGCCT	ANATATTCTA	AGCATTCAAT	TTGTCAGTTT	CTGAGATTTT	60
CTTTCCATCT TAGTTTTTTA	GAAGTCAGAA	AATGACTTTT	CACATTCAGT	TAGGGTATAT	120
AACAATGTTA ACGTAAGTTT					180
TAATGCTTTG AAATAGCATA					24.0
TATTTTACAG TCATTTGTAG					300
TCACCTTTAG TATATTACTO					360
AAATCCCTTG GTTTAGTGAT					420
CTTTGAGTAG TTCATGAAAA					480
AGGAAGTTCA AGGTAGGGAA					535

- (2) INFORMATION FOR SEQ ID NO:132:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 401 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GAATTCGGCC	TTCATGGCCT	AAGGGGATCA	TCAAAGATGT	TGGACACCTT	GTGTTCAAAT	60
CTTGGTTCAG	GTGCGGCCTG	TGCAGATCGG	CTTTTTGGTT	TGGTTGTCTT	GGCCTGGATA	120
CCAGTGGAGA						180
TTGGACTTTT	CTTTTGGTTT	TACAGTTAAG	TCAGCAAAGA	TATCAATGTT	ATCATCAAAT	240

AAATTAGATT CCAATGTTTT CTCCTTCTCT CTGGTTTTCT GAGAGGGTTT AATTGCTTCC GTAGCAAATA TATCATCCTC AAAAATATCT TGTGTTGTTA ATATGACATC CTGCTGACTA CTGGATTTTG TCTCATTCTT CTTGACTTTC TGATCCTCGA G	300 360 401
(2) INFORMATION FOR SEQ ID NO:133:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 497 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

(D) TOPOLOGY: linear

GAATTCGGCC	TTCATGGCCT	AGTAGATGAA	CTAGAAGATG	GATAAACGAA	GATAGATAAA	60
ATGAAGAAAA	ACAAAAGTCA	AGGAGAACTC	AGGCGTCCAA	GAGTGTGTAA	ACAACTTCTG	120
GTGTGAGACG	CGCTACATTG	CGCTAAATGG	CCTGTGCGCT	TCTGGTTTTT	CCCTTCCTCT	180
GTTGATTTTT	TATAGTTGTC	TTTTATTTTA	AACACGCCTC	CCCCCCCCT	TTTTAAACTG	240
ATTTTACCAT	CACTCTCTCT	AGCCCTGCCT	CCCTAGAATT	AGCTGCTTCT	TACCTCCCTT	. 300
GGATCTGGAA	CTTAAATATT	AACGTGTATA	TAAGTTAATA	GTAAGTAGAC	CGTGAATTTA	360
GAAGAGTAAA	ACAGAATCAT	GAGTACGTAG	TCACTGTGGC	CCCTTTTTTG	CTGGATTTCA	420
AGTTCGTAAG	CATTTTTGGA	AGAGAGTCGA	AGGGGAAGGG	GTGGCTTGCC	AGTCAGTTGA	480
GTGATGCATG	GCTCGAG					497

- (2) INFORMATION FOR SEQ ID NO:134:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 362 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAATTCGGCC	TTCATGGCCT	AGGCTGGTCA	TTGAGAGTGT	TGGTGCAGTC	AAACTGGAAC	60
ACGATGTGAT	TGGTAAACAT	GTGCTTGATA	CATCGAACAA	AATATTCTGT	CTCTGCTTCT	120
GTAAGTTGAA	CAGGCTCAGA	AGACTTGAAC	AAGGGTCCTA	TATTCAGAAA	CTCAGGAATG	180
GCAGCCAATT	GTTCTTGGGG	ATATATTTCT	AATGAAGTGC	TAGACTATCC	AATTACTTAA	240
TTTCTTATAC	CTTTAGATAA	TCAGTATGAA	AAGTTCCCAT	TTATAATGGA	AATGAAAATT	300
CTTAACTAAA						360
AG						362

- (2) INFORMATION FOR SEQ ID NO:135:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 377 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GAATTCGGCC TTCATGGCCT ACCCCAATCA ATGGATCCTC AACTCCAAAT CCAAAGATAG

WO 98/45437

PC1/US98/00950	
CATCTTCTGT CACTGCTGGA GTTGCCAGTT CACTCTCAGA AAAAATAGCC GACAGCATTG GAAATAACCG GCAAAATGCA CCATTGACTT CCATTCAAAT TCGTTTTATT CAGAACATGA TACAGGAAAC GTTGGATGAC TTTAGAGAAG CATGCCATAG GGACATTGTG AATTTGCAAG TGGAGATGAT TAAACAGTTT CATATGCAAC TGAATGAAAT GCATTCTTTG CTGGAAAGAT ACTCAGTGAA TGAAGGTTTA GTGGCTGAAA TTGAAAGACT ACGAGAAGAA AACAAAAGAT TATGGGCCCA CCTCGAG	120 180 240 300 360 377
(2) INFORMATION FOR SEQ ID NO:136:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 333 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:	
GAATTCGGCC TTCATGGCCT AAGCAAACTT CATGCAGCTG GTGGAACTAG ATGTGTCTCG AAATGAGATT CCTGAAATTC CAGAAAGCAT TTCATTCTGT AAAGCACTGC AGGTAGCTGA CTTCAGCGGA AACCCACTGA CTAGGTTGCC AGAAAGCTTT CCTGAATTAC AGAATTTAAC ATGTCTTTCT GTAAATGACA TCTCACTACA GTCTCTACCT GAAAATATTG GCAATCTTTA TAACCTGGCT TCACTGGAAC TGAGAGAGAA TCTTCTTACA TATCTTCCTG ACTCTCTTAC CCAGCTGCGA AGACTAGAAG AACTTGACTC GAG	60 120 180 240 300 333
(2) INFORMATION FOR SEQ ID NO:137:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 309 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:	
GAATTCGGCC AATGAAGCCT ACTTTAGTAT TTTGGCACTT CCTAATTGAC ACCTTGGGAG ACTGCAGGAA GGGAACGAGA ATCATTNNTA GGNTATTTGT GTGTGTGTG GGTTTTTTTTTT	60 120 180 240 300 309
(2) INFORMATION FOR SEQ ID NO:138:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 599 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:	

60 120

GAATTCGGCC AAAGAGGCCT AAACTCAGAA TGGTGCTACT TGAAGACTCT GGATCTGCTG ACTTCAGAAG ACATTTTGTC AACCTGAGTC CCTTCACCAT TACTGTGGTC TTACTTCTCA

GTGCCTGTTT	TGTCACCAGT	TCTCTTGGAG	GAACAGACAA	GGAGCTGAGG	CTAGTGGATG	180
GTGAAAACAA	GTGTAGCGGG	AGAGTGGAAG	TGAAAGTCCA	GGAGGAGTGG	GGAACGGTGT	240
GTAATAATGG	CTGGAGCATG	GAAGCGGTCT	CTGTGATTTG	TAACCAGCTG	GGATGTCCAA	300
CTGCTATCAA	AGCCCCTGGA	TGGGCTAATT	CCAGTGCAGG	TTCTGGACGC	ATTTGGATGG	360
ATCATGTTTC	TTGTCGTGGG	AATGAGTCAG	CTCTTTGGGA	TTGCAAACAT	GATGGATGGG	420
GAAAGCATTA	TTGCAATCAC	AATGAAGATG	CTGGCGTGAC	ATGTTCTGAT	GGATCAGATC	480
TGGAGCTAAG	ACTTAGAGGT	GGAGGCAGCC	GCTGTGCTGG	GACAGTTGAG	GTGGAGATTC	540
AGAGACTGTT	AGGGAAGGTG	TGTGACAGAG	GCTGGGGACT	GAAAGAAGCT	GAACTCGAG	599

- (2) INFORMATION FOR SEQ ID NO:139:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 541 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCGGCC	TTCATGGCCT	AACCTTCCTG	AATATCTGCC	GTTTGTCCTG	CAAGAAATAA	60
CTAGTCAACC	CAAAAGGCAG	TATCTTTTAC	TTCATTCCTT	GAAGGAAATT	ATTAGCTCTG	120
CATCAGTGGT	GGGCCTTAAA	CCATATGTTG	AAAACATCTG	GGCCTTATTA	CTAAAGCACT	180
GTGAGTGTGC	AGAGGAAGGA	ACCAGAAATG	TTGTTGCTGA	ATGTCTAGGA	AAACTCACTC	240
TAATTGATCC	AGAAACTCTC	CTTCCACGGC	TTAAGGGGTA	CTTGATATCA	GGCTCATCAT	300
ATGCCCGAAG	CTCAGTGGTT	ACGGCTGTGA	AATTTACAAT	TTCTGACCAT	CCACAACCTA	360
TTGATCCACT	GTTAAAGAAC	TGCATAGGTG	ATTTCCTAAA	AACTTTGGAA	GACCCAGATT	420
TGAATGTGAG	AAGAGTAGCC	TTGGTCACAT	TTAATTCAGC	AGCACATAAC	AAGCCATCAT	480
TAATAAGGGA	TCTATTGGAT	ACTGTTCTTC	CACATCTTTA	CAATGAAACA	AAAGTCTCGA	540
G						541

- (2) INFORMATION FOR SEQ ID NO:140:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 403 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTTCATGGCC	TAGTGGTTCT	TCTGAAATCG	GCCTTCAGAC	ACCTGTCTTT	GGTAGTACCA	60
ATATCTAAGA	AGTGGTTTCA	GTTCAATTTT	GTTTTCCTCC	ATGCCAGAGA	GAAGCCACAG	120
TTTCCTAAGC	TGGGGAGGAG	GTATATCCTT	CAAGAGATCG	GCTTGTTAGA	ATAGACCACT	180
TAACACCATA	TGAAAAAGCA	ACAGACTGAA	ACATGGATGT	CCTCAAGAAG	GGCTGCTGAC	240
ACCTATGATT	TGGCAAGGAG	ATAAATAACA	GAATGTGCAA	AGGGTCATAA	GAGTGCAGAC	300
ACCCTAATGT	CTGTTGGCTG	GAAGGTCAGA	GCAGTTCACC	AGTGAAAATG	GGTACGCCAT	360
GAAGGCCGGC	CTTCATGGCC	TATAGGCCAT	GAAGGCCGAA	TTC		403

- (2) INFORMATION FOR SEQ ID NO:141:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 439 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

PCT/US98/06956 WO 98/45437

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAATTCGGCC	TTCATGGCCT	AGTCCTCATC	TGCTGGCATT	TTGTGGGGTG	TTAGTGCCAA	60
ACTTGAATAG	GGGCTGGGGT	GCTGTCTTCC	ACTGACACCC	AAATCCAGAA	TCCCTGGTCT	120
TGAGTCCCCA	GAACTTTGCC	TCTTGACTGT	CCCTTCTCTT	CCTACCTCCA	TCCATGGAAA	180
ATTAGTTATT	TTCTGATCCT	TTCCCCTGCC	TGGTCTAGCT	CCTCTCCAAA	CAGCCATGCC	240
CTCCAAATGC	TAGAGACCTG	GGCCCTGAAC	CCTGTAGACA	GATGCCCTCA	GAATTGGGGC	300
ATGGGAGGG	GGCTGGGGGA	CCCCATGATT	CAGCCACGGA	CTCCAATGCC	CAGCTCCTCT	360
CCCCAAAACA	ATCCCGACAA	TCCCTTATCC	CTACCCCAAC	CCTTTGCGGC	TCTGTACACA	420
TTTTTAAACC	TGGCTCGAG					439

- (2) INFORMATION FOR SEQ ID NO:142:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 292 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCGATTGAAT	TCTAGACCTG	TGTGTCTAGC	TGTGATGGAA	TCTGAAATGA	AGTTTGACAA	60
GGACCATGAT	GGACTCATTG	AAAATGGAGG	CTATGCAGAC	CAGACCTATG	ATGGATGGGT	120
GACCACAGGC	CCCAGTGCTT	ACTGTGGAGG	GCTGTGGCTG	GCAGCTGTGG	CTGTGATGGT	180
CCAGATGGCT	GCTCTGTGTG	GGGCACAGGA	CATCCAGGAT	AAGTTTTCTT	CTATCCTCAG	240
CCGGGGCCAA	GAAGCCTATG	AGAGACTGCT	GTGGAATGGC	CGCTTACTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:143:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 457 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GAATTCGGCC	TTCATGGCCT	AGGGAGGCTG	AGGTGGGAGG	CTCACTGGAG	GCCAGGAGTT	60
CGGAACCAGC	CTGAGCAACA	TAGGGAGACC	TCAGCTCTAC	AACTGAAAAA	AAGATAGCCA	120
GGTGTGTTCA	TGGTGGCACC	TGTCTGTATT	CCAGCCGCTT	GGGAGGCTGA	GGCAGGAGGT	180
TTGCTTGAGT	CCAGGAGTTT	GAGGTTGCGG	TGAGCTACAC	AATGAGCTAT	GGTGGCACTA	240
CTACACTCCA	GCCTGGGCCA	TAGAGTAAGG	CCCTGTCTCT	AACTGGAAGT	CCAAAGAGGG	300
ATCTACTTCC	TAGACTATTA	ATTTAATAGA	TCAATAAATT	AATCAAGAAT	ATGATTTTTT	360
TCTCATCTTT	CTCTGTAGTC	ATATTTTATA	CAGACTTTTT	GTTTAAGTAA	TCTCTCTTTA	420
TGGGCAGACA	ATGATTTCAG	AAACACCCTG	CCTCGAG			457

- (2) INFORMATION FOR SEQ ID NO:144:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GAATTCGGCC TTC	ATGGCCT AGTCAGCCGT	GACTGCACCA	CCATACTCCA	GCCTGGGTGA	60
CAGAGCGAGA TCT	TGTCTTA AAACAAAACA	AAACAAAACC	CAGACTTCCT	ATAATTCCTA	120
AAAATAAATG TGG	GTTTGAG AGGCCTACCT	TGAAATGTAC	AAGATCCTGG	CCAGACTTCA	180
CCTATCTAAC AAT.	ATGCTAG TAACTATTTG	TTGACATGTC	TTAAAGAAAT	GTTCATCAGG	240
GCCTCAGAAA GCA	AGGCAGA GAACAGGTCC	CTGAAATTTA	CTAGCTTGCA	CCAAACCATC	300
AGATAAAGAT AGG	TTAATAT TTGACAGAAA	AAACTCTTCA	AAAAGAGACA	GTGAAATACT	360
CTTGAGATGA ATC	CAGGCGG CTCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:145:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 303 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAATTCGGCC	TTCATGGCCT	AGGCAGTGGA	GGCCTCTGTA	ATTCTAGCAT	ACAGGTGGCA	60
AGTTATTACA	TTATTTCTTT	CCTCCTGTCT	ACCTGCAGTT	GGTTTTATGT	GGGGCGTTAG	120
TACACTTCCC	AAAGGGCTTG	CCCGCAGGTG	AGAGGTGCAC	ATTGAACTCC	CTCACCAGGC	180
AGATGGGAAG	TGTGGCCATG	AGAGAGAGCT	TCAGGGGCCC	TGGGTTTATG	ACATCGCTGG	240
GCCAGGAATG	AGGTTAATAT	TTTTAATGGC	GAAGGGTGAG	CCCCGTTATT	ACCCGAGCTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:146:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 376 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAATTCGGCC TTCATC	GCCT ACTGGATGGC ATC	TACTTCG TATGACTATT	GCAGAGTGCC	60
CATGGAAGAC GGGGAT	RAAGC GCTGTAAGCT TCT	GCTGGGG ATAGGAATTC	TGGTGCTCCT	120
GATCATCGTG ATTCTC	GGGG TGCCCTTGAT TAT	CTTCACC ATCAAGGCCA	ACAGCGAGGC	180
CTGCCGGGAC GGCCT	rcggg cagtgatgga gtg	TCGCAAT GTCACCCATC	TCCTGCAACA	240
AGAGCTGACC GAGGCC	CCAGA AGGGCTTTCA GGA	TGTGGAG GCCCAGGCCG	CCACCTGCAA	300
CCACACTGTG ATGGC	CCTAA TGGCTTCCCT GGA	TGCAGAG AAGGCCCAAG	GACAAAAGAA	360
AGTGGAACAA CTCGAG	3			376

- (2) INFORMATION FOR SEQ ID NO:147:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 412 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GAATTCGGCC	TTCATGGCCT	AATGGAAAGG	ACAAGGAAAA	GGGAGAAGGG	GTGAGAGTCT	60
GTCCTAGGGG	CCAACGAGAA	CAGTGAGCTG	TTTCAGGGGA	GCCATTTCCT	TGTCCATGCT	120
CACAAGCCTG	TGGATTCTTC	CCCCTCTGCA	GGAAATTACC	TGATGTTCCA	AACCCCCTCC	180
AGATCCTGTA	TATCCGCAGC	ATCTCCCCTT	TCCCTGAGCT	GGAACAGTTT	CTACAGGACA	240
CTATCAAGAG	GTACTAGGGG	CCTGGAGGTT	TGGGCTCCAA	GAGAAGCTTG	ACAGAGCCCA	300
CGCCCGACCC	CTACTTCTGT	TTCTTCCTAA	GGTATAATCT	GCAGATGTTG	GAAGCTGAGG	360
GCAGCATGAA	GCAGGCCCTG	GGTGAACTGC	AGGCACAGCA	GCCCCCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:148:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GCCTGGCCAT	CCGGAGAGCT	AAGAACCTCA	GGCGGCTGCT	GTACGTNTCA	TGCAACCCCC	60
GGGCAGCCAT	GGGCAACTTT	GTGGACCTCT	GCAGAGCCCC	ATCTAACCGG	GTGAAGGGCA	120
TTCCCTTCCG	GCCGGTCAAG	GCTGTGGCAG	TGGACCTGTT	CCCGCAGACC	CCTTCTTTTT	180
TCATACTTAT	ATGAAAGACT	ACATACTTAA	AATACTGGTG	ATTATATTTA	GGACCTGAAA	240
TCATAAGATT	GTGGTCTTGC	TTTTTACTTA	TTTTTGTATC	TTAGCGATGT	CTAGAGTTAA	300
TAAGTGTTGC	TTTTCTAATC	ACAGCAAATC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:149:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GGATTCGGCC	TTCATGGCCT	AGTGGGGCAC	TAGGATCATC	ATTTGGGTGA	GAGCCCTCGG	60
CAATGGTGGA	GAGGGAGAAG	TTATCATTGT	GGAGCTCAGA	TGGGGTCCGG	AATTTGTTGG	120
TCCTACGCAG	CTTGGTATTC	TCCGTCTTGA	GCAGGTAGAG	CTTCTTGGCA	AAGAACACCG	180
TCATCATGAA	GAGCAGGAGC	AGGACGAGGG	CAGCCGAGCC	CACGGCCACG	CACATCACCT	240
GGAAGTCGGT	GATGATGGAC	TCGCAGCGCA	TCCCCTTGTG	CCAGATGTAG	TCCTGCGTGT	300
TGCACCTGCA	GAAGGCCCCT	ATGTTCTCCA	CCAGGTAGCA	CTGGCCGCCA	TTGTGACAGT	360
AACTTGGGAA	GAGGTCGCAC	ACTGACCGGC	AGGAGCCGTT	ATGCCGCACA	AAGCCACTGC	420
GGCACTCAGT	GCCATTTTCA	CTGGAGGCCA	AGTCCCTGCC	TGGCTCTCCT	TAGGCCATGA	480
AG						482

- (2) INFORMATION FOR SEQ ID NO:150:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 277 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTTCCTTACT	AACTTTAATG	GCCACAACAT	TTAGGCGAAA	GGGGGGCAAT	CATTGGTGGT	60
TTGGCATTCG	CAGAGACTTC	TGTCAGTTTC	TGCTTGAAAT	TTTCCCATTT	TTAAGAGAAT	120
ATGGGAACAT	TTCATATGAT	CTCCATCACG	AAGATAGTGA	AGATGCTGAA	GAAACATCAG	180
TTCCAGAAGC	TCCGAAAATT	GCTCCAATAT	TTGGAAAGAA	GGCCAGAGTA	GTTATAACCC	240
AGAGCCCTGG	GAAATACGTT	CCCCCCTCT	CCTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:151:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 272 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GCTCGCCCAC	TTTATGAAGA	GCGATTTCAC	GGCTGCTTGA	ACCATTCGAA	TTTGGATTTG	60
TGTTCAGCAC	TTTAAAAGGT	TCAACTTTTT	GCTTCTACCC	AGATTGGTCT	CAGGTCTGTC	120
TTCTCCAGAT	GACCGGTGGT	TTCCTGAGCT	GCATCTTGGG	CTTGGTGCTG	CCCCTGGCCT	180
ATGGCTTCCA	-GCCTGACCTG	GTGCTGGTGG	CGCTGGGGCC	TGGCCATGGC	CTGCAGGGCC	240
CCCACGCTGC	ACTCCTGGCT	ACAATACTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:152:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCGGCC TTCATC	GGCCT AGGGGCGGTG	AAACGTCCTG	AAGAGCGTCC	AGCTCGTGGC	60
CGAGAGGACT CGGGC	GCTCC CCACGCTGGA	GGCCGTGGAC	CGCTCCCTTT	AAAAGTTGAA	120
ACGGCCGCCG TTCGG	GACGG CCTGGCGGGA	GGAGGGCCCG	ACGAGGGGAG	GCTTCAGGGA	180
CAACTGGGGC TTCTC	GACGT CCACCCTTTT	CAGGGCGCGG	CCCCGGTAGC	CCTCGGGCCG	240
GCCCAGGTAC AGGAG	GTGCT TCCCGGGACC	CCCGGAGTAC	CTGGAGGGAC	CTCCCGAGGG	300
GACTCGAG					308

- (2) INFORMATION FOR SEQ ID NO:153:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 438 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCGGCC	TTCATGGCCT	ACAATCCCAA	ATGTAGGATC	ATGCCCATTG	CCCTAAGCCC	60
AGGCATGAGA	GTCGACATCT	CTCCTCTTAT	ATACAGATCC	AGTCCACAGG	TGAAGTGGGA	120
ACTCTCCAAC	CAGGATTCAG	CACACCATTG	ATGTTGCGAC	TCCTCTACTG	GAACACAGCT	180
TGGAGAAGGG	ATTGGGGCTC	TCATGGCAGG	ATGCAATCCA	CTGTTGAGAT	TGTGACTCAT	240
GCACTTGAAC	CTAAGTCTCA	GGAGTTGTTG	ACTCTTACAC	CCAGCACCCA	GGTGATAGGA	300
CTCTCATGTC	TGGTTCCTGC	CCACAGGTGA	AATTGTGACA	TATACATGGT	CACAGCTCAC	360
AGGTGAGGTG	ATAACTCACA	TACCTGGATC	CAGCTAAGAG	AACAGATTTT	GACTCTGATA	420
TCTTAGGCCA	TGAAGGCC					438

### (2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 297 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GAATTCGGCT	TCATGGCCTA	CAAGATGACT	AAAGTCTTCA	CTCACCAAGG	AAAAGTGGCT	60
CTGTATGGCA	AGCTGGTGCA	GTCAGCTCAG	AATGAGAGGG	AGAAACTTCA	AATAAAGATA	120
GATGAGATGG	ATAAAATACT	TAAGAAGATC	GATAACTGCC	TCACTGAGAT	GGAAACAGAA	180
ACTAAGAATT	TGGAGGATGA	AGAGAAAAAC	AATCCTGTGG	AAGAATGGGA	TTCTGAAATG	240
AGAGCTGCAG	AAAAAGAATT	GGAACAGCTG	AAAACTGAAG	AGGAGGATGC	TCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:155:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCGGCC	TTCATGGCCT	AAATTTAGGA	AGGTCAAACG	TGAATCTCCA	TTTGACAAAC	60
GTCCAACTGC	AGCAGAGATT	AAAGTGGAAC	CCACCACTGA	GTCATTGGAC	AAAGAGGGCA	120
AAGGTGAAAT	TAGAAGCCTA	GTGGAGCCAC	TCAGTATGAT	CCAATTTGAT	GATACTGCTG	180
AGCCACAGAA	AGGAAAAATA	AAAGGAAAGA	AACACCATAT	CTCTTCAGGA	ACTATCACAA	240
GCAAAGAAGA	AAAAACTGAA	GAGAAGGAAG	AGTTGACCAN	ACAAGTCAAG	TCTCATCAAC	300
TTGTTAAATC	ACTCTCAAGA	GTGGCTAAAG	AGACTTCAGA	ATCTACCAGA	GTTCTAGAAA	360
GTCCAGATGG	CAAAAGTGAA	CAGCGTAACC	TCGAG			395

- (2) INFORMATION FOR SEQ ID NO:156:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 422 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCGGCC TT	CATGGCCT ACAG	AGTACT GAGTG	GAACA TACGATO	ATA GATTTACAA	A 60
TAATGTAGCA TA	CTTCTACT TCAT	IGTATC TTAAG	TTTCT TGAAATA	TTG CTACTGGAG	A 120
TTGGAAAGAA AT	CTTAATGT TATG	GGTAT TGTCT	AAGAA GCTTTAT	TTT AAAACCATC	T 180
CATTAAATTT TO	TTGCATTT TAGA	FAATCG TCCCC	AGATG CCATGTT	ACC CTAGTGCAG	A 240
GTTTGGGGCT GG	ATAAGTTT TTGT	TGTAGG TGGCT	ATCCT GTGTTTT	GTA GGGTATTTA	.G 300
CAGCATCCTG GC	CTTAAAAC AAAA	ATGTTT TCAGA	CATTG CCAAATG	TCC CCCGAGCGG	T 360
AAAGTCACCC CC	AAGTTGAG AACC	CTCTA TACAA	AGAGC TGTTATI	'AGA GCCAGACTC	G 420
AG					422

- (2) INFORMATION FOR SEQ ID NO:157:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 492 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAATTCGGCC	TTCATGGCCT	AGATTGCTTG	AGGCCAGAAG	TTCAAGACAG	GCTGCCCAAC	60
ATAGTGAGAC	CCCCTTCTCT	ACCAAAATTT	TAAAAATGAG	CATGCATCTG	TAGTCCTAGC	120
TATTGGGAAG	GCTGAGGCAG	GAGGATCATC	TGAGCCCAGG	AGTTTGAGGC	TGCAGTGAGC	180
TAAGAAGGTG	CCACTGCACT	GCTGTTGTCT	CTCAGCAGAT	CATTTTCAGC	TTTCTTTGGA	240
GAGTAGCCAT	TAGCAATGCA	AATGTGAAGT	TTGATAGCAC	AATAAATAAA	ACACTGAAAA	300
CTGTAGATGT	TACTTATAAA	ACACTGGCAC	TCAGATAAAT	TGGGTTTGGT	CAAGAAGACA	360
GTGAAGCATA	TCCCTGTTGG	GCCAGAGGCT	GTTATCGTTT	TGCTCTGAAT	TCAAAACCTG	420
ATATGTCTCC	AAATTTGCTT	AGGGTTGTTA	TCCTGGAAAA	TAGAATCTGA	TAGAAGGTGG	480
GCACATCTCG	AG					492

- (2) INFORMATION FOR SEQ ID NO:158:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCGGCC T	TCATGGCCT	ACTGCTTTCG	TGAAGACAAG	ATGAAGTTCA	CAATTGTCTT	60
TGCTGGACTT C	TTGGAGTCT	TTCTAGCTCC	TGCCCTAGCT	AACTATAATA	TCAACGTCAA	120
TGATGACAAC A	ACAATGCTG	GAAGTGGGCA	GCAGTCAGTG	AGTGTCAACA	ATGAACACAA	180
TGTGGCCAAT G	TTGACAATA	ACAACGGATG	GGACTCCTGG	AATTCCATCT	GGGATTATGG	240
AAATGGCTTT G	CTGCAACCA	GACTCTTTCA	AAAGAAGACA	TGCATTGTGC	ACAAAATGAA	300
CAAGGAAGTC A	TGCCCTCCA	TTCAATCCCT	TGATGCACTG	GTCAAGGAAA	AGAAGCTTCA	360
GGGTAAGGGA C	CAGGAGGAC	CACCTCCCAA	GGGCCTGATG	TACTCAGTCA	ACCCAAACAA	420
AGTCGATGAC C	TGAGCAAGT	TCGGAAAAA	CATTGCAAAC	ATGTGTCGTG	GGATTCCAAC	480
ATACATGGCT C	AGGAGATGC	TCGAG				505

- (2) INFORMATION FOR SEQ ID NO:159:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 373 base pairs

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- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTCGGCC	AAAGAGGCCT	AGCCGGAGCA	GCTGTCTGGG	AGTCAAGGCT	GCAGTAGCGT	60
TTCTTCATGG	GGTGCTCCAG	GGGGTGCCAC	AGACCGACAG	GCAGCCCAAG	GGCCTGGACA	120
CCCCTCCCCA	GGCAGGTGCT	GCCCCAGGAG	GACTGTCCTC	GGGAATGAAC	CTCCCGCGGG	180
CTTTGGACTG	AGGTCCCTGT	GGCCTCGGTC	TCCTCCCCAT	GAAGTGGGAG	CGAGGCTCCC	240
CAATGGTGCT	TTTGGCTTTA	GTGTACGATG	TTTGCTGTGC	TTCCCGCCGT	GGAGGGCAGA	300
GCCACCCCAC	ATCAGGATCG	GACGTGCTAC	CCCTCCCGGT	CCCGGCCCTG	GCCCAGCCAG	360
CCCAGCCCTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:160:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 362 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GAATTCGGCA	AAGAGGCCTA	ATGAATTCTC	TGATCACAAA	ACAGACCCAG	GAAAGCATTC	60
AGCATTTTGA	GCGACAGGCA	GGGCTGAGAG	ATGCTGGCTA	CACACCCCAC	AAGGGCCTCA	120
CCACCGAGGA	GACCAAGTAC	CTTCGAGTGG	CCGAAGCACT	CCACAAACTA	AAGTTACAGA	180
GTGGAGAGGT	AACAAAAGAA	GAGAGGCAGC	CTGCATCAGC	CCAGTCCACC	CCAAGCACCA	240
CTCCGCACTC	TTCACCTAAG	CAGAGGCCCA	GGGGCTGGTT	CACTTCTGGT	TCTTCCACAG	300
CCTTACCTGG	CCCAAATCCT	AGCACCATGG	ACTCTGGAAG	TGGGGATAAG	GACGGGCTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:161:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 419 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAATTCGGCC AAAGAGGCCT	AGTTTTACAA	AACGCGATTT	GTAATATAAA	CTAGTTAGAT	60
AACTCAGAGG GTTTTATTGG	CCATATTTTT	GTTTATGCTT	TGTCACAGGC	TTTAGTCATT	120
GCTTCCATGT GTTTTCATCC	TTCAGGATAT	CTTCAAGAAG	CCTACTTATG	GACCAAACAA	180
GTTCTGACCA TCATGGAGAA	ATCTCTGGTC	TTGCTCAGGG	AGGTGACGGA	TGGCTCCCTC	240
TATGAAGGAG TTGCGTATGG	CAGCTACACC	ACTAGATCAC	TCTTCCAATA	CATGTTTCTC	300
GTCCAGAGGC ACTTCAACAT	CAACCACTTT	GGCCATCCGT	GGCTTAAACA	ACACTTTGCA	360
TTTATGTATA GAACCATCCT	GCCAGGTATA	GTGAGGAGTC	AGAAGTGTGA	AAACTCGAG	419

- (2) INFORMATION FOR SEQ ID NO:162:.
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:	
GAATTCGGCC AAAGAGGCCT ACAGGTAGTA TCTTTATAGC GGTATAAAAA CAGACTAATA CAAACAGGTA GCTCTAAATT GTGAGTTTTT CTTAACTCCT TTGATCTTCT GTGATAGCGA TTTTTCACAT TTCACACTTC CCTAATGCCA AAAATCCACC TCCAGCAGCT GTTTTGCCTC TTTCTTATCC TGCCCCTTGG AAGAATGTCA TCATTATTGC TGCCACAGCA CTGTGTTCTT TTTCAGAAGT TACAGCTCGA G	60 120 180 240 261
(2) INFORMATION FOR SEQ ID NO:163:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 108 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:	
GAATTCGGCC AAAGAGGCCT AGTGGTCTGG GGCAAAATTT AGTAAGACCT GGAAAGCATA GGTAATCAAA GCAGAAACTG ACAAATGAGA TGGTATCAAG CTAAAAAG	60 108
(2) INFORMATION FOR SEQ ID NO:164:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:	
GAATTCGGCC AAAGAGGCCT AGTTTAACCT CATCAGACAT TATTGCAGCC AGCTGTCAGC CAAGCTCAGT AACCTTCCAA CGCTCATTC CATGAGGCTA GAGTTCC1GA GAATCCTCTG TAGCCATGAG CATTACCTCA ATCTGAACCT TTTTTTTATG AATGCTGATA CTGCTCCAAC ATCTCCATAT CTTCCCAGAA CTCAAGCTCC TGCTCCAGCT TCCAGGACCA GAAGATCGCC AGCATGTTCG ATCTGACTTC CGAGTACCGC CAGCCCCTCG AG	60 120 180 240 292
(2) INFORMATION FOR SEQ ID NO:165:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 135 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:	
1.45	

GAATTCGGCC AAAGAGGCCT AGCAAAAACT GTTCAAAAGA GTTGTTGATT ACTTTCATTT	60
CCACTTTCTC ACCCCCATTC TCCCCTCAAT TAACTCTCCT TCATCCCCAT GATGCCATTA	
TGTGGATTCC TCGAG	135
(2) INFORMATION FOR SEQ ID NO:166:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 449 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:	
GAATTCGGCC AAAGAGGCCT AGAAAAAGTA GCACAGTGGA GTCTGAAATA GCAAGCGAAG	60
AGAAAAGCAG AGCTGCTGAG AGGAAAAGGA TTATTATTAA GATGGAGCCA GAAGATATTC	120
CTACAGATGA ACTGAAAGAC TTTAACATTA TTAAAGTTAC TGATAAAGAC TGTAATGAAT CCACTGACAA TGATGAATTA GAAGATGAAC CTGAAGAGCC ATTTTATAGA TACTATGTTG	180 240
AAGAAGATGT CAGCATAAAA AAAAGTGGTA GGAAAACTCT AAAACCTCGA ATGTCAGTAA	300
GTGCTGATGA AAGAGGTGGT TTAGAGAATA TGAGGCCCCC TAACAACAGC AGTCCAGTAC	360
AAGAGGATGC TGAAAATGCA TCTTGTGAGC TGTGTGGACT TACAATAACC GAGGAGGACC	420
TGTCATCTCA TTACTTAGCC AAACTCGAG	449
(2) INFORMATION FOR SEQ ID NO:167:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 565 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:	
GAATTCGGCC AAAGAGGCCT AAAAGGAAAC TTGGACAAGT AGAAAGTGGA TGACCCAGGC	60
TCCGTTACAT ATACTTGGAT TCCAGCTGGG ACCTAGATTT GCTGAGGACG GAAGCCAAGG	120
AGACAGGAAC ATGTGGCTGC TCCCAGCTCT ACTCCTTCTC TGCCTCTCAG GCTGTTTGTC	180
TCTGAACGGC CCCGGCTCTG TGACTGGCAC TGCGGGGGAC TCTCTGACAG TGTGGTGTCA	240
GTATGAGAGC ATGTACAAGG GATATAACAA GTACTGGTGC CGAGGACAGT ACGACACGTC	300
ATGTGAGAGC ATTGTGGAGA CCAAGGGAGA AGAGAAGGTG GAGAGGAATG GCCGCGTGTC	360
CATCAGAGAC CACCCGGAGG CTCTCGCCTT CACTGTGACC ATGCAGAACC TCAATGAAGA	420
TGATGCTGGA TCTTACTGGT GCAAAATTCA GACAGTGTGG GTCCTGGATT CATGGTCACG	480 540
CGATCCCTCG GACCTGGTTA GGGTGTATGT TTCCCCAGCA ATTACAACCC CAAGGAGGAC	565
CACACATCCÁ GCCACCCCGC TCGAG	505
(2) INFORMATION FOR SEQ ID NO:168:	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 158 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCGGCC AAAGAGGCCT AGTTTCCTTT ATATGTTTGC ACTTAATTTG ATTCCATCCT TCATGCTGTT TTCATTATTC TTAGTTCATC TACACCACAT AAATTATCAC CTTTGTTTTC AGTTCCCCAA TTTCCATGTG CCACAAACAA ATCTCGAG	60 120 158
(2) INFORMATION FOR SEQ ID NO:169:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 383 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:	
GAATTCGGCC AAAGAGGCCT AGTCTCACCA TCTATTCTAA ACCTTATATT ATCAATCCTA TTCCCTCTCA CCAAAAGAAT CCCTTTATAC AAGTAATTAT CCTGTCTATG TCTTTCAACT CTAGTTTCCC CACTGCAACT CTTCCCTTAA TATATGTACC TGCTCTGTTA TCCCTCCA GCTACTTCCC TATTTTCTGT TCCCCTTTAC AGGAAAACTT TTCTCCAGCA TTTCCCAATG CCATTGTCTT ACTTCCTCAC ATTCTATTT CTTCTCAAAC CATTTTTATT AGGCTTCTTT CCCCAATGGC TATTGTCAAG CTTCACTTAA TGCCGTGCAA ATCACCCTAT TCTCCAGGTC TTCTTTCTTC CCAGTCTCTC GAG	60 120 180 240 300 360 383
(2) INFORMATION FOR SEQ ID NO:170:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 282 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:	
GAATTCGGCC AAAGAGGCCT AAATATTGTC TGAAAAAAAT ATATGAGACC CATTACTCAG TCTCTCCTCC TGCCATTAT ACTGCAGGTA TTCCCCAAGT TTCTCTTCTC	60 120 180 240 282
(2) INFORMATION FOR SEQ ID NO:171:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 350 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:	
GAATTCGGCC AAAGAGGCCT AGTGGAAGAG AAGAATGTTT CTGTCTCTTC CTACGTTGAC TGTTCTTATT CCACTGGTTT CTTTAGCAGG ACTGTTCTAC TCAGCCTCTG TGGAAGAAAA CTTCCCACAG GGCTGCACTA GCACAGCCAG CCTTTGCTTT TACAGCCTGC TCTTGCCTAT TACCATACCA GTGTATGTAT TCTTCCACCT TTGGACTTGG ATGGGTATTA AACTCTTCAG	60 120 180 240

	GCATAATTGA TGCAACTAGA GTCAATATGC TGTATATATT AATGATAGCT CTTGGGCATC GATCTCTGAA AGCTCAAATG GATGGAATTT AGTTTGCGGG AACTCTCGAG	300 350
	(2) INFORMATION FOR SEQ ID NO:172:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 140 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:	
7	GAATTCGGCC AAAGAGGCCT AGGGGTGTAC ATTTTATTGG AAACCTTAAA TACTGTTCAG AAAGAATATA TCTTCAATCA AGGCTCTTGT GCAGCCTACA CAGAAAAATG AAGCTTTTTG GGTTAGGTGC AACGCTCGAG	60 120 140
	(2) INFORMATION FOR SEQ ID NO:173:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:	
(	GTGGTCTCTC CTCCCCTGCC ACTCCCCTCT TCTTTTTTT CCAACATGGC CTTGCTCCGC GTACATCGCC ACCCAGGGAC CGCTGCCCGC CACCGTGGCT GACTTTTGGC AGATGGTGTG GGAGAGCGGC TGCGTGGTGA TCGTCATGCT GACACCCCTC GCGGAGAACG GCGTCCGGCA GTGCTACCAC TACTGGCCGG ATGAAGGCTC CAATCTCTAC CACATCTATG AGGTGAACCT GGGTCTCCGAG CACATCTGGT GTGAGGACTT CCTGGTGAGG AGCTTCTATC TGAAGAACCT CGAG	60 120 180 240 300 304
	(2) INFORMATION FOR SEQ ID NO:174:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 188 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:	•
<u>;</u>	GCGATTGAAT TCTAGACCTG CCTCTCTTAT ACCTCGGTGT GGCCGAAAGG AAATAAGCAG AGGCGCTATT GGCAGGACCT AGAAACTTTC CTTGTAACAT AGCTAGTATG TTCCCTCTGC CCCTTCTTCA TCTTTTCCTC ACACTTGCTG GAGCTGGAGC AGCTATCCTG ACCGCAGGTG CACTCGAG	60 120 180 188
	(2) INFORMATION FOR SEQ ID NO:175:	

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GAATTCGGCC	TTCATGGCCT	ACTATCTGCC	TTGCGCTCCC	ACTGCCCTGA	CCTGTGCCCT	60
CTCACAGGCC	CCCGTGATGG	CTCGCTGGCC	TCCCTTCGGC	CTCTGCCTCC	TCCTGCTGCT	120
GCTGTCCCCA	CCGCCACTGC	CCTTGACAGG	GGCCCATCGC	TTCTCCGCAC	CTAATACCAC	180
TCTCAACCAC	TTGGCACTGG	CACCTGGCCG	AGGCACACTC	TATGTCGGCG	CAGTGAACCG	240
CCTCTTCCAG	CTCAGCCCCG	AGCTGCAGCT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:176:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GGTCAGCCGA	GCATGATAGG	AGACATCATC	AACCTCGGCC	TGAAAGGGAG	GGAGGGGAGA	60
GCAAAGGTCG	TCAACGTGGA	GATCGTGGAG	GAGCCCGTGA	GTTATGTCAG	CGGGGAGAAG	120
CCGGAGGAGT	TTTCCGTCCC	ATTCAAAGTG	GAGGAGGTCG	AAGATGTGTC	GCCAGGCCCC	180
TGGGGGTTGG	TTAAGGAGGA	GGAAGGTTAT	GGAGAAAGCG	ATGTCACATT	CTCAGTTAAT	240
CAGCATCGAA	GGACCAAGCA	GCCTCAGGAG	AACACGACTC	ACGTGGAAGA	AGTGACAGAG	300
GCAGGTGATT	CAGTGGGCGA	GCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:177:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 408 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTCGGCC	AAAGAGGCCT	AAGCAATGTC	TCCACCACTG	CTGCTGCTAC	CCTTGCTGCT	60
GCTGCTGCCT	CTGCTGAATG	TGGAGCCTGC	TGGGGCCACA	CTGATCCGGA	TCCCTCTTCG	120
TCAAGTCCAC	CCTGGACGCA	GGACCCTGAA	CTACTGAGGG	GATGGGGAAA	ACCAGCAGAG	180
CTCCCCAAGT	TGGGGGCCCC	ATCCCCTGGG	GACAAGCCTG	CCTCGGTACC	TCTCTCCAAA	240
TTCCTGGATG	CCCAGTATTT	TGGGGAAATT	GGGCTGGGAA	CGCCTCCACA	AAACTTCACT	300
GTTGCCTTTG	ACACTGGCTC	CTCCAATCTC	TGGGTCCCGT	CCAGGAGATG	CCACTTCTTC	360
AGTGTGCCCT	GCTGGTTCCA	CCACCGCTTC	AATCCCAATG	TCCTCGAG		408

- (2) INFORMATION FOR SEQ ID NO:178:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 305 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GAATTCGGCC AAAGA	AGGCCT AGGAGGAATT	TCCATCTTGC	TCTCAAAGTG	AGTCTGAATG	60
TGCTCGGTGG TGTC	ACCCCC GCCGAGCTGC	CAGTGCAGAA	GGCCACTATT	GAACTCCTGC	120
ACACGCCCCA ACTTO	GTCAGA TCGGTCAACA	ACAAACAGGT	TGTTCTTTTT	GACTATCTTT	180
ATTGGCAGCT TGTC	GAACTT ACTGGCTTGC	TTGGGCTTCT	CCTTTGGGTC	TGCAGCGGCG	240
TCCGGGGCAG TCAG	AGCGAT GCTGCTCTTT	TCATCGCTTT	CTGTCTTCTC	GCTGTCTACC	300
TCGAG					305

- (2) INFORMATION FOR SEQ ID NO:179:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 247 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAATTCGGCC AAAGAGGCCT AGTGCAGCAA	TTTAGAGAGT	GTCTCAGGAG	TGTGGCTCAC	60
TGGCAGCTGC AGCTATGTTA GTGCTTCTTT	CTGCCTCAAG	TTCAGAAACA	AGCTGGACTA	120
TCTCAGGGTG ATTGAATTTT CCTGCTGTGG	AATCATAGAA	GTCTTGCAGT	CTCCCAGGTT	180
TGTGTTCAAG GTCTTCATAT TCAGATGCTT	GAAGAATCAT	TTCACATTGG	TCTAGCATTC	240
AATCGAG				247

- (2) INFORMATION FOR SEQ ID NO:180:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 315 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GAATTCGGCC AAAGAGGCCT	AGTCAAGTTC	ATTTCCCAGA	GTCTTAAGAC	TAAGTTCTGC	60
CTCCTCATTG CAGGTGTGCC	GAGAGTTTTT	TTTGAACAAC	AAAAATTACT	AAGGAACCTC	120
ACTACCTTTG GCGGTAGAAT	TAGAAAACAG	ATTCAGCAGT	CACCTACTCC	CCTTCAGTAA	180
TTCGAGACAA TTATTTTCT	CCTGACACAA	CATCAGGTCC	CATGAAAAAT	GACACCGTGC	240
CTGGTGTTTT TGGGTTCTTT	AATGCTTCTT	TTAGAGCCAC	ATTTTTCTTT	TCAAACCGAG	300
TTCCCATCGC TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:181:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCGGCC	AAAGAGGCCT	AATTTTTCTT	CACGTTCTTT	ATCACCACCA	TGGTTATGTT	60
GGCTGCCCTG	GCTCACCATT	TGTTTTACTG	GGATGTTTGG	TTTATATATA	ATGTGTGTTT	120
AGCTAAGGTA	AAAGGCTACA	GGTCTCTTTC	CACATCCCAA	ACTTTCTATG	ATGCTTACAT	180
TTCTTATGAC	ACCAAAGATG	CCTCTGTTAC	TGACTGGGTG	ATAAATGAGC	TGCGCTACCA	240
CCTTGAAGAG	AGCCGAGACA	AAAACGTTCT	CCTTTGTCTA	GAGGAGAGGG	ATTGGGACCC	300
GGGATTGGCC	ATCATCGACA	ACCTCGAG				328

- (2) INFORMATION FOR SEQ ID NO:182:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 123 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GAATTCGGCC AAAGAGGCCT AGTTGTGGAA AAGAAAGACT GTGAGGGTAG GCACAAGAGC 60
ACTCAAATGT CCCAGGTAGA GAAAACAACA TGTATGATGG CCCAGAAGGA GGCAAGTCTC 120
GAG 123

- (2) INFORMATION FOR SEQ ID NO:183:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 311 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC	AAAGAGGCCT	ACTTGGACAA	GTAGAAAGTG	GATGACCCAG	GCTCCGTTAC	60
ATATACTTGG	ATTCCAGCTG	GGACCTAGAT	TTGCTGAGGA	CGGAAGCCAA	GGACACAGGA	120
ACATGTGGCT	GCTCCCAGCT	CTACTCCTTC	TCTGCCTCTC	AGGCTGTTTG	TCTCTGAAGG	180
GCCCGGCTC	TGTGACTGGC	ACTGCGGGGG	ACTCTCTGAC	AGTGTGGTGT	CAGTATGAGA	240
GCATGTACAA	GGGATATAAC	AAGTACTGGT	GCCGAGGACA	GTACGACACG	TCATGTGAGA	300
GCTCACTCGA	G					311

- (2) INFORMATION FOR SEQ ID NO:184:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 130 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC AAAGAGGCCT AGTTCAATCT GTAACAAGCC TTCTTCAATT TCCTCTCCAC
ATACCCTGCA TAGACTTTAA GATTCCTCTG CTCGATGCTA ATAAGAAGAC ACACACCCCT
120

CGTTCTCGAG 130

- (2) INFORMATION FOR SEQ ID NO:185:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 416 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GAATTCGGCC A	AAAGAGGCCT	AGGAGGGGGA	AGAGAGTCCG	TTTTGCAGAA	GATGAAGAAA	60
AGAGTGAAAA T	TTCCTCGGAG	GACGGTGACA	TAACGGATAA	GAGTCTTTGT	GGAAGTGGTG	120
AAAAGTACAT C	CCCACCTCAT	GTGAGGCAAG	CTGAGGAGAC	AGTGGACTTC	AAGAAAAAGG	180
AAGAACTAGA A	AAGC TTGAAG	AAACATGTAA	AAGGTCTACT	TAACAGGTTG	AGTGAACCCA	240
ACATGGCTTC C	CATCAGTGGG	CAGCTGGAGG	AACTGTACAT	GGCCCACAGC	AGAAAGGACA	300
TGAATGACAC (	CCTGACCTCC	GCTCTCATGG	GTGCCTGCGT	CACTGCCTCG	GCCATGCCCA	360
GCAGACTGAT C	GATGGAGCAT	GTTCTCTTAG	TCAGCATCCT	TCACCACTTA	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:186:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC	AAAGAGGCCT	ACTACATTTT	TACCTAAATT	TATAGAAAAT	CAATTCGGAT	60
			GGGCTGTTTT			120
			AATTCAGAAT			180
			TTACGCTGAG			240
			CTGAATCATA			300
			GTAACGTACT			344

- (2) INFORMATION FOR SEQ ID NO:187:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 488 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCA	AGAGCCTAAA	ATCTACAAGC	ACCAGGAAGT	CAAGATGCAA	GCACCAGCCT	60
TCAGGGACAA	GAAACAGGGG	GTCTCAGCCA	AGAATCAAGG	TGCCCATGAC	CCAGACTATG	120
			ACCATGCAAA			180
CGAGCCAAGT	CCCAGCCCAG	TGCAGGCCGC	CCTCAGACTC	CACCCAGGTC	CCCTGCTGGT	240
TGTACAGAGC	CATCCTGAGC	CTGTACATCC	TCCTGGCCCT	GGCCTTTGTC	CTCTGCATCA	300
TCCTGTCAGC	CTTCATCATG	GTGAAGAATG	CTGAGATGTC	CAAGGAGCTG	CTGGGCTTTA	360

AAAGGGAGCT TTGGAATGTC TCAAACTCCG TACAAGCATG CGAAGAGAGA CAGAAGAGAG GCTGGGATTC CGTTCAGCAG AGCATCACCA TGGTCAGGAG CAAGATTGAT AGATTAGAGC GACTCGAG	420 480 488
(2) INFORMATION FOR SEQ ID NO:188:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 163 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:	
GAATTCGGCC AAAGAGGCCT AGGTCAGATG CATTAAAACA TATCAAAATG TTACAAAAAT GTATGGCTCC CTTGCTGAGG CCCTGTCAGA TTATGTTAGA TGAGTAAACG CATCAGTGTG TAAGTTCAGA ACCAAACGTT GAATCAAGTC ATGTACTCTC GAG	60 120 163
(2) INFORMATION FOR SEQ ID NO:189:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 310 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:	
GAATTCGGCC AAAGAGGCCT ACCTGCTCAT ACCTGTGGCC AAAAGCATGA TGCCCCAGGC TCTGCCTCCA ATTCTACCAT CTTCTTCCAT CTTTCTCTTT TATCAGGTCT CTGCCCTCCT GTACTTTGTA CTTAGATTCT CCTCTGCCAA GCCCATTCAG ACTGTGACTG GTAGGAGTGC TGTGCTCAGC TTTCCACTTG AGTGTTTATC CAAGAAGTTG GATAACCCTC TCAAGTTATG GCCTCCATTC CAGTGCGCCT CAGTCTATGG GGATGCATTC CACTCACCCT TGGGCCTAGG GCAGGTCGAG	60 120 180 240 300 310
(2) INFORMATION FOR SEQ ID NO:190:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 516 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:	
GAATTCGGCC TTCATGGCCT AGGGCCTCAG TCTTTTTACT TTTGCGGCTG TGTTTCTCTG AAGGCTTGGC ATTAGTAGAT TGAAAAGAAT AACCATCTAG GGAAATGTGA ATTCAGTTTC TTTCTGACAT TCTGCTCTCT ACAAGGGGAT ATTATGTACA CATAAACCTA CTTCCAAAAT AATGAAGTGA GGCCTAATTC CTTACTCTTC AGGAGGCCCA CTGTGGGAGG GTCACTGACC TTGTGTATGG GCTGCCCTTC ATGGCTCTG GAGTCATTAT AAAGGGCAGC ATTTGGCGTG GTGCGTCCTA AGCCAGTGTT TCTCGGCTCT GTTCCTTAAA CATGTGTTAG TGTTAATAGA TGTTCTTGGA AAAAAAAAAA AAAAAACAGC ATTCTGAGGT CAAACATGCT CAGAAAGCTT	60 120 180 240 300 360 420
GGAATCTGCA CTACGCTTCT CGTACACATT TCATATTAAA GATTTTGGAA AGTCCTGCAA	

WO 98/45437	PCT/US98/06956	<b>i</b>
TACAGAGCCC	TGTCTAATAT TGCCACAGCC CTCGAG	516
(2) INFORM	ATION FOR SEQ ID NO:191:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 319 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:191:	
CCAGTTTATT GCAGAGATTG CTCACCACTG	TTCATGGCCT ACTTGCTAGA TAGACAGATT AAGAATGTTG AAGACATGGT AATAACATTT TGGATGGCAC AGTAGAAGCC CAAGGAGGTG ATAGCATTTT AAAAGAATAG TATTTGATGC CAAATCTACT ATTGTGTCTA TATTCAAGAG ATGGGCTGCT TTCTCTTTGG CCTGCCACIG GGTGTCATCA GTATCATGTG TACACAGCCG ACACAGATGG AGGTTATATA GAAGAACGAT ATGAAGTGTC AATCTCGAG	60 120 180 240 300 319
(2) INFORM	ATION FOR SEQ ID NO:192:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 382 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:192:	
GGTAAAGAT AGTGGTCTCC TTATCTTTAT ACAGTTTAAT CATATCCTCA	TTCATGGCCT AAGCAGAAGG ACATATTAGA GAAGGATTGT ATAGTTTTCT GACAGTGAAT TGTATGGGCG ATGGATTAGC CGTGGAAGGT GTTGAGTATA AGCCAAACTC TATGGTTACT GGAATAAGAG AGTAGGAACC TTCTCAGGCT CTATTCTTGT CAACAGTATG TACATGTGC CCCCAGCCCC AAATAACTGT GATGTTCACT CTATACAGTT CCCAGAATCC ATTGGAAAATT GCTGTAACAG ATGCCCATCA ATTCTCCACG TCCAACTTCT CCATGGCCTC CTCTGCCTCT GAACTTCTCG AG	60 120 180 240 300 360 382
(2) INFORM	ATION FOR SEQ ID NO:193:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 474 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
· (xi)	SEQUENCE DESCRIPTION: SEQ ID NO:193:	

CAGGCAGGCT TAAGAGACAG GAAACATTTA GCATGTTGGT AAACCACTTT AGCACATCAG CAAAAGCATA TAAACAGCTT TAGGATTGGA AATTATTGCC AGGGGGGACT CGAG

(2) INFORMATION FOR SEQ ID NO:194:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 499 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:	
GAATTCGGCC TTCATGGCCT ACGTNNCTAT GTCTTCAAGC ACAGAGGTGT CCAGGTGTAT TGCACATCTT CATCGCACTG AGCTGCATGG ACAGCTGATT TCTGTGGAAA AAGTATAAGG TGATCCCTCT CAGAAAGAAA TGAAGAAGA AAATGATGAA AAGAGTAGTT CAAGAAGTTC TGGAGATAAA AAAAATACGA GTGATAGAAG TAGCAAGACC CAAGCCCTCTG TCAAAAAAGA AGGAAAAGA TCGTCTGAGA AATCTGAAAA AAAAGAAAGC AAGGATACTA AGAAATAGA AGGTAAAGAT GAGAAGAATG ATAATGGAGC AAGTGCCAA ACATCAGAAT CGATTAAAAA AAGTGAAGAA AAGAAGCGAA TAAGTTCCAA GAGTCCAGGA CATATGGTAA TACTAGACCA AACTAAAAGGA GATCATTGTA GACCATCAAG AAGAGGAAGA TATGAGAAAA TTCATGGAAG AAGTAAAGCAA ATGCTCGAG	60 120 180 240 300 360 420 480 499
(2) INFORMATION FOR SEQ ID NO:195:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 337 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:	
GAATTCGGCC TTCATGGCCT AAGCAAAAGA GCATTAAGAA GTGTCTGTTT TTGTTATTGC CATTTCATAA ATATTTTAGT AGGTGTTCAA TTTCATTGGA TATTCTTTTT TTTTAATTGT CTTTGTACCT ATGATTGAAA ACAGTAGTTG GTCTATGACT TTTGAGGAGA GGGAGAACCG AAGATTACAG GAGGCCAGCA TGAGGTTGGA ACAAGAGAAT GATGACCTTG CCCATGAACT AGTAACAAGC AAAATTGCTC TACGGAATGA CTTGGATCAG GCAGAAGACA AGGCAGATGT GTTGAATAAA GAGCTCCTTT TGACCAAAAC CCTCGAG	60 120 180 240 300 337
(2) INFORMATION FOR SEQ ID NO:196:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 386 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:	,
GAATTCGGCT TCATGGCCTA AAGGAAACTG ACAAATTATC CCCAGCTGCC AGAAGAAGAA ATCCTCACTG GACGGCTTCC TGTTTCCTGT GGTTCATTAT CTGATTGGCT GCAGGGATGA AAGTTTTTAA GTTCATAGGA CTGATGATCC TCCTCACCTC TGCGTTTTCA GCCGGTTCAG	60 120 180

PC1/0598/00950	
GACAAAGTCC AATGACTGTG CTGTGCTCCA TAGACTGGTT CATGGTCACA GTGCACCCCT TCATGCTAAA CAACGATGTG TGTGTACACT TTCATGAACT ACACTTGGGC CTGGGTTGCC CCCCAAACCA TGTTCAGCCA CACGCCTACC AGTTCACCTA CCGTGTTACT GAATGTGGCA TCAGGGCCAA AGCTGTCATC CTCGAG	240 300 360 386
(2) INFORMATION FOR SEQ ID NO:197:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 429 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:	
GAATTCGGCC TTCATGGCCT AGTTTTGTC TTTTTCTT TTTTGGTATT ATTTTGTTTG CCACTTATTC CTAAAATTCA TATTGCTATT AACCGTACAC ATCTTTCCAT GTTCTTATAA TAATCTACAA ACATCTCTCC CTTTCTGTAG CTCTCTCTGT CACACACACA CACATGCACA CACACACACA CACACACAC CACACGCTGT GCACTCTCCT GAAGCATGTG TGTACATACA TACATATGTG AGGGGTTTTA TGACTGTTTT ACCAAAATTGT GTTCTTAATA TATACAATGT TGGCTTCTTT TTAGCCATTC AGAAGTTATT TCAGTCATGG AATGATCTCT AGCCATATAA CTGAAAACAG GTAAGTTTCT TTCTTGGGGA AGAAGGGCGA ATGGTGATAG AGAAAATGGA GAGCTCGAG	60 120 180 240 300 360 420 429
(2) INFORMATION FOR SEQ ID NO:198:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 349 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:	
GAATTCGGCC TTCATGGCCT ACCAAGCTAT GCAGGAACAG TTGTCTAAGA ACAAAGAACT GACACAGAAA CTCCAGGTAG CCTCTGAGAG TGAGGAAGAG GAGGAGGCA CAGAAGATGT GGAAGAACTC CTTGTCCCTG ATGTAGTGAA TGAAGTGCAG ATGAATGCAG ATGGGCCGAA TCCCTGGATG CTCAGGAGCT GCACCAGTGA CACCAAAGAA GCTGCAACCC AGGAGGACCC TGAGCAACTG CCAGAGCTTG AGGCCCATGG AGTTTCTGAA AGTGAGGGAG AAGAAAGACC AGTGGCAGAA GAAGAAATTT TGTTGAGAGA ATTTGAAGAA AGGCTCGAG	60 120 180 240 300 349
(2) INFORMATION FOR SEQ ID NO:199:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:	
GAATTCGGCC TTCATGGCCT AGGGAAAGCT CCAACTTGCT TTACCTTTCT AAGATATCCC	60

120

GAATTCGGCC TTCATGGCCT AGGGAAAGCT CCAACTTGCT TTACCTTTCT AAGATATCCC ATTTTCTCTA TACCATTGT TGACTAATAT ATCTCTTGCC CACTGGTTTG TAACAGTGCC

TTAATTAGTT TTTGTGTTTG AAGTTCCAGA ATCTCTTCCT GGCCTATGTA TTGTGTTCCG TTGATGGATC TTTCCATCCC ATGGTACCCT TTACTATTAT TGTCTTCATT TTTATTACTA TTGTTATGCC CTTTTCTCTC TCCGTGCACA TCTTCATGTT TGAACTCTAA AAACACACCG CCAACGCTCG AG	180 240 300 312
(2) INFORMATION FOR SEQ ID NO:200:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 385 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:	
GAATTCGGCC TTCATGGCCT AATATATCCA AGTAATAGCA TGTACAGTTT GGTAAGCAAT ATAATAGAGA GATATTCACA GTGAAATAGG AAAGAGCAGT ATAGGTGCAA AGACAAAAAG CATGACACAG CTAGATACAG GGCAGCTGTT ATTGGTTTTG TATGGAGAAA ACCTGGAGAA ATGGTGAGAG AAGGGGCAGA CAGATGAGAGG GGCCAGATCA TGGAGTACCT GTTTGTGGCG CTCAGGAGTT TAGATGTTAT CATGCAGATA ACTAGGAGCC ATTTGAGGAA CTTAAATACA GGAGTGATAC CAGATTTATA TGTTTTTAAA ATGATTACTT GGTGGTAATT AAAGAAAAGA	60 120 180 240 300 360 385
(2) INFORMATION FOR SEQ ID NO:201:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 204 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:	
AATTCGGCCT TCATGGCCTA CGTTTTTTA AATTTTTTA ACTACATATT TGATACGATC TTTTCCTTCT TGCCTTCTTT TTGATACTT ACTTCTACC ATTCTATGTT TTTCGTCACT AGTTTGAAAA TTGTATACTT TGTTTTTATT CTTTCAGTGG TTACCCTAGA AATTACAACA AACAAAAATT GCAACAACCT CGAG	60 120 180 204
(2) INFORMATION FOR SEQ ID NO:202:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 450 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:	
GAATTCGGCC TTCATGGCCT AAAATCATCA TGCATATTTA TTTCTCCAAA GCACCTTTGA CAAGCATGAT TTGGATAGAG ACTGTGCTTT GTCACCTGAT GAGCTTAAAG ATTTATTTAA AGTTTTCCCT TACATACCTT GGGGGCCAGA TGTGAATAAC ACAGTTTGTA CCAATGAAAG AGGCTGGATA ACCTACCAGG GATTCCTTTC CCAGTGACG CTCACGACTT ATTTAGATGT ACAGCGGTGC CTGGAATATT TGGGCTATCT AGGCTATTCA ATATTGACTG AGCAAGAGTC	60 120 180 240 300

WO 98/45437

PCT/US98/06956	
TCAAGCTTCA GCTGTTACAG TGACAAGAGA TAAAAAGATA GACCTGCAGA AAAAACAAAC TCAAAGAAAT GTGTTCAGAT GTAATGTAAT TGGAGTGAAA AACTGTGGGA AAAGAGAGT TCTTCAGGCT CTTCTTGGAG AAGACTCGAG	360 420 450
(2) INFORMATION FOR SEQ ID NO:203:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 558 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:	
GAATTCGGCC TTCATGGCCT AACTGGTTTC TGGCTCGTGG ANTCTGTTTC AAGATCATAT AAGCCGTTGC CATTCCCAAG NAGCGCTGGG ATATGCTCCT TCTCAGATGC TGCTATTTCA GTGAAGGTAT TTAATGCTTG TTCAACATTA GATTTCTGTT TGGTAGCCAT TAAGCAATAG TTTTCCATTA TGCGAANCTG TACGTGACCC TGAACAGTCT GAGGTTTTAG TTCCTTAANA AGTTTTTCTG CTGTTCTTAC TGCCAGTTGC ACAGATTCTT GCTTCTCAGT TGAATAACCC AGGTCTCCAT CCAGGTTTTC AAATACTTCA CCTCCAACAG TTTCATTATC TGGATTCAAA CAGATCTCTA TCATATTATA AAGGGCATTT TGGCCCCAGT CACGATCTTT CCGAGCTTTA TTAAAATGTC GAAGGGCATC ATTTGGTTCT CCAGTGTACC AAAGATACAG TCCTTTACAA TACTGAAATC CTGGTTCCAA TTTTGCTCTG GAGNNACGTT TCTCAGCCAT TGAGAAAAAT CTTGGGACAT CCCTCGAG  (2) INFORMATION FOR SEQ ID NO:204:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 348 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	60 120 180 240 300 360 420 480 540 558
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:	
GAATTCGGCC TTCATGGCCT ACAAGTAGGG ACTGACTTCT CTAGGTTCCT ACAAAGCTCT TCAACCACAC TCATTTCAAG CTCTGTCAGA ACAGCATCTG AATTAGGAGG ACTTTGGGAT TCTGGGATAC AGGAAGTATC CAGAGCTTTG GATATAAAAA ACCCTGGGAC AGATATTTTG CAGCCTGAAG AGACCTATAT AGACCCTACT ATGATACAAT CTTTAACTTT TCCTTTGGCC CTTCATAATC AAAGCTCCGA TAAGACAGCT AACATTGTGG AAAACCCATG TCCTGAGATT CTAGGAGTGG ATGTAATATC TAAAGAGACA ACTAGGAGGA AGCTCGAG  (2) INFORMATION FOR SEQ ID NO:205:	60 120 180 240 300 348
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

CGCTTGGGTC CAGATCTGTA TTCCCAGGGC TCATAGAGAT ATTGGCAAAC TGACAGATTT CATGGCTCAA GAAACCTAAA GACACCTACT TGAATTCCTT TGGTTGGCAG TCAAATGTTA ACTAGTGTGT TTTCAAGCTT CTATTCTTAG GCATGTTACT TCCTTTTGGA AGTCAAAACC AACCATCTTT TAAGTAAGAG GGCTAACCAA ATATGTGCCA CACTAACTCG AG	120 180 240 292
(2) INFORMATION FOR SEQ ID NO:206:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 220 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:	
GAATTCGGCC TTCATGGCCT AAAATATTAA AATCTTTGAA GAAGAAGAAG TTGAATTTAT CAGTGTGCCT GTCCCAGAGT TTGCAGATAG TGATCCTGCC AACATTGTTC ATGACTTTAA CAAGAAACTT ACAGCCTATT TAGATCTTAA CCTGGATAAG TGCTATGTGA TCCCTCTGAA CACTTCCATT GTTATGCCAC CCATCTCGAG GCAGGTCTAG	60 120 180 220
(2) INFORMATION FOR SEQ ID NO:207:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 333 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:	
GAAAAAATGG CCAAGGCTAC TGGGAAACTA AAGCCAACTT CTAAAGATCA GGTATTGGCC ATGCTAGAGA AAGCCAAAGT TAACATGCCA GCCAAGCCTG CTCCACCCAC TAAAGCAACT TCTAAACCAA TGGGAGGGTC CGCTCCAGCC AAATTCCAGC CTGCATCAGC ACCTGCTGAA GATTGTATTT CCAGCAGTAC AGAACCCAAA CCTGATCCAA AAAAGGCCAA AGCTCCAGGA TTATCCTCTA AAGCAAAGAG TGCACAAGGG AAGAAGATGC CAAGCAAAAC CAGCTTAAAG GAGGATGAAG ACAAATCCGG GCCTATACTC GAG	60 120 180 240 300 333
(2) INFORMATION FOR SEQ ID NO:208:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 316 base pairs  (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(C) STRANDEDNESS: double	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	60 120 180 240 300

CCCCGGACCA CTCGAG

## (2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 517 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GAATTCGGCC AAAGAGGCCT	ATGTCCCTGT	CCATCTTAGA	GGCTGACCAA	GCCCAGCCAT	60
GGGTGGTCCA AATTGCTTAG	GTGGTCCCAA	TTGCTTGGCT	GGCCCAAGAG	ATGTCTGGTT	120
CTTAACAATA CAAGAGCCTA	TAGAAATTGC	TAAAGGGATT	TCAGCCACAA	CTGAAGCTCA	180
CCAAGAATGA GTTTTCTGGA	ACTGGTTAAA	GTGTCACAGT	AGGGAGTAAG	GAAATAAGAA	240
TCCCCACCAA ACATAAGAGA	ACAGAATGAT	AATAGTCCCT	ACTAGTCCAT	GACAAGGCTG	300
CCAATTAGGC ATT' AAAGCT	ATCAAAGATG	ATGCTGTGAG	GGACCTGGCA	ACTTTTGTAA	360
TAGTCTGACT TTAAATGTTT	TATTAATGGC	CAAGCAGCAA	ATATTTTAGG	ATTTGTAGGC	420
TATATGGTCT CTGTCCCAAT	TACTCCATTC	TGCTACTGTA	GCATAAAAGC	AGCGATACAT	480
CCTAAACCCG TCGATTGAAT	TCTAGACCTG	CCTCGAG			517

- (2) INFORMATION FOR SEQ ID NO:210:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 829 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GAATTCGGCC	AAAGAGGCCT	AAGAACATGA	AACATCTGTG	GTTCTTCCTT	CTCCTGGTGG	60
CAGCTCCCCG	ATGGGTCCTG	TCCCAGGTGC	AGCTGCAGGA	GTCGGGCCCA	GGACTGGTGA	120
AGCCTTCGGA	GACCCTGTCC	CTCACCTGCA	$\mathtt{CTGTCTCTGG}$	TGATTCCATC	AGTCATTACT	180
ACTGGACCTG	GATCCGGCAG	CCCCCAGGGC	AGGGACTGGA	GTGGATTGGA	TATTTCTATT	240
CACCCGGGAA	CTCCAACTAC	AATCCCTCCC	TCAAGAGTCG	AGTCACCATG	TCAGTCGACA	300
CGTCCACGAA	CCAGTTCTCC	CTAAAACTCA	${\tt NTTCTGTGAC}$	CACTGCGGAC	ACGGCCGTCT	360
ATTACTGTGC	GAGAGACCTA	TATTGCCGTG	GGGGAACCTG	CTACCCCGCG	AGACTTGACC	420
GCTGGGGCCA	GGGAACCCGG	GTCATCGTCT	CGTCAGCCTC	CACCAAGGGC	CCATCGGTCT	480
TCCCCCTGGC	ACCCTCCTCC	AAGAGCACCT	CTGGGGCACA	GCGGCCCTGG	GCTGCCTGGT	540
CAAGGACTAC	TTCCCCGAAC	CGGTGACGGT	GTCGTGGAAT	TCAGGCGCCC	TGACCAGCGG	600
CGTGCACACC	TTCCCGGCTG	TCCTACAGTC	CTCAGGACTC	TACTCCCTCA	GCAGCGTGGT	660
GACCGTGCCC	TCCAGCAGCT	TGGGCACCCA	GACCTACATC	TGCAACGTGA	ATCACAAGCC	720
CAGCAACACC	AAGGTGGACA	AGAAAGTTGA	GCCCAAATCT	TGTGACAAAA	CTCACACATG	780
CCCACCGTGC	CCAGCACCTG	AACTCCTGGG	GGGACCGTCA	GTCTTCCTC		829

- (2) INFORMATION FOR SEQ ID NO:211:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 142 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

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TATATACCTT CCACCACTCG AG

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

GAATTCGGCC AAAGAGGCCT AGTTAATCTG ATAAATTCAC CATCAATTTG GTAAGCTTTA ATATAACTAC CCTGTTTTTT GAATACAGAT AATGCAAAAG AAAACCATTT TATACTCGGC

120

(A	A) LENGTH: 555 base pairs	
( E	B) TYPE: nucleic acid	
	C) STRANDEDNESS: double	
(I	D) TOPOLOGY: linear	
(ii) MOL	ECULE TYPE: cDNA	
(xi) SEQU	UENCE DESCRIPTION: SEQ ID NO:212:	
GTACAAACAT ACCA CCAAAACTAA ATTG TCTATTTTAC TTGC CCAGGAAAAA TTAT GCCTTTCAAC ATCC AGTGGCTGCC CAAG AATGACCTCT TTCC	AGAGGCC TAGTGGAATC ATTCTGCCAC ACCATTTCCT ACTCAAATAG ACAGACA CTCCCATATA CACATGCTCC TCTATCCGCC AACTCTGGAA GGTCTTC AAGAGAGATG ATGGCTTTAA GAACAAAAAAT AGCCTTATCC TGTACT GTTGTACTG TTATTTAAGA AACAAGCTGG TGGTTGATGT TCTTTTC AAAATGAGGG AAGAGGAGGT TCACCATCTG GATATGGTGT TTTAAGG ATTGTTGATA TCATTATTGT TAATCAATTG TTGTCAGCAC GCTGTGC AAATGAAACA GCCAATCAGC AGGAGAAAGT GATGAAATTA TTTAACC ACTCATCCGT AAGCCTTGTT ATTTTTCATA CAAACCTCGA GGGCGGC GGCGAATGCT GGGAGAGTCA GGTCTAGAAT TCAATCGTAG AA	60 120 180 240 300 360 420 480 540
(2) INFORMATION	FOR SEQ ID NO:213:	
( ) ( E	ENCE CHARACTERISTICS: A) LENGTH: 97 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: double D) TOPOLOGY: linear	
(ii) MOL	ECULE TYPE: cDNA	
(xi) SEQ	QUENCE DESCRIPTION: SEQ ID NO:213:	-
	BAGGCCT ACGAGAAGGG CGGTGTGTAC AAAGGGCAGG GACTTAATCA ACCCGCA CTTACTGGGA ATTCCTC	60 97
(2) INFORMATION	N FOR SEQ ID NO:214:	
. (7 (1	DENCE CHARACTERISTICS:  A) LENGTH: 487 base pairs  B) TYPE: nucleic acid  C) STRANDEDNESS: double  D) TOPOLOGY: linear	
(ii) MOL	LECULE TYPE: cDNA	
(xi) SEQ	QUENCE DESCRIPTION: SEQ ID NO:214:	
AAAACGTAAT CAGG	GAGGCCT AAGAAGAAT TGGTAGATTG CGAGAAGAGA TAGAAGAATT GAACTTT TACAAAGCCA GCTGACTGAA AAGGACTCTA TGATTGAAAA CAAACAT CTGGCACAAA TGAACAGTCT TCAGCAATAG TTTCAGCTAG GTTGCAG AATTAAAACA GGAACTGGCA ACTTTAAAGT CTCAGTTAAA	60 120 180 240
	161	
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CTCACAATCT	GTGGAGATCA	CCAAACTACA	GACAGAAAAG	CAGGAACTGT	TACAGAAAAC	300
					TAGCCACCAA	360
AACTACTGAT						420
					ATTCATCTAA	480
TAGTACC						487

- (2) INFORMATION FOR SEQ ID NO:215:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 584 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GAATTCGGCC A	AAGAGGCCT	ACTGGGCCTT	TCAGCACCTG	CTCCAGCTTC	ACCTTGGTGA	60
ACATCAGGTT G	BAAGTTCTCA	GGGTGCTCGG	TGATGGCCAT	GTTGACAACA	TCCAGGGCAT	120
GCTGGTGGTG C	TTCTGGGCA	GAGAAGAGCA	GTGCCAGCAG	GTGGAGGGCG	TGGGCATCAT	180
CCTTGCGTAC C	TTCAGGGCC	TCCTGCAGCT	GCTCCATGGC	ACTGGAGATC	TGTCGGACGA	240
GGGCCAGCTG C	CAGCGAGACA	TAGAGGATGA	CCTGGGGGTC	ACTGGGCGCC	AGCTGCTGAG	300
CCCTCTCCAG C	CGTCTGCAGT	GCCTTCCGGT	GCAATTCATC	TTGCTTGGAC	TTCAGGGTGG	360
CGTCGGTGGC C	TGCAGGCTA	TAGGTGAGAC	CCAGAGCCAG	GTAGCCCTTG	GGGAGGAACT	420
CCCCGGCTTC C	CTCTCCGAGG	CTGATCACCA	TCATGGCAAA	GTGCTCTGCT	TCCTCTAGCC	480
AGCGAAGGGA C	CCGATGCAG	ACCTTCGCGG	CCATCAGGGG	CACGGTGGGG	TCCGAGGGCC	540
GCAACTTCAC A	ACACTCCCGC	AGCAGGGACA	CAGCGTAGGC	TGAC		584

- (2) INFORMATION FOR SEQ ID NO:216:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 532 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

AGGTTTCAGT	CCAAGAGTGA ACGAGCAGGG CCAAAGCAGC TTGCAAACAT GCCCAGGACC TTGGGCGTGG GCTTTTTCTG	GTAGTGCACA CAGGAAAGAA CCAAATCAGT CACTGCCCCG AGAGCCCCTT CATGAGAGGG GGGACATTGG	GAAGTCTCCT AAAAAAAACC TACCTTGACA CTTCTAACAG CTACCCAGGG AAATAAAGAG TGCCTATCTC	GGCACCCTGG CAAACCCCAT ACTCTCATGC GAAGAGATAC CCCTTCCAAA ATTTGGCTGT TATTCTGAGA	GAATCCTGCA CACTCTGCCA ACAGACTGCA TCTTTTGGGG GGCAAAGCAC AGTGGGAGGG GTTGTTCTCC	60 120 180 240 300 360 420 480
				TATTCTGAGA AGGGTACTCG		532

- (2) INFORMATION FOR SEQ ID NO:217:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 269 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTCGGCC	AAAGAGGCCT	AGTGTGTCCG	GGTCTTATAC	AAAAACAACA	CAGTGAATGA	60
AGGAATAAAT	ATTTATTGAA	TGGAAAATCA	GCAAAGGAAA	AAATTGTATA	ATTGTCAATG	120
			TGATTTGGAA			180
TGTTCACGCA	TTTCGGTTGT	GTTTTCAGAA	AGTAACTACA	ACATAGCATC	ATGTAGCAGA	240
ATTGCTGGTT	GTAAGCAAAA	AGGCTCGAG				269

- (2) INFORMATION FOR SEQ ID NO:218:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 675 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC AAAGAGGCCT	AATTCTTTTT	CTTTTTAATT	TGAAGAAAA	TCATCAGTCT	60
TGGAATACAG AAGAGAAACT	AGAAATATAC	GTATTTTGTT	TCACATTTGA	ACAGTCATTC	120
TTGAGGAATA CTCCATACCT	GAGTAGACAG	CCATGTGGCC	ATCGCAGCTA	CTAATTTTCA	180
TGATGCTCTT AGCTCCAATA	ATTCATGCTT	TCAGCCGTGC	CCCAATTCCA	ATGGCTGTGG	240
TCCGCAGAGA GCTATCCTGT	GAGAGCTATC	CTATAGAGCT	TCGCTGTCCA	GGAACAGACG	300
TCATCATGAT AGAAAGTGCC	AACTATGGCA	GGACTGATGA	CAAAATTTGT	GACTCTGACC	360
CTGCTCAGAT GGAGAATATC	CGATGTTATC	TGCCAGATGC	CTATAAGATT	ATGTCTCAAA	420
GATGCAATAA CAGAACCCAG	TGTGCAGTGG	TGGCAGGTCC	TGATGTTTTT	CCAGACCCGT	480
GTCCAGGAAC CTATAAATAC	CTTGAAGTGC	AGTATGAATG	TGTCCCTTAC	ATTTTTCTTT	540
GTCCTGGACT ACTAAAAGGA	GTATACCAGA	GTGAACATTT	GTTTGAGTCC	GACCACCAAT	600
CTGGGGCGTG GTGCAAAGAC	CCTCTGCAGG	CATCTGACAA	GATTTATTAT	ATGCCCTGGA	660
CTCCCTACAG AACTG					675

- (2) INFORMATION FOR SEQ ID NO:219:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 414 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTCGGCC	AAAGAGGCCT	ACTCCCTGTT	TTGAACAAGT	TTTTTTGAGA	ATTCTTAGTT	60
TTAGTTTTTG	TTTAGCTTAC	ACACTGAAAA	TTTTGAGAAG	CATCTAAAAA	AATCCACAAT	120
TAGTGCAAAA	AGAGGGGACA	ATACTTTAAG	TCATTCCTTC	TATAAAAAGA	ATTAAGGTTA	180
			TTTCCTATTT			240
			AGGTTTGAAC			300
			CTTGGAAAAA			360
			CTTATTTAGG			414
1100001110	11410000	10011.011				

- (2) INFORMATION FOR SEQ ID NO:220:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 120 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GACCGTCGAT TGAATTCTAG ACCTGCCTCG AGATTGGAGA CAGAAGGTCC CGGGAGCAGA
AAGCCAAACA GGAGCGGGAG AAAGAACTGG CAAAAGTCAC TATCAAGAAG GAAACTCGAG 120

- (2) INFORMATION FOR SEQ ID NO:221:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 333 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GAATTCGGCC	AAAGAGGCCT	AAGCAGCAGC	TGCTTATATG	CATGTGAACA	GCTGGGGAAT	60
TAATTTGGTA	TGCATTCTCA	GGAGCCACTC	ATCTGCTGGC	AGAGGTAGCA	GAAGAATGCC	120
CTTAGTGTAA	GTCCTCTACA	ACCATACACC	AAATGTGCTC	CCTGCATTTC	AAATTCCATT	180
GTAGAAAGTC	TCTGATAATC	TCACTTATAC	CATGAGCCAT	TCCTCAGTAT	CTGTCCTCTT	240
CCTGTTAGTG	TTCTACAATT	CCTTTCTCCT	TAATTTTTCT	CCGCTTTACA	AAATGTCACA	300
CAGACAAGTG	CATAATACTT	AAACAAGCTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:222:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 817 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GAATTCGGCC	AAAGAGGCCT	AAGAAAAGCA	CCCTTATTAA	GAATTGCAGC	AAGTAAGCCA	60
ACAAGGTCTT	TTCAGGATGA	TTTTCTTATA	TCAAGTGGTA	CATTTCATTT	TATTTACTTC	120
AGTTTCTGGT	GAATGTGTGA	CTCAGTTGTT	GAAGGACACC	TGCTTTGAAG	GAGGGGACAT	180
TACTACGGTC	TTCACACCAA	GCGCCAAGTA	CTGCCAGGTA	GTCTGCACTT	ACCACCCAAG	240
ATGTTTACTC	TTCACTTTCA	CGGCGGAATC	ACCATCTGAG	GATCCCACCC	GATGGTTTAC	300
TTGTGTCCTG	AAAGACAGTG	TTACAGAAAC	ACTGCCAAGA	GTGAATAGGA	CAGCAGCGAT	360
TTCTGGGTAT	TCTTTCAAGC	AATGCTCACA	CCAAATAAGC	GCTTGCAACA	AAGACATTTA	420
TGTGGACCTA	GACATGAAGG	GCATAAACTA	TAACAGCTCA	GTTGCCAAGA	GTGCTCAAGA	480
ATGCCAAGAA	AGATGCACGG	ATGACGTCCA	CTGCCACTTT	TTCACGTACG	CCACAAGGCA	540
GTTTCCCAGC	CTGGAGCATC	GAAATCTTTG	TCTCCTTAAA	ACATCTGAGA	GTGGATTGCC	600
CAGTACACGC	ATTAAAAAGA	GCAAAGCTCT	TTCTGGTTTC	AGTCTACAAA	GCTGCAGGCA	660
CAGCATCCCA	GTGTTCTGCC	ATTCTTCATT	TTACCATGAC	ACTGATTTCT	TGGGAGAAGA	720
ACTGGATATT	GTTGCTGCAA	AAAGTCACGA	GGCCTGCCAG	AAACTGTGCA	CCAATGCCGT	780
CCGCTGCCAG	TTTTTTACCT	ATACCCCAAC	GCTCGAG			817

- (2) INFORMATION FOR SEQ ID NO:223:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 587 base pairs

entre production of the second

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GAATTCGGCC	AAAGAGGCCT	AGGAGATACA	TCATCATATC	ACGGAAAGAG	ATGCAGATAG	60
ATCTTTGACC	ATACTTGATG	AACAGTTATA	CTCATTTGCG	TTTTCCACCG	TGCACATTAC	120
GAAGAAAAGA	AATGGAGGTG	GGAGTTTAAA	TAACTATTCC	TCCTCCATTC	CATTGACTCC	180
CAGCACCAGC	CAGGAGGACC	TTTATTTCAG	TGTTCCTCCC	ACTGCCAACA	CACCCACGCC	240
CGTTTGCAAG	CAGTCCATGG	GCTGGTCCAA	CCTGTTTACA	TCTGAGAAAG	GGAGTGACCC	300
AGACAAAGGG	AGGAAAGCCC	TGGAGAGTCA	CGCTGACACC	ATCGGGAGCG	GCAGAGCCAT	360
CCCCATTAAA	CAGGGCATGC	TCTTAAAGCG	AAGTGGGAAA	TGGCTGAAGA	CGTGGAAAAA	420
GAAATATGTC	ACCCTGTGTT	CCAATGGCGT	GCTCACCTAT	TATTCAAGCT	TAGGTGATTA	480
TATGAAGAAT	ATTCATAAAA	AAGAGATTGA	CCTTCGGACA	TCTACCATCA	AAGTCCCAGG	540
AAAGTGGCCA	TCCCTAGCCA	CATCGGCCTG	CGCACCCATC	TCTCGAG		587

- (2) INFORMATION FOR SEQ ID NO:224:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 534 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GAATTCGGCC AAAGAGCCTA	AGTAGTTGCT	GCCTTTCTTC	AGATCAGGTT	ACCACAATGC	60
CTCCCCGCTG CTGACGCTTC	ATCCCCCACA	CCTCCAGCCC	CAGTTACCTG	GAGCTTCTCA	120
GAACCCACTT TGCCGGTGCT	AAAACACAAG	AGGGGGTGAA	AGTGGCTGCC	AGTAATGGCC	180
AGAAACCAAC CACCAGAGGC					240
GCCAACCATG TGGCAGGTCC	CAGGCCCCAC	CCACTGCGCC	ATCCGTCTCT	GAGCTCCACA	300
GTGGTCCCAC TAATGGGAAC	CTCCTCTAGG	GAGAGTGATA	CTGCACCTTC	ACCCGTAGGA	360
CTCATATTTA TAACAATGTG	TAATGGCTGT	AGCAAAAAGC	CCTTGTTTCT	AGATGTAAAT	420
GGTCAAAGAA ACAAGCGCTC					480
TTGTATCTCC TATTCTGGAT	TAGTGCCTTT	TGGACAGTAG	ACTGTAACCT	CGAG	534

- (2) INFORMATION FOR SEQ ID NO:225:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 118 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GCTCCACTCT CTCCCTATCC ATTTGTAAGA ACAGGCTCCC CTCGCCGAAT ACAGTTGTCT 60
CAAAATCATC CTGTCTACAT TTCCCCACAT AAAAATGAAA CAATGCTTTC TCCTCGAG 118

- (2) INFORMATION FOR SEQ ID NO:226:
  - (i) SEQUENCE CHARACTERISTICS:

WO 98/45437

PCT/US98/06956 (A) LENGTH: 582 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226: GAATTCGGCC AAAGAGGCCT AAATTTTAGT AGAGATGGAA TTTCACCATA TTGGCCAGGC CGGTCTCAAA CTCTTGACCT CAAGTGATCT GCCCGCCTCG GCCTCCCAAA ATGTTGAGAT 120 TACAGGCGTG AGCCACCATG CCTCTCTTAC ATTCTTTTCT TCTGTTCACT ACAGCCGTGG 180 AGAGCTCCGG GTTGTCCTGC ACATGTGCAC TGCCCTCTCT TTTATGGACC TTTTAGGCTG 240 GCTGCACCCT CCGTCTGTGT CACCCTCCTG CTCCTCCTCC ACCTGGCTAG TTCCTGTTGG 300 CCACTTTTGG AAATTCATGC CAGTCCAGTC CACCCTGAGT ACATCCTCTT TCTGTGTCAC 360 TGAGCTCACT ATGCTGGGTT TTATCTATGT CTCCCTCGCA ACTAGATCAT TCACGTCTTG AAGTTAGGCA TCATGCGTTC TTCATTTCTG TACCTCCCAA CTCAATGCTT AGCACCCAGC 480 AGGGGCTCAA GACTGTGTGT GGAATGAAGG ATTCGTGTGA AAATGCAGGG AGATGGAAGG 540 CTGAGCGTTT CTGTTCCTTG ACCATTCCCG GGTTGGCTCG AG (2) INFORMATION FOR SEQ ID NO:227: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 461 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227: GAATTCGGCC AAAGAGGCCT AAAAACTTAT AAATAAGTGA GACTACTGCC CCCTAGCCTA 60 AAATTCATTC CCTGCGCTCA CTCAACATCA TAGTTCTTTA GGAAGACAAG TTGTTCTATA 120 GCATAAAGAT ACAACCTATT TAGATAGTCT AAAGATTCTC CTCTGTTTCT CAAATACAGT CAGTTATGCA GCTCAAAATG CCTCTCATTT TCCTGCTTTT TTTTCTTCTA CTATTGTTGC CTCCAGGCTT TGCAGAAACA CATGTTATTC TCCCCCTAAA ATCTGTTCCT CTTCTAGTTT 300 360 TCTCTCTGCC AGCAATGGCA CCACACAGTC TTTTGGTTTT GCACCAGAGA ATTAGAGATG AACCCCTCAT CTCTAATCTA TCACAAGTTT CCTCAGATTT AAACTCTCAA ATCAAGATGT 420 TTCTCACCAT TTCCATTACT ATTGTCCCCA GCTTTCTCGA G (2) INFORMATION FOR SEQ ID NO:228: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

60 GCCTAAACCG TCGATTGAAT TCTAGACCTA TCTCGAGAAA GAGTTGTTCT GGAAAGAAAT GAAGAAAGA GCAGAACCAA TCTCAAGCAG CCAAGTGGTG AAGTTGGATG TATGTGACCC 120 133 TACGTCTCTC GAG

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 482 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GAAAGGGATC A	AAAAAGAAAA	AGTGATCGAA	TGGAATCTAC	TGATACCAAA	CGACAAAAGC	60
CTTCTGTCCA	TTCAAGACAA	CTGGTTTCTA	AGCCACTGAG	CTCATCTGTT	AGCAATAACA	120
AAAGAATAGT	TAGTACAAAA	GGAAAGTCAG	CCACAGAGTA	TAAAAATGAG	GAATATCAAA	180
GATCTGAAAG	AAACAAGCGT	CTAGATGCTG	ATCGGAAAAT	TCGTCTATCA	AGTAGTGCCT	240
CCAGAGAACC '	TTATAAGAAT	CAACCTGAAA	AAACCTGTGT	CCGGAAAAGG	GATCCTGAAA	300
GGAGGGCCAA .	ATCTCCTACG	CCAGATGGTT	CTGAGAGAAT	TGGGCTTGAA	GTGGATAGAC	360
GTGCAAGCAG .	ATCCAGCCAG	TCTTCTAAGG	AAGAAGTGAA	CTCTGAAGAA	TATGGCTCTG	420
ACCATGAGAC	TGGCAGCAGT	GGTTCTTCTG	ATGAGCAAGG	GAACAACACT	GAAAATCTCG	480
AG						482

- (2) INFORMATION FOR SEQ ID NO:230:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAATTCGGCC	TTCATGGCCT	AGGGGATAAA	TGTAAGCTTG	TTAAAGTAAG	CACCACACCA	60
TGTTTCTGTC	TCCCCAGCAC	CCAGCACAGT	GCTGTGAACC	TTGGCAGATG	CTAGATAAAT	120
GTGTGTTGAA	TGAATGTGCC	TATGAAGCCA	CAAAGATGCC	ACATGTTAGT	ATATCAGTGA	180
GAGGTGACTC	CACAGTGCTC	TCTGGAGAAG	CAATATGAGT	GACTGAAGAG	TGGGGCCTTT	240
TGCTTTTGCC	TGGATATAGG	GGTGCTCTTC	TACTGTAATT	GGGTGTGGAA	AAACTCTGGC	300
TTTATGGTAT	TCCATTAGGT	TCTTTTCATT	TAAAGTAGTC	TTAAAATCAA	AGTATCCAAT	360
ATTTTAAAGC	CACAAAGTAG	ATTACATAAT	TAGCAGAGAT	TTTAGTCAGT	AAAATGTTAG	420
AAATCAAACT	ATAAGAAAAT	TCAAGTCCTT	TATTTTGTGT	CTTGGGTATA	TGTCATTATT	480
TTAAATTCCA	CAGCTCTCGA	G				501

- (2) INFORMATION FOR SEQ ID NO:231:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAATTCGGCT	TCGATTGAAT	TCTAGGACTT	GACAGAATTC	GAGTTATCCT	TCTCAGAACA	60
TGTGCAGAGT	CTCTTTTTGC	CTCACCATGT	GGTCCTGTGC	TCTTTCAGGT	GGGAGTTTTG	120
GGGCCTCCAG	GGCAGCAGGC	ACCACCTCCA	TATCCCGGCC	CACATCCAGC	TGGACCCCCT	180
GTCATACAGC	AGCCAACAAC	ACCCATGTTT	GTAGCTCCCC	CCCAAAGACC	CAGCGGCTTC	240
TTCACTCAGA	GGCCTACCTG	AAATACATTG	AAGGACTCAG	TGCGGAGTCC	AACAGCATTA	300

GCAAGTGGGA TCAGAGCAAT CTCGAG

- (2) INFORMATION FOR SEQ ID NO:232:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAATTCGGCC	TTCATGGCCT	AATCAGAAGC	TTTTCAAAAT	TCCGTCTTCA	AGAAGAAACA	60
CCCGTGGAGG	AAGAAGACAT	TATACAAAAC	AAATTTAGAA	ACTGGGATCA	TGAGTGGAAA	120
AACAAAGGCA	AGAAGGGCTG	CCATGTTTTT	TAGACGTTGC	TCTGAAGACG	CCAGCGGTAG	180
CGCCAGTGGC	AATGCTTTGT	TATCAGAGGA	CGAAAATCCT	GATGCGAATG	GGGTAACTCG	240
ATCATGGAAG	ATTATTCTAA	GTACAATGCT	TACACTGACT	TTTCTTCTTG	TAGGACTCCT	300
AAATCATCAG	TGGCTTAAAG	AAACAGATGT	TCCTCAGAAA	TCCAGACAAT	TATATGCCAT	360
GCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:233:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GAATTCGGCC	TTCATGGCCT	AAAGAAGAAT	TGACACCTCT	TGGAGTCCAC	TTGGCACGAT	60
TACCCGTTGA	GCCACATATT	GGAAAAATGA	TTCTTTTTGG	AGCACTGTTC	TGCTGCTTAG	120
ACCCAGTACT	CACTATTGCT	GCTAGTCTCA	GTTTCAAAGA	TCCATTTGTC	ATTCCACTGG	180
GAAAAGAAAA	GATTGCAGAT	GCAAGAAGAA	AGGAATTGGC	AAAGGATACT	AGAAGTGATC	240
ACTTAACAGT	TGTGAATGCG	TTTGAGGGCT	GGGAAGAGGC	TAGGCGACGT	GGTTTCAGAT	300
ACGAAAAGGA	CACACTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:234:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 358 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAATTCGGCT TCATGGCC	TA CGATGAGGCT	GCTGTCATTT	GTGGTGTTGG	CTCTATTTGC	. 60
TGTCACTCAA GCAGAGGA					120
CGCCGTGGAG GGACGAGA					180
TGCATTAGAC GTGGAACT.					240
TGGAATGCTC AATGTCAA					300
GGTCCTGCGC CCTCTCAA					358

- (2) INFORMATION FOR SEQ ID NO:235:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 513 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GAATTCGGCT	TCATGGCCTA	GTTGTACGTA	ATGTATTTAT	ATGTTAATTT	GTTATGTATA	60
TAGATGTGCA	AGTCTTGTCA	GAATTGGCCT	CAGTGTAGTT	AAAGGGCAGA	AGGGGAAGAT	120
ACTGACTAGT	CATAGAAATA	CCTCATTCGC	CTGTGGGAAG	AGAAGGGAAG	CCTCTTCAGG	180
GTGAGTGAAT	GGCAAAGCGG	TTGCTTCTGG	CTCCTCCTTC	CCCTGTGGTC	TTGGAAGTGT	240
GTGGAAGGCA	GGGACAGAGA	TGGAGGCCGA	GCCAATAGAC	TGAAGAGACC	ACAGCAATTG	300
GCTCCTCCAT	CTAGAGATTT	TCTTGGCAGT	ATTCCATGGG	ATGTTAAGCA	AAGGAAACCA	360
AAGGAATCGT	TTCAAATGGA	CTCATGGCTT	AGAAATCTTT	ATTCTTAGGG	CAGTCAGTAG	420
TATTCTAAAG	CTTTCTGACA	AGATAAAGGA	AGTCACCAAA	ATTTCTTTTT	TTAAATTGTA	480
TCTAATCCTC	AACAACAAAC	CAAAACTCTC	GAG			513

- (2) INFORMATION FOR SEQ ID NO:236:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 412 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GAATTCGGCC	TTCATGGCCT	ACTTGGAAAT	GTTTGATGCT	ACTCTGAAAG	ATCGAGAACT	60
GAGCTTTCAG	TCGGCTCCAG	GTACTACCAT	GTTTCTGCAT	TGGCTAGTGG	GAATGGTATA	120
TGTCTTCTAC	TTTGCCTCCT	TCATTCTACT	ACTGAGAGAG	GTACTTCGAC	CTGGTGTCCT	180
GTGGTTTCTA	AGGAATTTGA	ATGATCCAGA	TTTCAATCCA	GTACAGGAAA	TGATCCATTT	240
GCCAATATAT	AGGCATCTCC	GAAGATTTAT	TTTGTCAGTG	ATTGTCTTTG	GCTCCATTGT	300
CCTCCTGATG	CTTTGGCTTC	CTATACGTAT	AATTAAGAGT	GTGCTGCCTA	ATTTTCTTCC	360
ATACAATGTC	ATGCTCTACA	GTGATGCTCC	AGTGAGTGAA	CTGTCCCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:237:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 337 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TTCATGGCCT AGAGA	ATATGC TTCTTTGTAC CAA	TATGGAA AATCTAAAAG	AAAAAACCCA 60	
CACTCAGCAC TATGA	AATGTT ATAGGTACCA AAA	ACTGCAG AAAATGGGCT	TTACAGATGT 120	
GGGTCCAAAC AACCA	AGCCAG TTAGTTTTCA AGA	AATCTTT GAAGCCAAAA	GACAAGAGTT 180	
CTATGATCAA TGTCA	AGAGGG AAGAAGAAGA GTT	GAAACAG AGATTTATGC	AGCGAGTCAA 240	
GGAGAAAGAA GCAAG	CATTTA AAGAAGCTGA AAA	AGAGCTG CAGGACAAGT	TCGAGCATCT 300	

TAAAATGATT CAACAGGAGG AGATAAGGAA GCTCGAG

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 750 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GAATTCGCGC	ATTCGGTACA	ACAAGAGAGA	TAAACGATGA	AACCGTTACA	TTATACAGCT	60
TCAGCACTGG	CGCTCGGACT	GGCGTTAATG	GGGAATGCAC	AGGCAGTGAC	GACCATTCCG	120
TTCTGGCATT	CTATGGAAGG	GGAACTGGGT	AAAGAGGTGG	ATTCTCTGGC	CCAACGTTTT	180
AACGCCGAAA	ACCCGGATTA	CAAAATTGTA	CCGACCTATA	AAGGCAACTA	CGAACAGAAT	240
TTAAGCGCGG	GGATTGCCGC	ATTTCGTACC	GGCAACGCGC	CGGCTATTTT	GCAGGTTTAT	300
GAAGTTGGCA	CCGCCACCAT	GATGGCGTCG	AAAGCCATTA	AACCGGTGTA	TGACGTGTTT	360
AAAGAGGCAG	GGATTCAGTT	CGATGAGTCG	CAGTTTGTGC	CGACGGTTTC	AGGTTACTAC	420
TCCGACAGCA	AAACGGGCCA	CTTACTCTCC	CAGCCATTCA	ACAGCTCGAC	CCCCGTTCTC	480
TATTACAACA	AAGACGCCTT	CAAGAAAGCA	GGATTAGACC	CGGAACAGCC	GCCGAAAACC	540
TGGCAGGATC	TGGCGGACTA	TGCCGCGAAA	CTGAAAGCCT	CCGGCATGAA	GTGCGGCTAC	600
GCCAGCGGCT	GGCAGGGCTG	GATCCAACTG	GAAAACTTTA	GCGCCTGGAA	CGGTCTGCCG	660
TTTGCCAGCA	AAAACAACGG	CTTTGACGGC	ACGGACGCGG	TGCTGGAGTT	CAATAAGCCG	720
GAGCAGGTGA	AACACATCGC	CATGCTCGAG				750

- (2) INFORMATION FOR SEQ ID NO:239:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 490 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAATTCGGCC TTCATGO	CCT ACTTACAGAA C	CTATTCACT GGGAAGGAAG	CCCTCATTAT	60
AATGATTTTC ATTCTTA	ATGT GTGTTTCAGG A	CGACTGGGT TTGGATTCAG	AAGAGGATTA	120
TTATACACCA CAAAAGG	TGG ATGTTCCCAA G	GCCTTGATT ATTGTTGCAG	TTCAATGTGG	180
CTGTGATGGG ACATTTC	CTGT TGACCCAGTC A	GGCAAAGTG CTGGCCTGTC	GACTCAATGA	240
ATTCAATAAG CTGGGTC	TGA ATCAGTGCAT G	TCGGGAATT ATCAACCATO	AAGCATACCA	300
TGAAGTTCCC TACACAA	ACGT CCTTTACCTT G	GCCAAACAG TTGTCCTTT	ATAAGATCCG	360
TACCATTGCC CCAGGC	AAGA CTCACACAGC T	GCTATTGAT GAGCGAGGC	GGCTGCTGAC	420
CTTTGGCTGC AACAAGT	IGTG GGCAGCTGGG C	GTTGGGAAC TACAAGAAG	GTCTGGGAAT	480
CAACCTCGAG				490

- (2) INFORMATION FOR SEQ ID NO:240:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 425 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GAATTCGGCC	TTCATGGCCT	ACTTCTGGAC	TCTATAGAAC	CCACTGCCTC	CTGATGAAGT	60
CCCTACTGTT	CACCCTTGCA	GTTTTTATGC	TCCTGGCCCA	ATTGGTCTCA	GGTAATTGGT	120
ATGTGAAAAA	GTGTCTAAAC	GACGTTGGAA	TTTGCAAGAA	GAAGTGCAAA	CCTGAAGAGA	180
TGCATGTAAA	GAATGGTTGG	GCAATGTGCG	GCAAACAAAG	GGACTGCTGT	GTTCCAGCTG	240
ACAGACGTGC	TAATTATCCT	GTTTTCTGTG	TCCAGACAAA	GACTACAAGA	ATTTCAACAG	300
TAACAGCAAC	AACAGCAACA	ACAACTTTGA	TGATGACTAC	TGCTTCGATG	TCTTCGATGG	360
CTCCTACCCG	TTTCTCCCAC	TGGTTGAACA	TTCCAGCCTC	TGTCTCCTGC	TCTAGGATCC	420
TCGAG						425

## (2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 461 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GAATTCGGCC TTCAT	GGCCT AACCAGAACT	AATTTGCTAA	GTCTTTTGTT	TAGTCCTGCA	60
AGACTGATGC TTAAT	ACACA GTCTGTTCTC	CTGTGTCTAG	GTCAGGAACT	CCAGTTTGCT	120
TTTCTGTTTT GTGTC	CTGGT AGCAGCTGTT	GAGTAACTTT	CATTGGAGGT	TGGGAAGGAA	180
GTGAGGAGAA AGTGT	TCTTG TTTAGTGTTT	TATTTCCTAT	AATAGGATGC	TGCCTAACCC	240
AGTTCATCTC TATGT	CCTGT TCACTGAATA	TTCCGGGTAA	TTGAAAGAAA	ATATAATGGA	300
TGGGCTCCAT TAAAA	CCAGC TCAAAAATAA	ATTCŤTGTCA	GTAAAGATTT	CTTGTCAAGA	360
TGTCTTGGAT TGCAC	TTTTG TTGAGGAAAG	ACAGTGTAAA	TAGTTAAAGA	ATGTTGATAA	420
AATTGAAACA TTTGG	TTGTG GAATTGTGTG	TGGTACTCGA	G		461

- (2) INFORMATION FOR SEQ ID NO:242:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 508 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GAATTCGGCC T	TCATGGCTT	ATGGACAAGG	AAGCATTCAG	AGCATGGTGT	CATCTGACTC	60
CACATCACCA G	SATTCTTCTT	TAACAGAAGA	ATCACGTTCT	GAGACAGCCA	GTAGTTTATC	120
CCAGAAGATT T	TGTAATGGGG	GATTATCTCC	TGGTAACCCA	GGAGATTCTA	AGGACATGAA	180
GGAAATTGAG C	CCCAATTATG	AAAGTCCCTC	TAGTAATAAT	CAGGATAAAG	ATTCATCACA	240
GGCTTCCAAA A	AGCTCAATAA	AAGTTCCAGA	GACCCACAAA	GCAGTCCTTG	CTCTCCGATT	300
AGAAGAGAAA G	GATGGCAAGA	TTGCTGTACA	AACTGAGAAG	GAAGAAAGTA	AAGCCTCTAC	360
AGATGTTGCT C	GGCAAGCAG	TAACCATAAA	CCTTGTCCCC	ACAGAAGAGC	AAGCAAAACC	420
TTACCGAGTT C	STGAACCTGG	AACAGCCATT	GTGCAAGCCA	TATACTGTCG	TGGATGTGTC	480
AGCAGCCATG C	GCCAGTGAGC	ACCTCGAG				508

- (2) INFORMATION FOR SEQ ID NO:243:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 323 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GAATTCGGC1	TCATGGCCTA	GGTTTTCTGT	ACATGGAGAT	TAAACTGTCT	TCCAAAGTGA	60
AGAGTTTATT	GTTCTAGATC	TTGAGCACAA	AGGTTGGTAT	ACGTTAATAA	AAAAAATAGC	120
AAGGGAAGA	AATCATTTCC	TTCATACCAA	GTAAGAGAGC	ACTTATCATG	GTAGGCACTG	180
GCTTTGCAAT	TATGAGACCA	GTAGTAGAAA	TAGCTTTAGT	TTCCTCAATT	TTCCTGGAGT	240
ATTCTTCAGA	CTTTCTTTAC	ACTGCTCAAG	GTGGGGCGAG	TGGCAGGGCG	GACCCTGGCG	300
ACCTGACGCT	GCGGAGGCTC	GAG				323

- (2) INFORMATION FOR SEQ ID NO:244:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A, LENGTH: 396 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GAATTCGGCC I	TCATGGCCT	AGCTTCAGTA	GCAAATAAGG	ACATCATCTG	CTATAACCTA	60
CAAGCAGTTG G	GACAGATATT	CTACATTTCC	TCATTTCTCT	ACACCGTCAA	TTACATCTGG	120
TATTTGTACA C	CAGAGCTGAG	GATGAAACAC	ACCCAGAGTG	GACAGAGCAC	ATCTCCACTG	180
GTGATAGATT A	TACTTGTCG	AGTTGGTCAA	ATGGCCTTTG	TTTTCTCAAG	CCTGATACCT	240
CTGCTATTGA I	GACACCTGT	ATTCTGTCTG	GGAAATACTA	GTGAATGTTT	CCAAAACTTC	300
AGTCAGAGCC A	ACAAGTGTAT	CTTGATGCAC	TCACCACCAT	CAGCCATGGC	TGAACTTCCA	360
CCTTCTGCCA A	ACACATCTGT	CTGTAGCACA	CTCGAG			396

- (2) INFORMATION FOR SEQ ID NO:245:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GAATTCGGCC	TTCATGCTTA	GCCTCAGCTC	TTTCTTCTGG	GTTGTTTGTA	TTTTCTTTTC	60
TGTCCCAAAC	AGTTTCCCCC	ACAAAAAGAA	CTTTATGTCT	TTCTCTGTCT	TCCCTCAGTC	120
CTTCCAGTCA:	GCAGCCTGTG	ATTGGGCTTT	TCCCCTCAGA	AACGAACAAT	CCAGAACCCA	180
CTGTTTAAAA	CAACTGTATT	TTGCCTTGGG	AAGTCCCATT	GCCTTCCCTG	AAAACATTAA	240
ACATTCCTCC	GATCCCCAGC	CTGAGTCTCT	CTGTCTCTGG	GCCCCATCCT	GCTCCACAGC	300
AGGGCTGGTG	TGTCCAGCAC	AGAGTGACCC	TCCGATGCCC	TTTCCCACCC	GCCGCCCTGC	. 360
CTCCCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:246:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAATTCGGCC	TTCATGCCTA	GAGAACTTGA	AGCTTTGCGG	CAGGAATTTA	AAAAGAAAGA	60
CAAGACGTTG	AAAGAGAATT	CCAGAAAGTT	GGAGGAAGAA	AATGAGAATC	TCCGAGCAGA	120
GCTACAGTGT	TGTTCTACAC	AACTGGAATC	CTCTCTCAAC	AAATACAACA	CCAGCCAGCA	180
AGTCATCCAA	GACTTGAATA	AAGAGATAGC	CCTTCAGAAG	GAGTCCTTAA	TGAGCCTGCA	240
GGCCCAGCTG	GACAAAGCTC	TGCAGAAGGA	GAAGCACTAT	CTCCAGACTA	CCATCACCAA	300
AGAAGCCTAT	GATGCATTAT	CCCGGAAGTC	AGCCGCCTGC	CAGGATGACC	TGACACAAGC	360
CCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:247:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 450 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GAATTCGGCC	TTCATGGCCT	ACGGCTTCAT	AGTAACTCTT	TGCCATATCT	CTAGCCAGCT	60
GCATAAAACG	TTCGCCATCA	GATGGAGACA	AAAGGTTTAA	AATACGCCTA	TAACCATCCA	120
TGGCCATTTT	ATGATCACCC	ATCTGTTCAT	AAAGGCTTGA	TCGCTCCCAC	AGATAACGGA	180
CATTAGTAGG	TTCATATTTA	AGAGCTTTTG	TATAGCAAAA	AATAGCCTGC	TTAATATTGT	240
CTTGTTCCAG	AGACATTTCT	GCCAGTCTAA	CCCATTCTTC	TGTGTCACTG	GGATTTAAAT	300
GCGCAGCAAT	CAACTCAAAC	TGCAATGATT	TTTCCATGTC	ACCTTGGTCC	TCATATATCA	360
TGGCTAGAGT	AGAGAATGGC	TCATAAGCCA	GAGGAGCTTG	TCTTATGATT	TCCATGCACA	420
TCAATATCGC	CTCTTCACGT	TCTCCTCGAG				450

- (2) INFORMATION FOR SEQ ID NO:248:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 408 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAATTCGGCC	TTCATGGCCT	AACGAAACTG	ACGTCTACCT	CATGGGGCTG	CTGTGTGGGT	60
TTGGGAGGCA	AAAATCTATG	AAGGGTTTTT	TGAAATCCCA	TAGGTGCCAC	ATCTATGAGA	120
TGTTTGATAA	ATGTGAATAT	GCTTTTACAT	TTGGGCTTAT	CTAATTTGCA	ATAAGAGAGC	180
CTCTCTCTAT	CAACACCAGC	TTCTCTCTCG	GGCTGTTTGC	TCAGGGAAGG	CAAGAAAGCC	240
ACGTGCTGGC	CCTCTGCCTT	CTCTAAAGTG	CTGTTGGAGC	ATGGAGGAGC	TGGAGGAGAT	300
GGGGATGGAC	TGACAGCTAA	GAGGGCGGCT	GCTGGGACTA	GATAGTGGAT	GAAGAAAGAA	360
GGACGAGGAA	GCCGTGGGGC	AGCCTCTTCA	CATGGGGACG	AACTCGAG		408

- (2) INFORMATION FOR SEQ ID NO:249:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 562 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GCCCATGACA	GAGAGCAGTG	CCAAAGACAT	GGCGTACGAA	CATCTGATAG	ATGACTTATT	60
GGCTGCTCAG	AAGGAAATTC	TGTCTCAGCA	GGAAGTCATC	ATGAAGTTAA	GGAAAGACCT	120
TACCGAAGCC	CACAGCAGAA	TGTCGGATTT	GAGAGGGGAG	CTAAACGAGA	AGCAGAAGAT	180
GGAACTGGAG	CAGAACGTGG	TGCTGGTCCA	GCAGCAGAGC	AAGGAGCTGA	GTGTGCTCAA	240
GGAGAAGATG	GCCCAGATGA	GCAGCCTGGT	AGAAAAGAAA	GATCGGGAGC	TGAAGGCCCT	300
TGAGGAGGCA	CTCAGGGCTT	CCCAAGAGAA	ACACAGACTC	CAGCTGAACA	CAGAGAAGGA	360
ACAGAAGCCC	CGGAAGAAGA	CCCAGACGTG	TGACACCTCT	GTGCAGATAG	AACCCGTCCA	420
CACTGAGGCC	TTCTCCAGCA	GCCAAGAGCA	GCAATCCTTC	AGCGATCTAG	GGGTCAGGTG	480
CAAAGGGTCC	CGGCACGAGG	AGGTCATTCA	GCGTCAGAJA	AAGGCCTTAT	CTGAACTTCG	540
AGCGCGAATT	AAAGAACTCG	AG				562

- (2) INFORMATION FOR SEQ ID NO:250:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 313 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GAATTCGGCC	TTCATGGCCT	ACCCAAACAG	ACAGAAAACG	CCACGAGGCA	AGTGTAGTCT	60
CTCACAGCCT	GGACCCTCTG	TCAGCAGTCC	ACATAGCAGG	TCCACAAAAG	GTGGCTCCGA	120
TTCCTCCCTT	TCTGAGCCAG	GGCCAGGTCG	GTCCGGCCGC	GGCTTCCTGT	TCAGAGTCCT	180
CCGAGCAGCT	CTTCCCCTTC	AGCTTCTCCT	GCTCCTCCTC	ATCGGGCTTG	CCTGCCTTGT	240
ACCAATGTCA	GAGGAAGACT	ACAGCTGTGC	CCTCTCCAAC	AACTTTGCCC	GGTCATTCCA	300
CCCTATGCTC	GAG ;					313

- (2) INFORMATION FOR SEQ ID NO:251:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 291 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GTCTTGACAA	AACCTAACTT	GCGCAGAAAA	CAAGATGAGA	TTGGCATGGC	TTTATTTGTT	60
TTTTTTTTTTT	TGTTTTGGTT	TTTTTTTTT	TTTTGGCTTG	ACTCAGGAGA	TCCCTCCCCG	120
GGGCTCCCGC	CGGCTTCTCC	GGGATCGGTC	GCGTTACCGC	ACTGGACGCC	TCGCGGCGCC	180
CATTTCCGCC	ACTCCGGATT	CGGGGATCTG	AACCCGACTC	CCTTTCGATC	GGCCGAGGGC	240
AACGGAGGCC	ATCGCCCGTC	CCTTCGGAAC	GGCGCTCGCC	CAACTCTCGA	G	291

(2) INFORMATION FOR SEQ ID NO:252:

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(i) SEQUENCE CHARACTERISTICS:
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(A) LENGTH: 384 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

CGGGAAATGA	AGCGGAAGCA	GGCGGAGTCC	GAGAGGCCCA	TCTTGCCAGC	CAATCAGAAG	60
CTCATTACTT	TATCAGTGCA	AGATGCACCC	ACAAAGAAAG	AGTTTGTTAT	TAACCCCAAC	120
GGGAAATCCG	AGGTCTGCAT	CCTGCACGAG	TACATGCAGC	GTGTCCTCAA	GGTCCGCCCT	180
GTCTATAATT	TCTTTGAATG	TGAGAACCCA	AGTGAGCCTT	TTGGTGCCTC	GGTGACCATT	240
GATGGTGTGA	CTTACGGATC	TGGAACTGCA	AGCAGCAAAA	AACTTGCGAA	GAATAAAGCT	300
GCCCGAGCTA	CACTGGAAAT	CCTCATCCCT	GACTTTGTTA	AACAGACCTC	TGAÀGAGAAG	360
CCCAAAGACA	GTGAAGAACT	CGAG				384

- (2) INFORMATION FOR SEQ ID NO:253:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 276 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GGGACGTTGG	TGTTGAGGTT	GGCATACGTA	TCAAGGACAG	TAACTACCAT	GGCTCCCGAA	60
GTTTTGCCAA	AACCTCGGAT	GCGTGGCCTT	CTGGCCAGGC	GTCTGCGAAA	TCATATGGCT	120
GTAGCATTCG	TGCTATCCCT	GGGGGTTGCA	GCTTTGTATA	AGTTTCGTGT	GGCTGATCAA	180
AGAAAGAAGG	CATACGCAGA	TTTCTACAGA	AACTATGATG	TCATGAAAGA	TTTTGAGGAG	240
ATGAGGAAGG	CTGGTATCTT	TCAGAGTGTA	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:254:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

GAGTTTGTTG	GGCTTACCTT	ATTTTAATTA	AAAAGAAGTC	GGGGCTACCA	GGGGTTTCAG	60
ACGTGCTCGA	TGGACACGTG	ATTTGTAAAC	AGCCAAGATT	CTGGGGGACG	GGGGGGTGCC	120
TCGGTGGGGT	TGACATTTGA	GTTACAGGGA	CTTAATAATG	GCCAGCCTTT	CACATCCCAT	180
GGGAAACCGC	CCCCCCGGGC	CTTGGAGAAT	${\tt GGGGGTCCAA}$	GTGCCTATCC	CCCTTTGGAT	240
GTAAAATTCA	TCGTTAGTAA	ACATCATCCG	CCCAGCAACA	AGCAAAGCAC	ATCGCAAGAT	300
TAAAACAAAG	AATCCGCCGT	GAACAGAAGG	CCTCCATCTC	TGCTCTCAGG	CAGGTGTCCT	360
TCAGGGAGGA	GCCTCAGGCA	GCTGTTCTAA	CCCTGCTGCC	AACGCCTGGG	CTGTTTCTGC	420
CGACAATCTT	CTATTTCTCT	AAAAGAGTAC	GCTGAACAGC	TGGCTCTGCG	TTGATTGAAT	480
TCTAGACCTG	CCTCGAG					497

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 470 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCGGCC	TTCATGGCCT	AGAGAACCGT	TGCTTTTCCG	AGTTGCTCTT	CTTCCAGGCT	60
CCGTTGGTGG	TCGGCATGGC	CCGTGGAAAT	CAACGAGAAC	TTGCCCGCCA	GAAAAACATG	120
AAGAAAACCC	AGGAAATTAG	CAAGGGAAAG	AGGAAAGAGG	ATAGCTTGAC	TGCCTCTCAG	180
AGAAAGCAGA	GGGACTCTGA	GATCATGCAA	GAAAAGCAGA	AGGCAGCTAA	TGAGAAGAAG	240
TCTATGCAGA	CAAGAGAAAA	GTGATGACTG	GCTATTTGGA	AAACCTGGGT	GCTACTGCCA	300
ACTGGGTGTA	TCATAAGCTC	TAAGATCAAG	ATTTTGTAGA	GTGGACAGTC	ATTACATATG	360
TTATAACTTA	TCCTTTAAAA	ACTATTTTAA	ACTTTATCCT	TTCAGCTTTA	CTTAGTGCGA	420
TGTTTTAGAA	GCAGTCTTCA	AAGAATAAAA	CACTAACCAT	GCTGCTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:256:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCGGCC	TTCATGGCCT	AATTTTGTAT	TTTTAGTGGA	GACGGGGTTT	CTCCATGTTG	60
GTCAAGCTGG	TCTTGAACTC	CCAACCTCGG	GTGATCCGCC	CGCCTTGGCC	TCCCAAAGTG	120
CTGGGATTAC	AGGCGTGAGC	CACCGCGCCT	GGCCAGTAGT	TTCTTAACAT	TAAATTATCC	180
GCAAAATGGA	AGAAATACTA	GAGGTCTGTG	AGGATGTTTC	TTCTCTTTCA	GTCTGTTGTG	240
GTGGTTTGTA	GTTTACAGGG	GCTTGGGTAA	CTGGATTTTT	AGGTTTATTA	TTTTAAATAG	300
TAGACTCAAC	ACTATTTTGT	ATTGCAGTAG	AGATCACTTA	TGCAGATCTT	TTTAATACCA	360
TTTCATAGAG	ATTAAGGGTC	ACCTCGAG			*	388

- (2) INFORMATION FOR SEQ ID NO:257:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 333 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAAACAGGGC	TCAAAGAAGT	GGTAACTGCT	GTGGAGGAAA	TGACAAGTAA	AGGAAAACCA	60
GGACAAGAAG	TCTTGGAAGA	CGACCAGGAA	AATACTTTAA	AATATGAGTA	TGAAGAAGAC	120
TTTGAAGTAG	ATGAGGAGAA	ACAAGGTGAA	AAATCTAATG	AAGAAGGACA	GGCTGATGTT	180
CAAATGAATG	GAATACCGCA	GTCACCTTTG	GATGATAAAA	AAGATAATTT	AGACCCTGAA	240
AAAGAGAGTG	AAACCTCATC	ACAGAAGGCA	CCAGATGCCC	GTGACAATGT	GAAAGATGAG	300
AATGATGGAT	GCTCTGAGAG	TGAACGTCTC	GAG			333

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 544 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

CACAGTGCTG	GNTCACAACA	AGATGNTCNA	GGTGTCAGCC	GTACTGTGTG	TGTGTGCAGC	60
CGCTTGGTGC	AGTCAGTCTC	TCGCAGCTGC	CGCGGCGGTG	GCTGCAGCCG	GGGGGCGGTC	120
GGACGGCGGT	AATTTTCTGG	ATGATAAACA	ATGGCTCACC	ACAATCTCTC	AGTATGACAA	180
GGAAGTCGGA	CAGTGGAACA	AATTCCGAGA	CGATGATTAT	TTCCGCACTT	GGAGTCCAGG	240
AAAACCCTTC	GATCAGGCTT	TAGATCCAGC	TAAGGATCCA	TGCTTAAAGA	TGAAATGTAG	300
TCGCCATAAA	GTATGCATTG	CTCAAGATTC	TCAGACTGCA	GTCTGCATTA	GTCACCGGAG	360
			AGACCATAGG			420
ATCCACCTGC	AAGCAGTGCC	CAGTGGTCTA	TCCCAGCCCT	GTTTGTGGTT	CAGATGGTCA	480
TACCTACTCT	TTTCAGTGCA	AACTAGAATA	TCAGGCATGT	GTCTTAGGAA	AACAGAATCT	540
CGAG						544

- (2) INFORMATION FOR SEQ ID NO:259:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GAATTCGGCC TTCATGGCCT	ACATCAGCAT	CCCTGGGAGC	ATCAGAAATG	CAGAGCTCAG	60
GCCCGCCCG GAGCTACCGA	ATCAGAACCT	ACATTTTACA	CACCCCTCAG	CTCAGAGCTT	120
GTTTCTCCCT GGATTCCATG	GCCCTGTGCT	GCTGGCAGCC	CGGGGTTAGG	GCATTTCGTT	180
GTCACCTGGC GACGGTGAAG	CCTAGTTTCC	TCCAGAGAGA	TTATGCTGCT	CTCCATCCAA	240
GTGAAGTGGC AATGGTGCCA	GCCTGAGATT	TCTGCCCTGA	GTTTTAAGTA	CGAGAGTGTG	300
GGCTGACAAT AAACTCCTTT	ATTCTACCCT	CTTCTGTTCT	CATAAGGAGA	TTAAATTTAA	360
CTGGAAGAGA TGAAGCTTGC	ATTTACCCAA	GAC			393

- (2) INFORMATION FOR SEQ ID NO:260:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 705 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

AAAG	AATACCAA	AAAAAAAACC	TATTCCTTTA	AAGGGATTGT	AAAGAGGCCT	GAATTCGGCC
				AGCCAAAATT		
				AGAAAATCAA		
CTCA 2	CTTAAACT	GTGAAGCAAA	TCTTTGGAAA	TAAACCTATT	CAATGGAAAA	GTTTTTAAAA
				CTCAAATCTC		
				AACAGATTTC		

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GGCAGTCTAA AACCCACATC TACCATTTCC ACAAGCCCTC CCTTGATCCA TAGCTTTGTT 420
TCTAAAGTGC CTTGGAATGC ACCTATAGCA GATGAAGATC TTTTGCCCAT CTCAGCACAT 480
CCCAATGCTA CACCTGCTCT GTCTTCAGAA AACTTCACTT GGTCTTTGGT CAATGACACC 540
GTGAAAACTC GTGATAACAG TTCCATTACA GTTAGCATCC TCTCTTCAGA ACCAACTTCT 600
CCATCTGTGA CCCCCTTGAT AGTGGAACCA AGTGGATGGC TTACCACAAA CAGTGATAGC 660
TTCACTGGGT TTACCCCTTA TCAAGAAAAA ACAACTCTAC CTACC 705
```

- (2) INFORMATION FOR SEQ ID NO:261:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 729 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GAATTCGGCC	AAAGAGGCCT	ACCTTACTTG	AGTCCACAGG	CAAGGCCCAA	TAATGCATAT	60
ACTGCCATGT	CAGATTCCTA	CTTACCCAGT	TACTACAGTC	CCTCCATTGG	CTTCTCCTAT	120
TCTTTGGGTG	AAGCTGCTTG	GTCTACGGGG	GGTGACACAG	CCATGCCCTA	CTTAACTTCT	180
TATGGACAGC	TGAGCAACGG	AGAGCCCCAC	TTCCTACCAG	ATGCAATGTT	TGGGCAACCA	240
GGAGCCCTAG	GTAGCACTCC	ATTTCTTGGT	CAGCATGGTT	TTAATTTCTT	TCCCAGTGGG	300
ATTGACTTCT	CAGCATGGGG	AAATAACAGT	TCTCAGGGAC	AGTCTACTCA	GAGCTCTGGA	360
TATAGTAGCA	ATTATGCTTA	TGCACCTAGC	TCCTTAGGTG	GAGCCATGAT	TGATGGACAG	420
TCAGCTTTTG	CCAATGAGAC	CCTCAATAAG	GCTCCTGGCA	TGAATACTAT	AGACCAAGGG	480
ATGGCAGCAC	TGAAGTTGGG	TAGCACAGAA	GTTGCAAGCA	ATGTTCCAAA	AGTTGTAGGT	540
TCTGCTGTTG	GTAGCGGGTC	CATTACTAGT	AACATCGTGG	CTTCCAATAG	TTTGCCTCCA	600
GCCACCATTG	CTCCTCCAAA	ACCAGCATCT	TGGGCTGATA	TTGCTAGCAA	GCCTGCAAAA	660
CAGCAACCTA	AACTGAAGAC	CAAGAATGGC	ATTGCAGGGT	CAAGTCTTCC	GCCACCCCCA	720
ACACTCGAG						729

- (2) INFORMATION FOR SEQ ID NO:262: .
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 686 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GAATTCGGCC	AAAGAGGCCT	ACTACCATGT	CCTCTTGGAG	CAGACAGCGA	CCAAAAAGCC	60
CAGGGGGCAT	TCAACCCCAT	GTTTCTAGAA	CTCTGTTCCT	GCTGCTGCTG	TTGGCAGCCT	120
CAGCCTGGGG	GGTCACCCTG	AGCCCCAAAG	ACTGCCAGGT	GTTCCGCTCA	GACCATGGCA	180
GCTCCATCTC	CTGTCAACCA	CCTGCCGAAA	TCCCCGGCTA	CCTGCCAGCC	GACACCGTGC	240
ACCTGGCCGT	GGAATTCTTC	AACCTGACCC	ACCTGCCAGC	CAACCTCCTC	CAGGGCGCCT	300
CTAAGCTCCA	AGAATTGCAC	CTCTCCAGCA	ATGGGCTGGA	AAGCCTCTCG	CCCGAATTCC	360
TGCGGCCAGT	GCCGCAGCTG	AGGGTGCTGG	ATCTAACCCG	AAACGCCCTG	ACCGGGCTGC	420
CCTCGGGCCT	CTTCCAGGCC	TCAGCCACCC	TGGACACCCT	GGTATTGAAA	GAAAACCAGC	480
TGGAGGTCCT	GGAGGTCTCG	TGGCTACACG	GCCTGAAAGC	TCTGGGGCAT	CTGGACCTGT	540
CTGGGAACCG	CCTCCGGAAA	CTGCCCCCCG	GGCTGCTGGC	CAACTTCACC	CTCCTGCGCA	600
CCCTTGACCT	TGGGGAGAAC	CAGTTGGAGA	CCTTGCCACC	TGACCTCCTG	AGGGGTCCGC	660
TGCAATTAGA	ACGGCACATT	CTCGAG				686

(2) INFORMATION FOR SEQ ID NO:263:

# (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 571 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GAATTCGGCC	AAAGAGGCCT	AGGAGAGAGG	AGGTGCTGCA	AGACTCTCTG	GTAGAAAAAT	60
GAAGAGGGTC	CTGGTACTAC	TGCTTGCTGT	${\tt GGCATTTGGA}$	CATGCTTTAG	AGAGAGGCCG	120
GGATTATGAA	AAGAATAAAG	TCTGCAAGGA	ATTCTCCCAT	CTGGGAAAGG	AGGACTTCAC	180
ATCTCTGTCA	CTAGTCCTGT	ACAGTAGAAA	ATTTCCCAGT	GGCACGTTTG	AACAGGTCAG	240
CCAACTTGTG	AAGGAAGTTG	TCTCCTTGAC	CGAAGCCTGC	TGTGCGGAAG	GGGCTGACCC	300
TGACTGTTAT	GACACCAGGA	CCTCAGCACT	GTCTGCCAAG	TCCTGTGAAA	GTAATTCTCC	360
ATTCCCCGTT	CACCCAGGCA	CTGCTGAGTG	CTGCACCAAA	GAGGGCCTGG	AACGAAAGCT	420
CTGCATGGCT	GCTCTGAAAC	ACCAGCCACA	GGAATTCCCT	ACCTACGTGG	AACCCACAAA	480
TGATGAAATC	TGTGAGGCGT	TCAGGAAAGA	TCCAAAGGAA	TATGCTAATC	AATTTATGTG	540
GGAATATTCC	ACTAATTACG	GACAGCTCGA	G			571

- (2) INFORMATION FOR SEQ ID NO:264:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 313 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GAATTCGGCC AAAGAGGCCT	ACCAAGCAAG	AACAGCTAAA	ATGAAAGCCA	TCATTCATCT	60
TACTCTTCTT GCTCTCCTTT	CTGTAAACAC	AGTCACCAAC	CAAGGCAACT	CAGCTGATGC	120
TGTAACAACC ACAGAAACTG	CGACTAGTGG	TCCTACAGTA	GCTGCAGCTG	ATACCACTGA	180
AACTAATTTC CCTGAAACTG	CTAGCACCAC	AGCAAATACA	CCTTCTTTCC	CAACAGCTAC	240
TTCACCTGCT CCCCCCATAA	TTAGTACACA	TAGTTCCTCC	ACAATTCCTA	CACCTGCTCC	300
CCCCATACTC GAG					313

- (2) INFORMATION FOR SEQ ID NO:265:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 343 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

60	TCTCATTGAT	ACACAGATGA	TCAGCTCAGA	GCCTCTGAGT	TTCATGCCTA	GAATTCGGCC
120	AGGACCGAGG	TCCACACATG	CCCTGGGACG	AATCTGGGTA	AACCTTGGGA	TCCTCACGTC
180	GGAAGTAAAC	GAGTAAAATG	CAGAAACAGG	GGCCTGGTCC	TCAAGGGACT	CTCAGGGACA
240	CTGCCATCTT	AACCATGCGG	TGGGCCACTG	CTCCAGAGTT	GTCTGCCTGA	TCAGTCCCAC
300	TTTGTGCAGG	CTGTGTCCCT	TCGTGTGATT	GTGCTGTGCA	GAGCTGTGAA	GGAGTTCTTT
343		GAG	GGAGCCACTC	CGACCTGTCA	TCTATGCATT	TACCAGGATT

- (2) INFORMATION FOR SEQ ID NO:266:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 340 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCGGCC	TTCATGGCCT	ACAGGAAGCA	CAGAAAGACA	AAATTGGAAA	TGTCTAGTTC	60
CATGTTGATG	CCTTCAGAAG	ATGCAGGTGA	ACAAAGAGAG	GCCGGGAAAT	CAGAGCTAGT	120
TGAAACCCAA	CATGTTACCT	TAGAGCCAGA	GCTACCACTG	AGTTCTCTAA	GCACAGTCAA	180
ATCCCAGGAT	TATGCTGAAA	CAGAGCAGGA	GGTCATTTTA	CAAGCTATAG	AGGCCATGGA	240
GGCCACAGAA	GCCCTGGAGG	CCACAGACGC	CATGGAAGCC	ATAGATCAAG	GTAGCATGAA	300
AGATTATGGA	GATGTGATCT	CTAAGCTGGA	AAGACTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:267:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GAATTCGGCC	TTCATGGCCT	AGGCACCCCT	AGGCGACTCA	GGGTTCGGGG	AGGAGGAGAC	60
CAGACGGGGC	CTTGGCTGGC	ATGGCCTCTT	CACAGGGCTG	CCGTGAAGAA	ACTTCGTGAC	120
AGCGGCGGAG	AGGTGGCCCA	GGAGTGAGAC	AAGCAGGCCC	CGGGCCTTGG	ACTCAGACAT	180
GCTGGGTCCG	GTCAGGCCCG	TGTGGGAACC	AGTGTTTTAG	GGACTGGGTA	CTCTCTTAGA	240
GAAGAACTGA	TGCTAAAGAG	TCAGGAAGAC	ACGAGCGGGC	CAAATAAAAG	AGGAAGAGAG	300
GCCCTCAGGA	CATCATGGCA	CTTACTGCTT	GGATTTGTCT	CCCCGTCCAG	AATTCTGTGG	360
ACTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:268:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GAATTCGGCC	TTCATGGCCT	ACTTGGGAAT	TAACATCTTC	GATAAATCCC	AGAAGTCTTT	60
AAGTGACAGT	AGAGAGCCTA	CAGAGAAGCC	TGGGAAAGCA	GAAAAATCTA	AGAGCCCAGA	120
AAAAGTGTCA	TCGTTCTCAA	ACTCCTCCTC	CAACAAGGAA	TCAAAAGTAA	ACAATGAGAA	180
GTTTCGTACT	AAGAGCCCCA	AGCCTGCCGA	AAGCCCCCAG	TCAGCCACTA	AGCAGTTGGA	240
TCAGCCCACT	GCTGCTTATG	AGTATTATGA	TGCTGGCAAT	CACTGGTGCA	AAGACTGCAA	300
CACCATCTGT	GGGACTCGAG					320

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 542 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GAATTCGGCC	AAAGAGGCCT	AGGGATATTT	ACTGAGGGCC	TACAGGGTGC	CCAATACTGA	60
GCTAGCTAGG	CTCAGGGACC	TGTACACACA	TGCATTCTCC	ATTAGGGTTC	TGCAATCCTG	120
ACACTATTAC	TATCCTCAAG	GACTCTGCGC	ATCCAGACCC	GTCTATTAGT	TAGCAATGAG	180
AACCCCTGCC	ATGGCCAAGT	TACACAAGAA	CACCCTTGCC	CTACCTCTGC	CCCCTGCNGA	240
TCTGAAAGTA	ACCTGGTCTG	AAAGAGAAGT	AAAGATGTGG	CTGTCCCTGG	GTGCTAGGGA	300
GAGAGGCCTG	TTGACAAAGC	CACCAGCTGT	CTCCAGTCAG	AGCCAGGGAG	ACAGGCTTCT	360
CCCTGCACCA	TCCGCACTGC	CATAGACACA	GCAGCCAGCA	ACAGCACTTG	GACCATTACG	420
GAGTTCCAGG	CCCAGTCTCC	AACTGACCTC	CCTCCTGCTC	CAGCTGCCCA	TGCTAACAAG	480
AGCCAGGGCA	CAAGACCTCA	CTTGGAACAA	GTACCAGGCA	GAAGAGAGCA	TNACCNGCCG	540
GT						542

- (2) INFORMATION FOR SEQ ID NO:270:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 613 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GAATTCGGCC	AAAGAGCCTA	GTCGATTGAA	TTCTAGACCT	GCCTCCTTTT	CCACTTGAAT	60
TGTTAAATTG	TTTACTCCAG	CATCTTTAAG	TATTCCTGTA	ACCTGCTGTA	CTATTCTTTG	120
TTCTAGCACA	TCAGATGTCA	CCTGTATATG	AATTGTTCCT	GCCACAATAC	TAGCAGAATG	180
ACGCCAAAAA	TGTGGGTCTC	GGTATGATAT	TAATCCTTCA	ATTTTCTGTA	TCTTTTCTAA	240
AGCAATATGT	AGTTCTTTTT	CATATTCTGG	TGGCAATCTC	AGGAGTAGAA	CCTGGCAGGC	300
ATCTTTAATC	AGTGGAACAA	CACTGAGAAA	TATTAATATA	GCAATAAAAA	GAGAACAGAG	360
TGGGTCAGCG	ATGAACCATC	CAAACTGCTC	TATAAGAACT	GTGGATACGA	TCACACCAAT	420
GCTGCCAAGA	GTATCTGCCA	AAACATGTAG	AAATACACCC	CTCATGTTAG	CATTCATGCC	480
TCCACCCGCA	GATCCGTGGC	TGTGACCATG	CCCATGGTCA	CTGTGTCCAT	GCATATGATG	540
TGAATGGCTG	TGATCAGATG	AGTGACAGCT	TCCTTGAGCC	TAAACCGTCG	ATTGAATTCT	600
AGACTGCCTC	GAG					613

- (2) INFORMATION FOR SEQ ID NO:271:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 763 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GAATTCGGCC AAAGAGGCCT AGTCTGGTTC TTGCTTGATC TGAGAGCTTC CATCAGTCTC 60
TTTTATTTCT TCTGTGGCTG GAACTTCCAA CTGGCTTGGT TCAGCTGATT CTTGTATCAC 120

GGGGCCTTCT	GACTCACTCT	GATCAACCAG	CTGGTTATTA	ATCACAAGTC	CTGGAAATGG	180
TCTAATGACC	GTGAATTTGA	TAAACTCGGC	AGAGTCTAAG	ATCCTTCTCA	TGGAGCTGAT	240
TTCCAGGTAG	CTGGGGGCTT	TGAAAGGACA	CCCCCGGGGG	CATGCCATCA	ACTACCACAC	300
AGCCAGGGTT	AATTGTGATT	TCCCTGTAGG	GAACTTTCAC	AGGAAAACCC	ATACCAATAG	360
CTTCACCAAA	TTTCCGACTA	AAGAGGTCAT	TCACTTGTTC	TCTTAGCTGT	CTAGCTTTTT	420
CAACTTTCGA	GAGTCTTTCA	TTATCATCAT	CTGGAATTGT	CACCTGAATG	ATGTTAAGGT	480
CTTCAACACC	TGATGCAGTA	GTATTAACAT	TGGGTGATGA	ATTTATTTTT	CTGGGAGGGC	540
TCTTAGAGGA	GGTGCTCTCC	TTAATCGCCG	TCTCAAACAT	TTCGGGCTTT	TTAATGATGA	600
ACTTAATTTT	${\tt GGCTTTGTTT}$	CTGAGTATCT	TCTCCAGCCT	CGGAATGCCA	AAAGTCGATG	660
GTCTTCGGAA	TGGCACACCC	TCAGGTAAGC	CTTCCACATA	AAAGTCTTCC	GGGAAAGACT	720
CAAATAACGC	GAACGGCACC	TTCACAGCTT	GTTTAAGGCC	AAG		763

- (2) INFORMATION FOR SEQ ID NO:272:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 102 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GAATTCGGCC AAAGAGGCCT AATTAAGGAA ATACTTTGCA TAAATTAATC AGCCCCACAG
TATTTCCTTA ATAAGAATAA AATGAATTTA ACACTGATTC TG 102

- (2) INFORMATION FOR SEQ ID NO:273:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 565 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GAATTCGGCC	AAANAGGCCT	ACNCCAGTCA	AGGAAAGTCA	AGTNGCAAGA	AGGAANTGTC	60
TAAAAGAGAT	GGCAAGGAGA	AAAAAGACAG	AGGAGTGACG	AGGTTTCAGG	AAAATGCCAG	120
TGAAGGGAAG	GCCCCTGCAG	AANACGTCTT	TAAGAAGCCC	CTGCCTCCTA	CTGTGAAGAA	180
GGAAGAGAGT	CCCCCTCCAC	CTAAAGTGGT	AAACCCACTG	ATCGGCCTCT	TGGGTGAATA	240
TGGAGGAGAC	AGTGACTATG	AGGAGGAAGA	AGAGGAGGAA	CAGACCCCTC	CCCCACAGCC	300
CCGCACAGCA	CAGCCCCAGA	AGCGAGAGGA	GCAAACCAAG	AAGGAGAATG	AAGAAGACAA	360
ACTCACTGAC	TGGAATAAAC	TGGCTTGTCT	GCTTTGCAGA	AGGCAGTTTC	CCAATAAAGA	420
AGTTCTGATC	AAACACCAGC	AGCTGTCAGA	CCTGCACAAG	CAAAACCTGG	AAATCCACCG	480
GAAGATAAÀA	CAGTCTGAGC	AGGAGCTAGC	CTATCTGGAA	AGGAGAGAAC	GAGAGGGAAA	540
GTTTAAAGGA	ATAGGAAATC	TCGAG				565

- (2) INFORMATION FOR SEQ ID NO:274:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 188 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GAATTCGGCC	AAAGAGGCCT	ACTTAAATCA	AGGCCAAAAC	TAAGGATTTA	GGTAGAGTGT	60
ATTAGCCTTT	CAATACCTGC	TTATTAAACA	GTTGTTTTCA	TACTTTTCAA	AGGTGTGTAG	120
AAGTTTTGTA	AATAAATTT	CTGATAGGAT	AAACTAGATT	CCCTATGATC	TCTTATTTAT	180
TTATCATT						188

- (2) INFORMATION FOR SEQ ID NO:275:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 555 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GAATTCGGCC AAAGAGC	SCCT AGTCCGTGAT	GCGTACACAC	CTGTCGAGCA	CGAGCTCCTC	60
TAGGCGGTGC AGGTCGG	CAGG CCACGTACTC	CAGCGCCATG	TCGGTGATNC	GTGGGCACCA	120
CGAGAGGTCA AGGNTG	CGCA GCTTGCGCAG	GTTCTCGGCC	ACGAGCTCCA	CGCCGTCGTC	180
GGTGACCTTG GAGCAGO	CCCG AGAGGCTGAA	CGCGGTGAGG	TTGGGCAGGN	TGTGCACCAC	240
GTTGACCACG CCGTGGT	TTGG TGATCTCCCA	GCAGGAGAGC	AGGCGCAGCG	TGTGCGTGCT	300
GTGGCCCTGG CGCGCCC	TGA AGTAGGCCAG	CGCCGTGTCC	GTCACGTGGT	AGGCCTGCAG	360
GCTCAGCTCC GCCAGGT	TTGG GCAGCAGCTG	CGAGATGGCC	GCGATGGCGT	CGTCGGCCAC	420
GTTGATGCAG TCACTC	ACGC TCAGCGAGGT	GATGCGCGCG	CTCAGGCTGG	ACCACAGCCC	480
GGCCTCGGTG AAGTCGT	TTGC AGCCCGACAG	CTCCAGACGC	ACCACGCCCT	GCATCTGTTC	540
AAGCATAACC TCGAG					555

- (2) INFORMATION FOR SEQ ID NO:276:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 496 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

GAATTCGGCC	AAAGAGGCCT	ACAGTGAATA	ATCAGAAGTC	AGTTTGGGAG	AAGTCAAAAT	60
GGACACAATC	TTCTTGTGGA	GTCTTCTATT	GCTGTTTTTT	GGAAGTCAAG	CCTCAAGATG	120
CTCAGCTCAA	AAAAATACCG	AATTTGCAGT	GGATCTTTAT	CAAGAGGTTT	CCTTATCTCA	180
TAAGGACAAC	ATTATATTTT	CACCCCTTGG	AATAACTTTG	GTTCTTGAGA	TGGTACAACT	240
GGGAGCCAAA	GGAAAAGCAC	AGCAGCAGAT	AAGACAAACT	TTAAAACAAC	AGGAAACCTC	300
AGCTGGGGAA	GAATTTTTTG	TACTGAAGTC	ATTTTTCTCT	GCCATCTCAG	AGAAAAAACA	360
AGAATTTACA	TTTAATCTTG	CCAATGCCCT	CTACCTTCAA	GAAGGATTCA	CTGTGAAAGA	420
ACAGTATCTC	CATGGCAACA	AGGAATTTTT	TCAGAGTGCT	ATAAAACTGG	TGGATTTTCA	480
AGATACAAGG	CTCGAG					496

- (2) INFORMATION FOR SEQ ID NO:277:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 491 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GAATTCGGCC	AAAGAGGCCT	ACACCCAGAG	ACTGTAATTT	GTGTAGTTTT	TCTTTTTTAA	60
CTTAAAGACA	ACTTTAAAAA	ATACTTACAT	TAATGTTTTT	TATATTCATA	GGTGGGTATA	120
TTCGCCTCAT	TCAAATGGCA	GTAGCCTTGG	CTCACATAAG	ACATGTTTCA	TGTGATCTGT	180
ATCCTGGCAT	ACCAGTTATA	TTTTGTGGGG	ACTTTAATAG	TACACCATCA	ACAGGAATGT	240
ATCATTTTGT	CATCAATGGC	AGCATTCCAG	AGGATCATGA	AGACTGGGCT	TCCAATGGGG	300
AGGAGGAAAG	ATGCAATATG	TCTCTTACAC	ATTTCTTCAA	GCTGAAAAGT	GCTTGTGGTG	360
AACCTGCTTA	CACAAATTAT	GTTGGTGGCT	TTCATGGATG	TCTAGATTAC	ATTTTCATTG	420
ACTTAAATGC	TTTAGAGGTT	GAACAGGTGA	TTCCATTACC	TAGTCATGAA	GAAGTTACCA	480
CTCCACTCGA	G					491

- (2) INFORMATION FOR SEQ ID NO:278:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 369 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

	120
TGTGGAATAC GGCAGAACCG TGTGTATGTT TCGCACAGAG AAGATTCGGA AGCTCGTAGC	
CATGGGCATC CCTGAATCTT TGCGAGGGAG ACTCTGGCTT CTCTTCTCAG ATGCGGTGAC	180
GGATCTTGCC TCACACCCTG GTTACTACGG GAATCTGGTG GAGGAGTCCC TGGGGAAATG	240
CTGCCTGGTA ACCGAGGAGA TAGAACGAGA CCTGCACCGC TCCCTGCCAG AGCACCCCGC	300
CTTCCAGAAC GAAACGGGAA TTGCTGCTTT GAGGAGAGTC TTGACGGCCT ATGCCCACCG	360
GAGCTCGAG	369

- (2) INFORMATION FOR SEQ ID NO:279:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 528 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GAATTCGGCC	AAAGAGGCCT	ACTCTCCCTT	TCCACTCCCT	GGTGTTCCCA	GGAGTGAGAT	60
GAGGGTGGAG	GGGCCCAGCA	CAGCACCTTC	AACCTCAGGA	TGAGAGAGGC	CCTTTCACAA	120
AACTCTAAGG	CAGGGGAACA	GGAAACAGAG	AAAGCCGGAG	AACCCCAGGA	GGGCCCCAAG	180
AGCGGATTCT	GGTGATTATT	AATGTGCTTG	CCCAATGAAG	AAAGAATACT	GGCACTCTCT	240
AGGTATGATG	AGAGCAGACA	GCAAACGTGG	GGCCTGTCTA	CAGTGATTCG	CTACCCCAAT	300
GTATGGTCAT	CCACGTTAGA	AGCAGCAGTG	AAAGGCGTGT	TGCTTTTCAT	TATTAACTTC	360
AAATCCCAGT	CCCTAAACCA	GCTCTTGACG	CCCCTCTGTC	AGGTGCTAAT	CCTGGAAACT	420
GGAGGCCACC	TGGTCTCCAC	TTTAGGTGAG	GAAAACCTGG	GAGAAGCCAT	CAGACTGCAC	480
CTGTGGCATG	AGATGCTTTG	AGACAGGTCA	AGAGGAGGAG	CTCTCGAG		528

- (2) INFORMATION FOR SEQ ID NO:280:
  - (i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 323 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:	
GAATTCGGCC AAAGAGGCCT ACAGTGTCGG AGTAGATTTG AAACTGGAGG TGAAGGTAGG AGTAAGTGAT AGATTTTAGA ATTAGTGCTC AGAGCTGAAA TATCCAGTCC GTGAACTTAG AGGCCAGCCT TCATACCACT GTGATGACAG GAACTACCCT AATCTTTTCT GTCCTTTTCT CTCTGCTGTC CCTCGGGCTG CCAGGCCAGC AGCAACACCC ACAGGTAATC TCCCCGCTGA CTCCATCCAC TTGCTCTGCC CTCTGCCCTC TCTGTGCCCC GTTGCACCTG AGCGTACACC CCAGCAGTGG CATCCAACTC GAG	60 120 180 240 300 323
(2) INFORMATION FOR SEQ ID NO:281:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 337 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:	٠.
GAATTCGGCC AAAGAGGCCT ACTCAGTCAG TACCATGCCA GTTACCTTTT TTCCTTGTGA CTTAATGAAT TGGATTTCC TCAATCTGTT ATTTGTAGGA GGTTTGTATG GGGCCAGGGT AGATTTCCAG ATTCTGCCT CAGAGGTAGT CTTTTTCACA TATGACACCT GGGTGTTTT CTCTGTGTGG CCACAAGTCT TCTGCCTCC TAAAAAAAATG TCTAGACCTT CTAGAAGGTC TTTTGCCGCT AATTCTGAAC TTTCCACTCC TTCCTTTGCA GCTGTGATTG GAGGGACATG GCTCCAGCAT GCCAATGTAA ACCACCGCCC CCTCGAG	60 120 180 240 300 337
(2) INFORMATION FOR SEQ ID NO:282:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 194 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii). MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:	
GAATTCGGCC AAAGAGGCCT AGGCTCTTCC ACTTAATTTC ATACTTTCAG GTCTGGATGC CCATTTTAAT TCTTCTGAAA GCATGCCTCC TTCTGGCTTC AGGACTCCAT CTCCAGCCTT ATGATCTAAA AATAATGGAA AATTACCCGG TATCGTTAGA GCTACACCAA AATTGCATTG AGCCAAAACT CGAG	60 120 180 194
(2) INFORMATION FOR SEQ ID NO:283:	
(i) SECTIONCE CHARACTERISTICS:	

185

(A) LENGTH: 296 base pairs

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GAATTCGGCC AAAGA	AGGCCT AAAATCATCA TAT	TCATAGA GATATTAAA	A GTGCAAATAT 60	)
CTTACTGGAT GAAGO	CTTTTA CTGCTAAAAT ATC	TGACTTT GGCCTTGCA	C GGGCTTCTGA 120	כ
GAAGTTTTGC CCAGA	ACAGTC ATGACTAGCA GAA	TTGTGGG AACAACAGC	r TATATGGCAC 180	)
CAGAAGCTTT GCGTG	GAGAA ATAACACCCA AAT	CTGATAT TTACAGCTT	r ggrgrggrrr 240	נ
TACTAGAAAT AATAA	ACTGGA CTTCCAGCTG TGG.	ATGAACA CCGTGAACC	A CTCGAG 296	5

- (2) INFORMATION FOR SEQ ID NO:284:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 456 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GAATTCGGCC	AAAGAGGCCT	AGCAACATCC	ACGCAGCTGC	TCATCAGGTA	CGAGTGCTTC	60
CATATCCATT	TACCCACCAT	TGGCAATTTG	AAAGGACCAT	CCAGACCCCC	ATAGGATCCA	120
CATGGAACAC	CCAGAGGGCT	TTCCAAAAGC	TGACTACTCC	CAAGGTCGTC	ACCAAGCCAG	180
GCCATATCAT	TAACCCCATA	AAAGCAGAAG	ACGTGGGCTA	CCGGTCTTCC	TCAAGGTCGG	240
ACCTGTCTGT	CATACAGAGG	AATCCAAAAC	GAATCACCAC	ACGTCACAAA	AAACAGCTGA	300
AGAAATGCTC	TGTAGATTGA	GTTGCTGGAG	GAGTGACAGC	CAGGAGCCCT	GACTTCACTT	360
CCTTTGGTCC	AGTTTTACTC	TGATACAGGG	TGGATTCCAA	AACTGGCTCA	GTACATTGCA	420
TGTAGTTAAG	CCACATTTTA	AAAATAAAGG	CTCGAG			456

- (2) INFORMATION FOR SEQ ID NO:285:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 150 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GAATTCGGCC AAAC	GAGGCCT AAGGTCGGC	TGTTCATCTT	GATTAGCATC	CAGGCCTTGG	60
AATATTTCAT CAAT	TGACAGC TTTATCTTT	ATATTCTTGA	TGGTGTTTGC	AAGCTCCTTT	120
GTAAGCAGCT GCTT	TCAGCTC ACCCCTCGAG	3			150

- (2) INFORMATION FOR SEQ ID NO:286:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 115 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

AATCCAAGCA ATAACCCAAG CAAAACTTCA GATGCACCTT ATGATTCTGC AGATGACTGG TCTGAGCATA TTAGCTCTTC TGGGAAAAAG TACTACTACA ATTGTCGAAC TCGAG 60

115

(2) INFORMATION	N FOR SEQ ID NO:287:	
(	UENCE CHARACTERISTICS:  (A) LENGTH: 278 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOI	LECULE TYPE: cDNA	
(xi) SEC	QUENCE DESCRIPTION: SEQ ID NO:287:	
AGATAAATGC TGG CAGTAGAGGA TGA CCTTTTATAT AAA	AGGAGAA GACTCAGATG AAGAAGAGA AATGGATACC TCTGAAAGGA TAGCCAA GATGATGAGA TGGGTTGCAC CTGGGGAATG GGAGAAGATG TGCTGAA GAGAACCCTA TTGTCTTAGA GTTTCAGCAG GAAAGGGAGG GGATCCC AAAAAGGCTC TCCAAGGCTT TTTTGACCGA GAAGGAGAAG ATTTGAT GAACAGGGAC AACTCGAG	60 120 180 240 278
(2) INFORMATIO	N FOR SEQ ID NO:288:	
(	UENCE CHARACTERISTICS:  (A) LENGTH: 364 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
. (ii) MOI	LECULE TYPE: cDNA	
(xi) SEC	QUENCE DESCRIPTION: SEQ ID NO:288:	
ATTTAACCTT CTC CATCCAGTAT AAC TTTAAAATTT TTT AACATTGATA ACA	CAACTGC CCAATAGTTT CCAGTAGAAA CATGGCCATA CCAGTCTAGA CATTTAAT CAATAGCACA ATCTAACCTA CACAAGAATA AGCAATCAAA CATGTTTT TCATTTTTAC TTTCTTGCGG TCAATTTTTT TAATGATCTA CCAAAATG ACAACTACTA TGGAATACTG AATACAAAGT TCAGTAACAC CACACACAC CACCACACAC CCACTGTTG TACTTAGTTA CGAAGAAGAG TGGGGACAGA AAATGAAGCT	60 120 180 240 300 360 364
(2) INFORMATIO	ON FOR SEQ ID NO:289:	
	UENCE CHARACTERISTICS:  (A) LENGTH: 471 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MO	LECULE TYPE: cDNA	
(xi) SE	QUENCE DESCRIPTION: SEQ ID NO:289:	
TCAGAGACGG ATC CCCTGTTTGC TGA ACGGGGGAGC ACC CCGGTGGTGA TCA	ATGTCCCA CCTAAAGGTC GGCTCTGCTG CCGACATCCC CATCAACATC CTCAGCCT GCTGACGGC ACTGTGGTCC CGCCCTCGGG CCGGAGGAG AAGCCGGCT GCGTAATGGC CACGTGGGGA TTTCATTCGT GCCCAAGGAG CTGGTGCA TGTGAAGAAA AATGGCCAGC ACGTGGCCAG CAGCCCCATC AGCCAGTC GGAAATTGGG GATGCCAGTC GTGTTCGGGT CTCTGGTCAG GGCCACAC CTTTGAGCCT GCAGAGTTTA TCATTGATAC CCGCGATGCA	60 120 180 240 300 360
	187	

GACCTGGAGG ACGGGACGTG CAGGGTCACC TACTGCCCCA CAGAGCTCGA G

GGCTATGGTG GGCTCAGCCT GTCCATTGAG GGCCCCAGCA AGGTGGACAT CAACACAGAG

420

471

(2) INFORMATION FOR SEQ ID NO:290:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 281 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:	
GAATTCGGCC TTCATGGCCT AGATTGAGTC ACATTGTTCT CTTTGATCCA TTTTCTTTTA GACAACATCA CTCAAACAAC CCTATTACTT CAGTAGCAAT GAACTGTCTC TGGATTTTAT TAAGCATCTC ACT.GTTCCT TTTCTTCAGC TGTATGGCAC CCTGTCTTCC TGTACACCAG AGGCTCCTCA GCTGGGTAAG GTGAGCCAAC GTTACCAGGA GTATATGCTG AGAGGCCATT TCAAAGTCTT TCATAGAAGG CTGTGCTTGG GCAAACTCGA G	60 120 180 240 281
(2) INFORMATION FOR SEQ ID NO:291:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 250 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:	
GAAACTCTGC CCCTGAAGGT TTGTTTTCTA ATTCAGAGGT TTAAATTAAT CTAGCCCACT TAATAAAACC AGAGATCCTA TGGGAAATTT AGCCTAAGAC AGTGCTGGAA ATTGCCATAT GTTGATACAA AGAAGTGTTT GGCCACATTA CAGGTCTCAG ACTCAACTGC TATGTGTGAC TGCCGCTCTG TGCCTATGTC TTGCTTTTTT GCTGAGTTCC CTATTTCCAT ATCTCCAGGT GATCCTCGAG	60 120 180 240 250
(2) INFORMATION FOR SEQ ID NO:292:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:	
GAAATGTCAG AGGCACATAA GCTTTTACAA AAATTGTTGG TTCATTGTCA GAAACTGAAG AACACAGAAA TGGTGATCAG TGTCCTACTG TCCGTGGCAG AGCTGTACTG GCGATCTTCC TCCCCTACCA TCGCGCTGCC CATGCTCCTG CAGGCTCTGG CCCTCTCCAA GGAGTACCGG TTACAGTACT TGGCCTCTGA AACAGTGCTG AACTTGGCTT TTGCGCAGCT CATTCTTGGA ATCCCAGAAC AGGCCCAACT CGAG	60 120 180 240 264

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 416 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:
GAATTCGGCC CTTCATGGCC TAGGTTTCTC CGTGTTGGTC AGGCTGGTCT CGAACTCCTG
                                                                       60
ACCTCAGGTG ATCCACCTGC CTCAGCCTCC CAAAGTGCTG GGATTACAGG CATGAGCCAC
                                                                      120
CATGTCCTGC TATAAATAAC TTTTAATAGG CTCTTTTTCT GGCTTTTTTT TTTAGTAACT
CAGCCCATTT TCTTCTTCTC AATCTGGTCT TTGTTAATGT TGATAACGCT GTCTTACTTT
                                                                      240
TAAATTGCCG TGATTAGAAA TTACTAGAGA TATATAAACC TAGTCTTTTG GGGGATTTTG
                                                                      300
AAAGGGTCAT AGTATTCTTA CTGTCTTTCA AAATGTACCT TATATTTGAA CATTGGAAGA
                                                                      360
TACGTGTTGC TGAATACAAG TTAGTTTCAT ACACACACAT ACACATGACA CTCGAG
(2) INFORMATION FOR SEQ ID NO:294:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 458 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:
GAATTCGGCC TTCATGGCCT ACTCCATTCC CAGATAGAAA GCTTGAATGA AGAGTTGGTC
                                                                       60
CAGCTGCTTC TCATCCGAGA TGAGCTGCAC ACAGAGCAGG ATGCCATGCT GGTGGACATT
GAAGACTTGA CCAGACATGC TGAAAGTCAG CAGAAGCACA TGGCAGAGAA AATGCCTGCA
AAGTGAAAAG AAGCCATTCA ACCAGAGAAC AAGCTAGAAT TTATTTTGCT TCTGTGGTTG
TAAAAATGCT GTTGCTAAAG GTGGCGCAGA AACAAATATC AGTGTTAGTC ATTGATAATG
                                                                      300
TCTGAAGCTT AATGTCCAGT GATTGCCCTT TGCTTCTTAA TTTATTTAA TTTTTTACTT
                                                                      360
GTGCCACTTA ATATCAGGCA TTTTAATAAA ATATTGTTAC AAAAAATGTA CAGTACTGAC
                                                                      45Ř
ACCACCACAA ATCATGGTTA ATAAAAGAGA GTCTCGAG
(2) INFORMATION FOR SEQ ID NO:295:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 302 base pairs
              (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:
GTGTAAAACC AATGCCAGGA AAACCAAATA CACAAAACCC TCCACGGAGA GGTCCTCTGA
                                                                       60
GCCAGAATGG GTCTTTTGGC CCATCCCCTG TGAGTGGTGG AGAATGCTCC CCTCCATTGA
                                                                      120
CAGTGGAGCC ACCCGTGAGA CCTCTCTCTG CTACTCTCAA TCGAAGAGAT ATGCCTAGAA
                                                                      180
                                                                      240
GTGAATTTGG ATCAGTGGAC GGGCCTCTAC CTCATCCTCG ATGGTCAGCT GAGGCATCTG
GGAAACCCTC TCCTTCTGAT CCAGGATCTG GTACAGCTAC CATGATGAAC AGCAGTCTCG
                                                                      300
                                                                      302
AG
(2) INFORMATION FOR SEQ ID NO:296:
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tilling Tilling og stiller i tilling Tilling og stiller

(A) LENGTH: 412 base pairs

(i) SEQUENCE CHARACTERISTICS:

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(B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:
CATGGATCTG CCTCCTGAGA GGGATGGAGA GAAGGGGAGG AGCACAAAGC CTGGCTTTGC
CATGCCAAAA CTTGCACTTC CCAAAATGAA GGCTTCTAAG AGTGGGGTCA GCCTGCCACA
GAGAGACGTG GATCCTTCCC TTTCTAGTGC CACAGCAGGG GGTAGCTTTC AAGACACAGA
AAAGGCCAGC AGTGACGGTG GTAGGGGAGG ACTTGGTGCA ACAGCAAGTG CCACAGGAAG
                                                                      240
TGAGGGTGTG AACCTCCACC GGCCACAGGT CCACATTCCC AGTTTGGGCT TTGCCAAACC
                                                                      300
TGATCTCAGA TCCTCCAAGG CCAAGGTGGA GGTGAGCCAG CCTGAAGCTG ACCTGCCTCT
                                                                      360
TCCCAAACAT GATCTGTCTA CCGAAGGTGA CAGCAGAGGA TGTGGGCTCG AG
                                                                      412
(2) INFORMATION FOR SEQ ID NO:297:
      (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 308 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:
GTGCTGGTGG CGCGGGGAGT GCGCGTCAAG GTGAACGAGG CCTACCGGTT CCGCGTGGCA
                                                                       60
CTGCCTGCGT ACCCAGCGTC GCTCACCGAC GTCTCCCTGG CGCTGAGCGA GCTGCGCCCC
                                                                      120
AACGACTCAG GTATCTATCG CTGTGAGGTC CAGCACGGCA TCGATGACAG CAGCGACGCT
GTGGAGGTCA AGGTCAAAGG GGTCGTCTTT CTCTACCGAG AGGGCTCTGC CCGCTATGCT
                                                                      240
TTCTCCTTTT CTGGGGCCCA GGAGGCCTGT GCCCGCATTG GAGCCCACAT CGCCACCCCA
                                                                      308
ATCTCGAG
(2) INFORMATION FOR SEQ ID NO:298:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 269 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:
GAATAAGTAA ATTCATGGAA AGGAAGAAAT TAAAAGAAAG TGAGGAAAAG GAAGTGCTTC
TGAAAACAAA CCTTTCTGGA CGGCAGAGCC CAAGTTTCAA GCTTTCCCTG TCCAGTGGAA
                                                                       180
CGAAGACTAA CCTCACCAGC CAGTCATCTA CAACAAATCT GCCTGGTTCT CCGGGATCAC
CTGGATCCCC AGGATCTCCA GGCTCTCCTG GATCCGTACC TAAAAATACA TCTCAGACGG
                                                                       240
                                                                       269
CAGCTATTAC TACAAAGGGA GGTCTCGAG
(2) INFORMATION FOR SEQ ID NO:299:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 458 base pairs
```

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GAGCGACCTT	TGGAATAGTT	AAGCACAGGT	CATTGTGGAC	ATGAATTCAG	GCCTCTGTAC	60
TAAAATCTAT	TTCAGGGAAT	GTTCTGTCTA	GTGATTTGCT	CACCATTTGA	TATATAATGA	120
ATTATAGGAC	AAGTATAAGC	TGATCTGCTA	TAGCTGTCCA	TCAGAGAGAA	TACACGTGGC	180
TATAACATCT	ATAACAAAAC	GACGATTCCT	CTACAAGAGG	CTGTTTCTCA	CTGCTAACGT	240
TGGTGTTTCT	GGCGTGGGAA	GAAATGCACA	GGCGTGCATG	GCATGCACGT	TCAGACAGCT	300
GCATTGTAAG	AGTTCTGTCA	TGCAGTCTGA	AAAGGGAAGA	AACAGGATGG	CTTTCTGTAG	360
CCACACCTGT	GAGGCGTGAT	GATTGTTGTA	TTATTAGATT	ACTGATTTTT	CTTTTCTGAA	420
AATACATTTG	AGTTTTAATC	ACATCTGTGG	AACTCGAG			458

- (2) INFORMATION FOR SEQ ID NO:300:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 99 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GGGATGCCTG	TTCTTGGGGT	AGAGAAGTCA	GGTAGCCCAG	GGCCCGCACT	CTCAATAGAC	6	0
CTTCAGAGAA	AAGGCATCGA	GGTAAATGCC	GCACTCGAG			9	9

- (2) INFORMATION FOR SEQ ID NO:301:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 569 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GGTCTAACAG	TAACACTACT	CAAGAGACCC	TGGAAATAAT	GAAAGAATCA	GAAAAAAAAC	60
TGGTGGAAGA	ATCTGTAAAC	AAAAACAAGT	TTATATCTAA	GACTCCAAGT	AAGGAAGAAA	120
TTGAGAAAGA	ATGTGAAGAT	ACCAGTTTGC	GTCAGGAGAC	ACAGAGGCGG	ACATCTAACC	180
ATGGTCATGC	CAGGAAAAGA	GCCAAGTCTA	ATTCCAAGCT	AAAGTTGGTG	CGTAGCCTGG	240
CAGTGTGTGA	GGAGTCCTCC	ACCCCATTTG	CTGATGGGCC	ATTAGAAACC	CAGGATATAA	300
TTCAATTGCA	CATCAGTTGC	CCTTCTGACA	AGGAGGAAGA	AAAGTCCACA	AAAGATGTCT	360
CTGAAAAGGA	AGACAAGGAC	AAAAACAAAG	AAAAGATCCC	AAGGAAGATG	CTGTCCAGAG	420
ACTCCAGCCA	GGAATATACG	GACTCCACTG	GAATAGACCT	ACATGAATTT	CTTGTAAATA	480
CACTGAAAAA	GAACCCAAGG	GACAGAATGA	TGCTGCTAAA	ATTAGAACAG	GAGATTCTGG	540
AATTTATTAA	TGACAACAAC	CCACTCGAG				569

- (2) INFORMATION FOR SEQ ID NO:302:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 311 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GCGATTGAAT	TCTAGACCTG	CCACCCAAAC	CCCAACTCTC	AGACTTACCT	CCCAAACCAC	60
AGATGAAGGA	CCTGCCCCCC	AAACCACAGC	TGGGAGACCT	GCTAGCAAAA	TCCCAGACTG	120
GAGATGTCTC	ACCCAAGGCT	CAGCAACCCT	CTGAGGTCAC	ACTGAAGTCA	CACCCATTGG	180
ATCTATCCCC	AAATGTGCAG	TCCAGAGACG	CCATCCAAAA	GCAAGCATCT	GAAGACTCCA	240
ACGACCTCAC	GCCTACTCTG	CCAGAGACGC	CCGTACCACT	GCCCAGAAAA	ATCAATACGG	300
GGGCACTCGA	G					311

- (2) INFORMATION FOR SEQ ID NO:303:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 683 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

ACAGCATGAA	GGCAGAAGCC	AATGCCCTGC	ATCACAAACA	CGACAAGAGG	AAGCGTCCGG	60
GGAAGAATGC	ACCCCCAGGA	GGTGATGAGC	CACTGGCAGA	GACAGAGAGT	GAAAGCGAGG	120
CAGAGCTGGC	TGGCTTCTCC	CCAGTGGTGG	ATGTGAAGAA	AACAGCATTG	GCCTTGGCCA	180
TTACAGACTC	AGAGCTGTCA	GATGAGGAGG	CTTCTATCTT	GGAGAGTGGT	GGCTTCTCCG	240
TATCCCGGGC	CACAACTCCG	CAGCTGACTG	ATGTCTCCGA	GGATTTGGAC	CAGCAGAGCC	. 300
TGCCAAGTGA	ACCAGAGGAG	ACCTAAGCCG	GGACCTAGGG	GAGGGAGAGG	AGGGAGAGCT	360
GGCCCCTCCC	CGAAGACCTA	CTAGGCCGTC	CTCAAGCTCT	GTCAAGGCAA	GCCCTGGACT	420
CGGAGGAAGA	GGAAGAGGAT	GTGGCAGCTA	AGGAAACCTT	GTTGCGGCTC	TCATCCCCCC	480
TCCACTTTGT	GAACACGCAC	TTCAATGGGG	CAGGGTCCCC	CCCAGATGGA	GTGAAATGCT	540
CCCCTGGAGG	ACCAGTGGAG	ACACTGAGCC	CCGAGACAGT	GAGTGGTGGC	CTCACTGCTC	600
TGCCCGGCAC	CCTGTCACCT	CCACTTTGCC	TTGTTGGAAG	TGACCCAGCC	CCCTCCCCTT	660
CCATTCTCCC	ACCTGATCTC	GAG				683

- (2) INFORMATION FOR SEQ ID NO:304:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 653 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCGGCC	AAAGAGGCCT	AGAGATGTCT	ACTCTCAGCT	CACGCCTGTA	ATCCCAGCAT	60
TGTGGGGAGG	TCAAGTTGGG	TGGATTGCTT	GAGCCCAGGA	GTTTGAGACC	AGCCTAAGCA	120
ATAGGCAAAA	CCCTGTCTCT	ACAAAAATCA	GCCAGGTATG	GTAGTGTGTA	CCTGTAGTCC	180
TAGCTACTCA	GGAGGCTGAG	GTGGGAGGAT	CGCTTGAGCC	TGGGAGGTGA	AGGCTGAAAT	240
TAGCCATGAT	CATGCCACTG	CACCCCAAGC	CTGGGCAACA	GAGCAAGACC	TTGTCTCAAA	300
AAAAAAAGGA	TGAGCTAGGT	TTGTATCTGT	AGACAGAGAT	TTATGATTAA	TTGGTAGGTG	360
AAAAAGTGTA	TTAAAGTACA	GTTATAGATT	AGAGTACAAA	ATGAATGAGT	ATATATGCGT	420

TTAAAAGTAT	GTATACATAT	CAGGAAAGGT	TACATGAGGA	TTTTCACTTT	CCACTTTATA	480
TCTCCCAGTA	TTTGAATTTT	TAATAACAAT	CTTTTTATCA	TAAAACTATA	TTAAATTAAA	540
CTTTTAGATT	TTTTAGTGGT	ATAAGTAGAA	CAGGAACCCT	AATACATTGT	TTTCTACTTT	600
TGTGATAAAG	ATAATTCATG	ATAGATGAAG	TTGCAAACCG	AAAGATCCTC	GAG	653

- (2) INFORMATION FOR SEQ ID NO:305:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 442 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCGGCC	TTCATGGCCT	AAGGTATTCC	AAAATGTCTA	ATTTATTTA	TCCGATGGTA	60
AATGTAATAA	TTAAAGAAAG	AGGAAAGAAT	CATGAAAGGT	GGCCCTTAAA	GAGGGCTTCT	120
GGCAGAGTTA	GGTCAGAGGC	ACACTTTCTT	ACAGACTAAG	AGTTTTTAAG	TACTCAAGGT	180
GATGTTTATC	AGAAGCTTGG	ACTGCTTCTG	TGTCTTTTTA	TTGTGCTTAT	CTGGGAGGGA	240
GAGTTCTGTG	TCTGCTCCTA	TACATCTTTC	TGCAGCTGCA	GACATACTCC	CTGAGTCTGC	300
TTTTAGCTTT	CCTATCTTAG	TGCACCTGAA	GGGAAAGGAA	TGAGCTTATT	AAGGCCCACT	360
GTTTTACTGG	GGCCCATTGT	ATGAGAGTGA	AGTTTGGCAG	TTACCCAAGA	GACGTTCCCC	420
TCACCTCCCT	CCGGCGCTCG	AG			•	442

- (2) INFORMATION FOR SEQ ID NO:306:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 412 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GAATTCGGCC	TTCATGGCCT	ACCAATATGC	AAATCAGTAC	CTCTTCTCTT	AGAGGTGTTC	60
ATGCCCAAGC	TCCTCAGACA	AGTCCATCCC	ACTGTGTGGG	AGGAAGTTGA	AGGGTGAGGA	120
TTTTTAAGAT	TTTTATCTTG	CTTGAAGTTG	TGAAGACTCA	ATGACAAATG	GCTAGGTTTT	180
GAAGGGGTCT	TGGAAGTCAT	TACTGGGGAT	AGACCCCTCT	TGATACTTGT	CACATTAATA	240
TCTGCCCAGA	CTCTCACACA	TTCAGATGTT	TAACGTCACA	TGCATTAAGT	TCTTTTGGTT	300
GCATGAGACA	GTGATGCACA	GAAACTCACT	TAGGAAAGGA	GATAGGTGGC	AATAAAGAAA	360
ACAGGGATTT	CATAGGAATG	CAGTAAAAA	AAAACCATGG	CCTAATCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:307:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 239 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GGGGTTGTCT GAGGCCCAGA GGTCGTATAA GGGCCGCTCT ACGGTGTCCT GGGGCCCGGG

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	PCT/US98/06956	
AGCTCGCCCT	GTTGCAGAAG GGTTGAGGAG CCGGGCTGGG CCCTGCGCAC CTCCCGGGGC GCTTGGCCAG CTTCTCCCAT AGCTGCTCCT TCCGCCTGAG CTTCTTGGCG GGTGGGCGAG GACGTCTTTG GGGGCAGGGA CTTTGGATGT GTTCTCGAG	120 180 239
(2) INFORMA	ATION FOR SEQ ID NO:308:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 533 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:308:	
CGCATCCTGC ACTCCAGCTT CCACGGAGAC AGCACATCCC GACCCCCAGA ATGGCTGTGA CCCTCCTTTG GCCAGCTCCA	CTGGGAAGTG CATGTCTCAG ACCAACTCCA CCTTCACCTT CACCACCTGT ATCCTTCAGA TGAGCTCACT CGGGTCACAC CAAGCCTTAA CTCAGCCCCA GTGGCAGCAC CAGCCACTTG AAATCCACGC CGGTGGCAC ACCATGCACT TGAGCCTGGC TGAGTCCTTC ACTAACACCC GTGAGTCCAC GACCACCATG TGGGGCTCGT GTGGCTGTTG AAGGAGCGG GCATTTCTGC TGCCGTGTAC GCTGGGACAG GGCCGGCCGG GGCTCCCTCC TGCACTCCTA CACGCCCAAG TCCCCTCTAC TCCGCCGAAC TCGCCTATGC AGACACCCAC ATCCTCCCA AGTTCAAGTG CACGAGCCCT CCCTACGACA ATTTCCTGGC TTCCAAGCCA TCCTGAGGGA AGTGAGAGAAA AAGAACGTCC GCAGGACCTC GAG ATION FOR SEQ ID NO:309:	60 120 180 240 300 360 420 480 533
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 297 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
·(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:309:	
GGCGCAAAAA GGTGGGATTC GGGCCCACAA	AAAGAGGCCT ACCCTAAAAC ATTTATTTCA AGGAGAAAAG AAAAAGGGGG TGGCTGGGC AATTATAGAA AACATGAGCA CCAAGAAGCT GTGCATTGTT TGCTCGTGTT CCAAATCATC GCCTTTCTGG TGGGAGGCTT GATTGCTCCA CGGCAGTGTC CTACATGTCG GTGAAATGTG TGGATGCCCG TAAGAACCAT AATGGTTCGT GCCTTGGGGA CCCAATCATT GTGGCAAGAT CCTCGAG	60 120 180 240 297
(2) INFORM	ATION FOR SEQ ID NO:310:	
(i <u>)</u> )	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 248 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:310:	

GAATTCGGCC AAAGAGGCCT AGGGTTTAAG AGCTGTGGAG GACTGAAAAC TGGATAAAAA GGGGGTCCTT TTCCTTGCCC CTGTCTCTCA CTCAGATGCG CTTCTTTTTC GCCACTGTTT

GGCAAAGTTT TCTGTTAAGC CCCCAGTTCT CCAGGTGCGT TACTATTTCT GGGATCATGG

60

120

180

GGTCAGTTTT ACCTCGAG	AGGACACTTG AACACTTCTT TTCCCCCCTC CCCAGTTCTC CAGGTGCGTT	240 248
(2) INFORMA	ATION FOR SEQ ID NO:311:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 343 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:311:	
TAGACTAGTA TCTCTTCCTC GAGTTGGTAG TATATTTAAT GACATCCCAA	AAAGAGGCCT AGGTAAATAA CTAATATTGA TGTATTTTTA TATTTTAATA AACTATGCAG AGTTAAGTGT TACATTAGAA TCTTGAACTC TCCTAACATT AGTTTCCTAT TGTTTTGGTA GAGTATGTAG ACATTTGCGA GATTAATTTA ATACATTCTG GATTTCATTT TACTTTAGAT AGCAGGTTTG GCACTTTAAA TCAGTAAGAG AATAACTGAG TATGAGCTGT ATCCTCATCT TACTGTTGAA ATAGTTGGGT GTGCACTGTG GCGGGATCTC GAG	60 120 180 240 300 343
(2) INFORMA	ATION FOR SEQ ID NO:312:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 268 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:312:	
ACTCCATGCC CCCAGCGCAC AGGCGTGGCC	AAAGAGGCCT ACGGGGAGGC GCGCCCGCGC TGAGTCGGCG GCGGTAGCC CTTGTCCGAT GGTTTGCAAC TCCGATTTTG CACACCGCTC CACCGTGCCC ACCCATTCAC ACTCACGCCA ACACTCTCGC TGAACACTTT TATAATTGTT GTTGGGACTT TGGGCGCAGC GCGGCTGATA CTGCGTCTGG AGGATTGATA CATTGCGGTT ACCTCGAG	60 120 180 240 268
(2) INFORM	ATION FOR SEQ ID NO:313:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 354 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:313:	
GTGGTGGGAA GACCCAAGCC CGAGGCGGCA CATGTTGAAG	GCCGGAGGAA GATGANGCTG AAGATTGGAT TCATCTTACG CAGTTTGCTG GCTTCCTGGG GCTAGTGGTC CTCTGGTCTT CCCTGACCCC GCGGCCGGAC CGCTGAGCAG GATGAGGGAA GACAGAGATG TCAATGACCC CATGCCCAAC ATGGACTAGC TCCTGGGGAG GACAGATTCA AACCTGTGGT ACCATGGCCT GAGTAGAAGT GGACTTAGAG TCTATTAGAA GAATAAACAA GGCCAAAAAT ACCATGCTGG AGGAGATTCC CAGAAAGATA TCATACTTCT CGAG	60 120 180 240 300 354

- (2) INFORMATION FOR SEQ ID NO:314:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 514 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GAATTCGGCC	AAAGAGGCCT	AGTGCAAGAA	CATGAAGCAC	CTGTGGTTTT	TCCTCCTGCT	60
GGTGGCAGCT	CCCAGATGTG	TCCTGTCCCA	GGTGCACCTG	CAGGAATCGG	GCCCGGGACT	120
GTTGAAACCT	TCGGACACCC	TGTCCCTCAC	CTGCTTTGTC	TCGGGTTACT	CCCTCAGTAG	180
TGTTCACTAT	TGGGGCTGGA	TCCGCCAGTC	CCCAGGGAAA	GGACTGGAGT	GGATTGGGAA	240
CATCCATCAC	AATGGTAGAA	CCAATTACAA	CCCGTCCCTC	GCCAGCCGCG	GTTCCATCTC	300
AGCCGACACG	TCC.AAGAACT	CCCTCTCCCT	GAATCTGACC	TCTGTGACCG	CCGCAGACTC	360
GGCCGTCTAT	TTCTGTGCGA	GCGGCCCTAT	TGCCTCCTTT	GAATCGACGA	CTCTAAAGGT	420
GGGCGGAGAC	TTTCACTCCT	GGGGCCAGGG	AATCCTGGTC	ACCGTCTCCT	CAGCATCCCC	480
GACCAGCCCC	AAGGTCTTCC	CGCACAGCCT	CGAG			514

- (2) INFORMATION FOR SEQ ID NO:315:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 215 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAATTCGGCC AAAGAGGCCT	AGGACACTAG	AATTATTAGT	GTTCATTTTC	ATCTAAGATC	60
TTTATTCTCT AACGTTCTTG	GTCCTATTGA	AACATTGCAG	TATGCAAAAC	TACTGCAATG	120
TTAAACCCAA GAGAAAAGCC	ATTATCATGT	GTATGCTGGT	CATCATGATC	AGTGTGGTAC	180
AATTTTTAAA AATAAACTAT	CATGCCCTTC	TCGAG			215

- (2) INFORMATION FOR SEQ ID NO:316:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 788 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GAATTATGTA	CGCCCTCTTC	CTCCTGGCCA	GCCTCCTGGG	CGCGGCTCTA	GCCGGCCCGG	60
TCCTTGGACT	GAAAGAATGC	ACCAGGGGCT	CGGCAGTGTG	GTGCCAGAAT	GTGAAGACGG	120
CGTCCGACTG	CGGGGCAGTG	AAGCACTGCC	TGCAGACCGT	TTGGAACAAG	CCAACAGTGA	180
AATCCCTTCC	CTGCGACATA	TGCAAAGACG	TTGTCACCGC	AGCTGGTGAT	ATGCTGAAGG	240
ACAATGCCAC	TGAGGAGGAG	ATCCTTGTTT	ACTTGGAGAA	GACCTGTGAC	TGGCTTCCGA	300
AACCGAACAT	GTCTGCTTCA	TGCAAGGAGA	TAGTGGACTC	CTACCTCCCT	GTCATCCTGG	360
ACATCATTAA	AGGAGAAATG	AGCCGTCCTG	GGGAGGTGTG	CTCTGCTCTC	AACCTCTGCG	420
AGTCTCTCCA	GAAGCACCTA	GCAGAGCTGA	ATCACCAGAA	GCAGCTGGAG	TCCAATAAGA	480

PCT/US98/00956	
TCCCAGAGCT GGACATGACT GAGGTGGTGG CCCCCTTCAT GGCCAACATC CCTCTCCTCC TCTACCCTCA GGACGCCCC CGCAGCAAGC CCCAGCCAAA GGATAATGGG GACGTTTGCC AGGACTGCAT TCAGATGGTG ACTGACATCC AGACTGCTGT ACGGACCAAC TCCACCTTTG TCCAGGCCTT GGTGGAACAT GTCAAGGAGG AGTGTGACCG CCTGGGCCCT GGCATGGCCG ACATATGCAA GAACTATATC AGCCAGTATT CTGAAATTGC TATCCAGATG ATGATGCACA TGCTCGAG	540 600 660 720 780 788
(2) INFORMATION FOR SEQ ID NO:317:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 214 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:	
GAATTCGGCC AAAGAGGCCT AAATCATCCT GATGATGGTT TTCTTACATA AACATGAGCT TCTGACCATG TACCATGGAT GGGTTCTCAC TTCCTGCTAT ATCCTGATCA TCACTATTGC AAATATTGCA AATTTGGCCA GTACTGCTAC TGCAATCACA ATCCAAAGGG ATTGGATTGT TGTTGTTGCA GGAGAAGACA GAAGCAAACT CGAG	60 120 180 214
(2) INFORMATION FOR SEQ ID NO:318:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 267 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:	
GTTGTCTTTT TTCCCCTTTA TAGCTGCTGG AGTGAATTTT AGAAAGCCTA AGTCATACAT CACATTGCTT CATGGCATC CCAGTACACT TTGGATTTTA TTTTACATCC TTACTGATCT GATTCTCATC TCTGTCTCTT CATGGTTCTC TGCCTTCTAG TTACACTGGT GACCTTTCAA AACCTTTACC ACATTGAGTT CATTCCTTAC TTTCCACTCT TTCCTGCCT GGAGTGTTCT GCCCCCATCTT TACGTGGCAC GCTCGAG	60 120 180 240 267
(2) INFORMATION FOR SEQ ID NO:319:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 256 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:	
GAAGCTTTCA GGCTATCTTC TAGTCAAGAT GAGTGATAAG CCAGACTTGT CGGAAGTGGA	60

- (2) INFORMATION FOR SEQ ID NO: 320:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GCTGCGTGTG	ATGGAGACCA	AACCCGACAA	GGCAGTGTCC	ATCATTGAGT	GTGACATGAA	60
CGTGGACTTT	GATGCTCCCC	TGGGCTACAA	AGAACCCGAA	AGACAAGTCC	AGCATGAGGA	120
GTCGACAGAA	GGTGAAGCCG	ACCACAGTGG	CTATGCTGGA	GAGCTGGGCT	TCCGCGCTTT	180
CTCTGGATCT	GGCAATAGAC	TGGATGGAAA	GAAGAAAGGG	GTAGAGCCCA	GCCCCTCCCC	240
AATCAAGCCT	GGAGATATTA	AAAGAGGAAT	TCCCAATTAT	GAATTTAAAC	TTGGCGCGCT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:321:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 298 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GAATTCGGCC	AAAGAGGCCT	ACTCTTACAC	CTTCCGCTCC	GTGGGCACCT	TCAATATCAT	60
CGTCACGGCT	GAGAACGAGG	TGGGCTCCGC	CCAGGACAGC	ATCTTCGTCT	ATGTCCTGCA	120
GCTCATAGAG	GGGCTGCAGG	TGGTGGGCGG	TGGCCGCTAC	TTCCCCACCA	ACCACACGGT	180
ACAGCTGCAG	GCCGTGGTTA	GGGATGGCAC	CAACGTCTCC	TACAGCTGGA	CTGCCTGGAG	240
GGACAGGGGC	CCGGCCCTGG	CCGGCAGCGG	CAAAGGCTTC	TCGCTCACCG	TGCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:322:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GCGCCGTGTC	CTTTTGCGTT	GGTACCAGCG	GCGACATGAC	GGGGTACACT	CCGGATGAGA	60
AACTGCGGCT	GCAGCAGCTG	CGAGAGCTGA	GAAGGCGATG	GCTGAAGGAC	CAGGAGCTGA	120
GCCCTCGGGA	GCCGGTGCTG	CCCCCACAGA	AGATGGGGCC	TATGGAGAAA	TTCTGGAATA	180
AATTTTTGGA	GAATAAATCC	CCTTGGAGGA	AAATGGTCCA	TGGGGTATAC	AAAAAGAGTA	240
TCTTTGTTTT	CACTCATGTA	CTTGTACCTG	TCTGGATTAT	TCATTATTAC	ATGAAGTATC	300
ATGTTTCTGA	AAAACTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:323:
  - (i) SEQUENCE CHARACTERISTICS:

	<ul><li>(A) LENGTH: 307 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:323:	
GCCCAAAATT GCCGGCAGGA CAGGAGGGCG	CAGGCCCCAG AAAAGCCTCT TGTCATCTCT CAGATGGGTT CCAAAAAGAA ATCCAGCAAA ACAAAAAAGA GACCTCGCCT CAAGTGAAGG GAGAGGAGAT AAAGACCAGG AGGCCAGCAG GGGCTCTGTT CCTTCAGGTT CCAAGATGGA CCAGTACCTC GCACCAAGGC CAGTGGAACA GAGCACAATA AGAAAGGAAC ACAAATGGTG ATATTGTTCC AGAACGAGGG GACATCGAGC ATAAGAAGGA	60 120 180 240 300 307
(2) INFORMA	ATION FOR SEQ ID NO:324:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 299 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:324:	
TGAGTCTTCT ATGGAAAGCC CCTCCAGCCA	GAGGATGCTG GGAATCTGCA GGGGGAGACG GAAATTCTTG GCTGCCTCGT CTGCATCCCA GCCATCACCT GGATTTACCT GTTTTCTGGG AGCTTCGAAG CGTGTCTCTG TCACCGCTGG AGTCCCAGGC ACACAGCCCC AGGTACACGG GCGGGAGCGC GAGAGCCTGG AGGTGCGCAT GCGCGAGGTG GAGGAGGAGA CCGCAGGCAG CTCAGCCTGG CCCAGGGCCG AGCCCCACCC ATCCTCGAG	60 120 180 240 299
(2) INFORMA	ATION FOR SEQ ID NO:325:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:325:	
TGGCTGTCTT GGTTTCCGCC CTCACCCTTT	TTCATGGCCT ACTCCAAACT CATGCCCTTG TTTTTATCTC TGCCCTTGGA CTATTTTCAC TCACAATTTC AACACATTTT GACTTGCTCG TGTCACCTAG TCAGGTATGT CTTCTTCCTT AATTTCTTTG CCGTCTTTGG TGCTGTTGAC CTGGGGTCTT CCTATTGGTC TCAGCTTCAG GTTTGCAGCC GCCCCTGGTT TCCTTCTGTG GGGTCTTCCC CTCCTTCTCA CCCACCCTCG AG	120 180 240 292
(2) INFORM	ATION FOR SEQ ID NO:326:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 345 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

# (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GAATTCGGCC	TTCAGACTTG	AAGTGGAGAA	GGCTACGATT	TTTTTGATGT	CATTTTGTGT	60
AAGGGCGCAG	ACTGCTGCGA	ACAGAGTGGT	GATAGCGCCT	AAGCATAGTG	TTAGAGTTTG	120
GATTAGTGGG	CTATTTTCTG	CTAGGGGGTG	GAAGCGGATG	AGTAAGAAGA	TTCCTGCTAC	180
AACTATAGTG	CTTGAGTGGA	GTAGGGCTGA	GACTGGGGTG	GGGCCTTCTA	TGGCTGAGGG	240
GAGTCAGGGG	TGGAGACCTA	ATTGGGCTGA	TTTGCCTGCT	GCTGCTAGGA	GGAGGCCTAG	300
TAGTGGGGTG	AGGCTTGGAT	TAGCGTTTAG	AAGGGCAAAC	TCGAG		345

- (2) INFORMATION FOR SEQ ID NO:327:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 474 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GAATTCGGCC	TTCATGNCCT	ACCTTTCCGT	CCGTTCTTTC	ACGCCTTCCT	CCTCATTTTC	60
CTTCCTTCTA	TTTTCCCTTC	CCTCTTTCCG	CTTTCCTGCC	CCGTTTCCTT	CCTCCCTCCC	120
TTCCTCCTTC	CTTCCTTCCT	CTGCGTTCTT	CCTCTCTCCT	TTGTTCCTTC	CTCCTCCTCC	180
CCACTCCCTT	TTCCTCTCCT	CTTCCCACCC	CAGTCTCCTA	CTCCCCAGTC	CTCCCATCCC	240
CATGGAACAT	ACACCTGCTT	TGTCTGGGAG	CCACGTTATT	CCTGCCAGCC	AGACCCTGGC	300
CAGGAGGATC	AGGGTCACGG	TCAGCTTGGG	CCGAGAACCC	TTCACATGAG	ACAAGCTCCT	360
CTGCCAGGGT	TTCCTGTGGG	AAAGGCCCCA	CTTCCCGACC	CTCCTGGGCC	ACTGCATGGG	420
GTCCCCTCTT	CGGCTTCTTC	TCCCCTCTCC	ACCCGGCAGC	CCCCCCAGCT	CGAG	474

- (2) INFORMATION FOR SEQ ID NO:328:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 556 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCGGCC	AAAGAGGCCT	AATTTACTCC	CCAATATAAA	ACATTTTACC	TGCGATCTAT	60
GTGTACATAT	TGAATGATGT	GTAACAATAT	CATAATTTTT	ATGTTCTGCA	TTTTTTCACT	120
TATATATCTT	TATTTAAATG	GACTTAACTT	TACTAATGGA	GTÄATTTTTA	GCTTTCAGAA	180
GGAGTTCTCA	CTCGAAGATA	AAGAACAGCT	CGCTAACCAC	GAAAGAGGAA	TCGATGCTCA	240
GCTTTTAGTT	GCACTTCCTA	AAGTTGCAGA	ATTAAGACAA	ATCTTTGAAC	CAAAGAAGAA	300
AGAATTCTTA	GAAATGAAAA	GAAAAGAAAG	AATTGCCAGG	CGCCTGGAAG	GGATTGAAAA	360
TGACACTCAG	CCCATCCTCT	TGCAGAGCTG	CACAGGATTG	GTGACTCACC	GCCTGCTGGA	420
GGAAGACACC	CCTCGATACA	TGAGAGCCAG	CGACCCTGCC	AGCCCCCACA	TCGGCCGATC	480
AAATGAAGAG	GAGGAAACTT	CTGATTCTTC	TCTAGAAAAG	CAAACTCGAT	CCAAATACTG	540
CACAGAAACC	CTCGAG					556

- (2) INFORMATION FOR SEQ ID NO:329:
  - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 385 base pairs

> (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCGGCC	AAAGAGGCCT	ACAAAACCAT	CCATAAATAA	ACAAAGCTAA	GAAAGCTAAG	60
AAACAAAGCT	AAGAAACAAA	GACTGAGGTG	AGGGAGATTT	GAGTATTTTT	TTTTCCTCTA	120
CCAACAAGTG	AAGAATTGAA	CACCTTAATC	CATCTGATCT	CCCAGGTGGA	AGCCACAAAT	180
CTTTTTTTTT	GTTTTGCTCA	GCATATTGGC	ACAGTGAGAA	ATTCATTTTA	TACTCTCTGG	240
CATCTCTCTT	GTAAACTCAC	CAAGTCTCAA	TAAGTTCACA	AAGAAGGCAG	AGACAAATAA	300
CCCTAGAATG	CAGGTGATTG	TTTATTTATG	TATTTTCCTT	GTTACATACC	CACCTATACC	360
CAAGGCCTTT	GCAGAAAAGC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:330:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 696 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

GAATTCGGCC	AAAGAGGCCT	AGGAAGCAGG	AGTTTATTTT	TATCCTTTTG	TAAGTATTAA	60
CTCGGTAATC	ACAACAAACA	CGGAGCAATC	TCAATGCTGT	TTATCCGGAG	GACAGTCTGC	120
GGGGTCGTGA	CGATTCTTTT	CTTCTTGAAG	TTTTTCCTTT	TCCTGAATCT	CATAATGATT	180
CTTGGCCATG	ATTCTGTCTT	TTCAATGACT	GTGGCTTCTA	CTCGAACAAG	ATCCTTTCCG	240
AGGAGTGGCT	TGCCAAGCAG	CGTGAAGTTG	TCTGCCCCAA	CCAGCAGGAC	CTTCTCCAGT	300
CGAATTCTCT	CTCCACACGC	AAGGTCTAGT	TCATTTCCAA	TTAAGATCAG	GTCTTCAGAG	360
GTCACCTTCC	ACTGGCGGCT	GGCAAAGTGC	ACCACGGCAA	AGAGCCTGCC	ATACTGCCCC	420
GTGACGATCA	TCTCATTCAC	TTTCTTCACG	ACCTCTGCAT	GGTGTCTGGT	CTCCTCAACT	480
GGGTCTGGCA	GAACAACTTC	TGGCCAAGGT	GGTGAACTCA	GGGATGTTTT	AGGAACATAT	540
CCTGGTAGAT	ATGAAGTGCT	CTGTGAATTG	AACCTTCGAG	AAGCAGACCA	AAGGGAGGCT	600
GCTCCGGGCC	CCGAAGGTCT	CAGGATGCTG	TGGCTGCACG	CGGACGCCAG	CCGCCCTAAG	660
GTGACCGTCA	GGGAAGATGC	TGCCATGGCC	GCCGCC			696

- (2) INFORMATION FOR SEQ ID NO:331:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 378 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GAATTCGGCC	AAAGAGGCCT	AATTTTTTGT	ACATCTGGGC	CCTTAGTTTT	TATTCTGTTT	60
ATTATATGTC	TCTGTCTCTC	TCTATTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	120
GTGTGTGTGT	GTGGTGCAGG	AGTGCCACCC	CCAGGGCCCT	GTCAACCTCT	CTTTTCTCCT	180
CCATGGCTGT	CTGCCTGCGT	ATCTGTCTCT	GAGAATCCTC	GGGGCGGTCA	GGGGATGTCA	240
GGAGGGGAAG	GAGCCGCCCT	CCCTATCTTG	CTGCTCCTCT	TGGCACTCAG	GGGCACCTTC	300
CATGGAGCCA	GACCGGGTGG	AGGGGCTTCT	GGGATTTGGT	GTCTGCTGCT	GCCAGAGCAG	360

GAACCCCCAG TACTCGAG 378

- (2) INFORMATION FOR SEQ ID NO:332:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 394 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GAATTCGGCC	TTCATGGCCT	ACATTGGGAT	TATTGGTGCT	GTGACCATGG	CTGGCATCAT	60
GGCGGCAGAC	AGAAGTGAAT	CACCTAGTTT	GACCCAAGAG	AGAGCCAACC	TGAGCGATGA	120
GCAGTGCACA	CAGGTGACCT	CCTTGTTGCA	GTTGGTTCAT	TCCTGCAGTG	AGCAGTCTCC	180
TCAGGCCTCT	GCACTTTACT	ATGATGAATT	TGCCAACCTG	ATCCAACATG	AAAAGCTGGA	240
TCCAAAAGCC	CTGGAATGGG	TTGGGCATAC	CATCTGTAAT	GATTTCCAGG	ATGCCTTCGT	300
AGTGGACTCC	TGTGTTGTTC	CGGAAGGTGA	CTTTCCATTT	CCTGTGAAAG	CACTGTACGG	360
ACTGGAAGAA	TACGACACTC	AGGATGGACT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:333:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 547 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GAATTCGGCC	AAAGAGGCCT	ACTTATTTTC	CTGTGAAAAT	GCCTACCACA	AAGAAGACAT	60
TGATGTTCTT	ATCAAGCTTT	TTCACCAGCC	TTGGGTCCTT	CATTGTAATT	TGCTCTATTC	120
TTGGGACACA	AGCATGGATC	ACCAGTACAA	TTGCTGTTAG	AGACTCTGCT	TCAAATGGGA	180
GCATTTTCAT	CACTTACGGA	CTTTTTCGTG	GGGAGAGTAG	TGAAGAATTG	AGTCACGGAC	240
TTGCAGAACC	AAAGAAAAAG	TTTGCAGTTT	TAGAGATACT	GAATAATTCT	TCCCAAAAAA	300
ACTCTGCATT	CGGTGACTAT	CCTGTTCCTG	GTCCTGAGTT	TGATCACGTC	GCTGCTGAGC	360
TCTGGGTTTA	CCTTCTACAA	CAGCATCAGC	AACCCTTACC	AGACATTCCT	GGGGCCGACG	420
GGGGTGTACA	CCTGGAACGG	GCTCGGTGCA	TCCTTCGTTT	TTGTGACCAT	GATACTGTTT	480
GTGGCGAACA	CGCAGTCCAA	CCAACTCTCC	GAAGAGTTGT	TCCAAATGCT	TTACCCGACT	540
CCTCGAG						547

- (2) INFORMATION FOR SEQ ID NO:334:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 397 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GAATTCGGCC TTCATGGCCT AGGGGAAATT GAGTCAAGAA AAGGTTCAAT ATTTTTTAAT 60
GGTAGAATTG ACCGTATGTG TATGTGCTTC TAGAAGTGAT TCAGGAGAGA GGGTGGAATG 120

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GATGGTGTGG	GACGGAGGGA	AGAATTGGTG	GAATGATGTT	GGCAAAAAGG	AATAGGCTTT	180
TGTGCATAAG	TTGAGGGATT	GGCCTTGCCT	AGAAACATGG	ACAATTCGTC	TATAGTAAGA	240
AGAGAAAAGG	TAGATCTATG	ACCACAGACA	TAGTCAGATA	ATCATTTTAA	AATTCTTTAA	300
TCAATAGATG	TTTCTGATGT	ATGGCAGGCA	GTAAGCTAAG	CAGTTTACAT	ACCTGATTTC	360
ATTTAGTTAT	TATAACAATC	CCAGTCTAAA	ACTCGAG			397

- (2) INFORMATION FOR SEQ ID NO:335:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 313 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC	TTCATGGCCT	ACTCCATCCT	TAAGGTCACC	ATTGGTATGT	TCCTGCTCTC	60
TGGAGATCCC	TGCTTCAAGA	CGCCACCATC	GACTGCCAAG	TCCATCTCCA	TCCCAGGCCA	120
${\tt GGATTCCTCC}$	CTGCAGCTGA	CGTGTAAGGG	TGGTGGGACC	AGCAGTGGGG	GCAGCAGCAC	180
CAACTCCCTG	ACTGGGTCCC	GGCCCCCAA	GGCTCGGCCC	ACTATTCTCA	GCTCAGGGCT	240
GCCAGAGGAA	CCCGACCAGA	ACCTGTCCAG	CCCTGAGGAG	GTGTTCCACT	CTGGCCACTC	300
CTCGCAACTC	GAG					313

- (2) INFORMATION FOR SEQ ID NO:336:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 467 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GAATTCGGCC	AAAGAGGCCT	AGATTGAATT	CTAGACCTGC	CTCGGCCTCC	CAAAGTGCTG	60
GGATTACAGG	CTTGAGCCAC	CACACCTGGC	CTAGTGATTT	GTAATTTCAT	GAGCTGTTGC	120
TGTATTGCCT	TCCACAGACA	GTCAATTTAT	AATCCCTCAG	TATTATATA	TCAGGAAGAT	180
TCAGTGAATG	GAATTTTGGG	TTGGTGGAGG	ACATATTTTT	TAATTGGTAG	ACCACTGAGT	240
GCTTTTGCAA	ATCTCCTTAA	ATCACATTAC	AGCAGGAACA	ACTATAGAAA	ATACAATTAT	300
TTAGGAGCAA	CCTGATCTGT	GAGCTAATTT	AATGAGTGGA	GCCCAGCCTA	CATGCTGAAG	360
AGCTCACATG	CCTCCTACCT	AGTTCCTTAA	CTAGGTTTTC	ACTCATGCCC	ATTTTGTCAT	420
ACTCTTGAAA	CCTTCCTATC	TTTGCATAGA	ACATTATTCT	TTCCACT		467

- (2) INFORMATION FOR SEQ ID NO:337:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 348 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GAATTCGGCC AAAGAGGCCT ACTTCTTTGA AGAACCATGA AGTCACACTA TATTGTGCTA

60

GCTCTAGCCT CCCTGACGTT CCTGCTGTGT CTCCCCGTGT CCCAGAGCTG TAACAAAGCA CTCTGTGCCA GCGATGTGAG CAAATGCCTC ATTCAGGAGC TCTGCCAGTG CCGGCCTGGA GAAGGGAACT GCCCCTGCTG TAAGGAGTGC ATGCTGTGCC TCGGGGCCCT GTGGGACGAG TGCTGCGACT GTGCAACCCT CGGAATTACA GCGACACCCC GCCCACATCC AAGAGCACCG TGGAGGAGCT GCACGAGCCC ATTCCGTCCG CTGTCGAG	120 180 240 300 348
(2) INFORMATION FOR SEQ ID NO:338:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 259 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:	
GAATTCGGCC TTCATGGCCT AGCCAGTCTT CAGTTATAAC CACTCCACCC TCCTCACTTT CTCTCTCTCT	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:339:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 183 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:	
GAATTCGGCC AAAGAGGCCT AGCCTTCTGC AAGATGCTTC TGATTCTGCT GTCAGTGGCC CTGCTGGCCT TCAGCTCAGC	60 120 180 183
(2) INFORMATION FOR SEQ ID NO:340:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:	
GAATTCGGCC TTCATGGCCT AGTTTTAACT GAGTGCAACA AGTATTTTCG TTAAGAGATT TTTTTTCGTA ATTTACCATT CTGCTGAATC AATTTTTAAT CCAGTTGGAA GCTCTAAAAT TCTAACATAA TTCAGAAGCA TTAAAAAAGA AGACTAAGGA AGAGAAAGCT ACATTTTAT TTCAGCTTGT ATTGCATTGT GCAGAAAGGA AAATAGTCTA GCTAATTTAC TTTTCCTATG AAAAACCTTA GAAGGCTCCT CGAG	60 120 180 240 264

- (2) INFORMATION FOR SEQ ID NO:341:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 412 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCGGCC	TTCATGGCCT	AGCCTTTCTA	GTCTTCCCTC	TTCTGTAGGA	ATANCATGTT	60
CCTCAAATGG	TCCTGAACTT	TTTCACCATT	TTGGTGAACC	CTTTTAAAGT	AAATTTACTC	120
AATGCTTTAA	AATTCATAGT	CTTAAAATAA	ATGTGAATTT	TGTTTCCAGG	TATTTATTCT.	180
GGGGTACAAA	AACTTCCCAG	AATTTACAGT	AGGAAAGGAA	ACCCCTTTAT	GATGTGGCTT	240
ATTATTACAA	GCATTCAGAA	ATGATGCTGG	CTAAGTCAAA	TCATTCCTTG	AGACAGTGAT	. 300
TCCTAAATGT	AATGCCGCCT	TCCTGAACTC	TCACATATTC	TATATCATGG	TTATTTTAAA	360
TTTATATAAA	TTAGCCTTTT	GTAACCTTAG	TCTTGTTTTG	AGCAATCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:342:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 466 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCGGCC	TTCATGGCCT	AGGGATTATA	GGTGTGAGCC	ACCGCGCCCG	GCCAGGAATC	60
ATTTTTATCC	AGGTAAGGCA	TACAGAACCG	GAGGGTTCTT	GTCTAAGTTG	TACCATGAAT	120
GTGTGCTCAG	TGGCTACTTT	GAAATAGACT	TACTGTACAA	TCCCTGAGCA	GGAATGAAAA	180
TAAAAGCTGG	AAATCACGGG	TTGCTCTGGG	GTTTTCAGGA	AGGTGTCGTC	CGTCTGGGGT	240
GAGTGTCCTC	CTTTCTCANG	GGATTTCATG	TGGCATTATT	TTGTTTTCAT	CTGAGAGGCA	300
ACATAAGCTG	GGAGGGAAGG	GCTGCAAAGA	GGGGGCCAGG	ACAAATGTGT	ACCTGGGGGC	360
CCCCATTTTG	ACTCCACCCT	GAGCTGGGGC	TGGGCCACAG	GAGGGCAGAG	GGAACACTTT	420
GGGACGGGGA	GGGAGCCCCT	GGACTGAAAG	AATGGGGTGA	CTCGAG		466

- (2) INFORMATION FOR SEQ ID NO:343:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GAATTCGGCC	TTCATGGCCT	AGAATTTTGG	AGTCTTTATC	ATAGGTAACC	TGGACCACAG	60
TTACTATTTA	TTGACAATGT	GATTGAGTGT	ATGGAGGAAA	GCACAGTGGA	TGCTAGGCTT	120
TGTAAATATG	GGGATGTAGA	AAAGCAGATA	GTTCAGTGTC	TACCTTTTTC	TAGAACTACC	180
TTGAACCTTA	AATTTTAAGT	CATGTTCATT	GCTAGAAAAT	TAAATGTACT	TATTAAAACC	240
AATGAAAAAG	CACATTTCTG	AAATGAAGTT	AGAGATAATC	TCTGTGTCTT	ATAAAAAGAC	300
ATTAATAAAA	ATCTGGTAAG	GACTCGAG				328

# (2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 416 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GAATTCGGCC	TTCATGGCCT	AGTGACCAGA	CATAAGAACT	CATTTTTAGT	TAAAGCATTT	60
TAAAAAAGTA	TACAAGGCAG	AGTTGCAAAC	AATCTCAGCC	TATGAAAAGG	ACAGCTGCAG	120
TCAATGTTCC	CACTAATATT	TTCCATCCGT	GTACTGAGTG	AATTTGTAAT	GTGCAACTCA	180
TGTCAAGAAA	ATAAACAGAT	GTGCACCACA	AGCGGAACAA	CAATGAAAGA	ACTTACATAG	240
ATTTTTATŢA	AGATTGAACT	TTTGATGTTG	ATTCCACTGG	TAAGAGAGCA	CTGTAGGCAA	300
AGGTCTTGTA	TTTATAAAGŢ	TATCTCCTAT	TGAGGAAGAT	GAAGATGTCA	ATACTCCCCA	360
ACAGAATGCT	TTGAGCTCTT	TCTAGTAGAT	CTGTGCCAAC	TCTGAAACAC	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:345:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GAATTCGGCC	TTCATGGCCT	AGTAAATACA	AAATACAAAA	ATACTGGTGA	GAGAATGGGA	60
TGATGATTAT	ATTCCTGGTT	CAGTTTTTCT	TCCTGAGAAA	TTTGATAATA	CATCTTTTGA	120
TTTTTAATAA	GTGAAATAAC	TGGTGACTGT	GTTGTATGTG	TGTGTGTGTG	TTTTTTTTT	180
AAATTTTTTT	TAGAAGTGTG	AAAAGAAACT	TCATCCACGG	AAACTTCAGG	ATAATTTTGA	240
AACAGGCAAG	TCATTTCCTA	TCTTTTTATA	ATCTCTGCCT	TGTGGGATTT	GGTTTGGTTT	300
ACCTAACTTT	CATTTTACTC	GGAGTATGTG	AGCTGTGACT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:346:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 544 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GAATTCGGCC	TTCATGGCCT	AGCCTTCGGA	ACCCCACCAG	AGTCACAGCC	AGGAAGGGCA	60
GCGGGGCGCA	CCAGGCCGAA	GGCTCACGCC	ACAGGGAGGG	CAGCTAGGAC	ATGGGGGGAA	120
GCGCGTTAAA	CCAGGGAGTC	CTGGAAGGGG	ACGACGCCCC	CGGCCAGTCC	CTGTACGAGC	180
GGTTAAGTCA	GAGGATGCTG	GACATCTCGG	GGGACCGGGG	CGTGCTGAAG	GACGTCATCC	240
GAGAAGGAGC	TGGAGACCTA	GTGGCGCCTG	ATGCTTCGGT	GCTAGATGCT	TCGTCTTGGG	300
TAAACTCCTC	GACTCCCAAG	GCCCCAGCTC	CATCTTTACC	TCAGAGCCTC	CTGAACCTCC	360
TCCTCCAGCC	TCACCTTCCT	CCAGCCTCAC	CACTCCTCCC	TGGACCTGCA	GCTCCGCACC	420
CCCGGGGGCC	TCAGAACTAC	CCCTTCCAGG	GCCTCAGAAC	TACCCCTACG	GTTTCTCCTG	480

CGTAACCTTC CGAG	TGCCTACCTT CCTGAGAGTG GTTGGTGACA GCAGCCGGGG CTAGAAACCT	540 544
(2) INFORM	ATION FOR SEQ ID NO:347:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 570 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	•
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:347:	
TGCATGATCC GAGACCTTGC GAGGCAGCAC ACTTTAGATG CAATTTGTGG TGCAGTGGGT TGTCACTCCG GTGGAGCAGA	CCTACCCAGT GATTGTCACC ATGGCCAGCA AGAGGAAATC CACCACACCA	60 120 180 240 300 360 420 480 540
(2) INFORM	ATION FOR SEQ ID NO:348:	
	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 300 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:348:	
ACTATTTTCT CTGTCCTAAT CAACAGGGTA	TTCATGGCCT AGAAAAAAGT TTTCAAAGGG AAGTAATCTT AAATCTGTAT ATGATGGAAA TTCTGTAGAG AAACAATAAC AAATTCTCCC TGACTCCTGT AGTAAGGTGG TCTTTCTTCT AATCTCCCCA TCCATCCACC CATCAGGAAG CCTTGTGTGA GTAACTGTAG ATTTCTGACT TCTTCTCGCA CCTTCAGCTG TGTAAGATGT GCTGCCGGAG GTTCTCCTGG GCAATCCCCA TTCGCTCGAG	60 120 180 240 300
(2) INFORM	ATION FOR SEQ ID NO:349:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 424 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:349:	
ATAGCCGGCC	TTCATGGCCT AACAACCACC ACCACCTGGA CGCCCAGCAG CACAACCACC TCAGGGTCAC AGAAAGCAAA GGGCACTCAG AATCATGGCA CCTAAGTCTG TCAGGGTTGC ATTGGCTCTC AAACCTGTCAT TTTGGGACTG	60 120

- (2) INFORMATION FOR SEQ ID NO:350:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GAATTCGGCC	TTCATGGCCT	AATTAGATTA	TTTTGAGCTT	GGGAACACTT	GTACATGGTT	60
CCCCGGGACA	TAAATGTAGA	AGTTCTGTAG	AGCAGTATCT	TCACATTGAG	GGATGTGAAG	120
			TTTAGAGTTC			180
CAGATATCTG	CCGATGATGA	CTTCTAACCC	ATTCAGAATC	TTTCTATGGT	ATATTGCCCT	240
GGGGTGTAAA	ATCCTCCAGG	ACCCTAAACA	GATGGACAGT	TGATGCATTT	CAGGGTAAGC	300
TGTAGACAAC	AATATATTTG	ACCCCTGAAA	CAATTCAGTA	TGCTTGTCAT	TTGTTAACTA	360
GAGTTATTTC	AAACATAATT	TTGAATAAAA	AATAAATTTT	AATAAATACA	TGTTCCCAAT	420
TATGCATATA	AAAGCAATCC	TCGAG				445

- (2) INFORMATION FOR SEQ ID NO:351:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 278 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

	AATTCGGTTC	ATGGCCTAAT	TTTGGAACTA	AGAGACAGAT	TTTTTGTTTT	TGTTTTTTA	60
	AATAGCTGTT	AACTAGTCTC	ATAAGGACAA	AATACAGAAA	GACAGTTCTT	ACAGAGAAAT	120
	AGAAGCAAAA	AAAGGAACCA	ATGGAAAATT	TAAAACTGAA	AAATAGAATA	TCTGAAATAA	180
.,	AAAATTCACT	AGATGACATA	ACTGTTGAGG	AAAGAGTATG	TGAATTTGAA	GAAAGAGCAA	240
	TAGAAATGTT	CCATTGTAAA	GAACAAAGAG	AACTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:352:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 457 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GAATTCGCCT TCATGGCCTA CAGATTATCT TACACTGAAC TGATCAAGTA CTTTGAAAAT GACTTCGAAA TTTATCTTGG TGTCCTTCAT ACTTGCTGCA CTGAGTCTTT CAACCACCTT  $^{\prime\prime}$  120

WO 98/45437

PCT/US98/06956	
TTCTCTCCAA CCAGACCAGC AAAAGGTTCT ACTAGTTTCT TTTGATGGAT TCCGTTGGGA TTACTTATAT AAAGTTCCAA CGCCCCATTT TCATTATATT ATGAAATATG GTGTTCACGT GAAGCAAGTT ACTAATGTTT TTATTACAAA AACCTACCCT AACCATTATA CTTTGGTAAC TGGCCTCTTT GCAGAGAATC ATGGGATTGT TGCAAATGAT ATGTTTGATC CTATTCGGAA CAAATCTTTC TCCTTGGATC ACATGAATAT TTATGATTCC AAGTTTTGGG AAGAAGCGAC ACCAATATGG ATCACAAACC AGATGGCAGG ACTCGAG	180 240 300 360 420 457
(2) INFORMATION FOR SEQ ID NO:353:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 295 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:	·
CCCCAAGCTT TAGTTTCTAG TGGGCCTGGA GCAATTGTGA AGGACAACTC CACCCAAGGC CCAGTATTGA AGAGGGGTAG GGTGGGAGGA TTGTACATAT CGCGAACGCT TGGCAAATCT	160 120 180 240 295
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 414 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:	
GCCTAGACAT GATGGTGGCC ACGTGCCAGG GGACCACACC CTATGTACAA AGCAGGAGAA TGATGCTCCC AGCTGAGCTG CAGGATGGGC GCTGGGCTGA CTGGAGGGT AGACGGGGTG GGGTCTGACC CCATTAGCCT TTCCCCATCC AACCTGGGCC CCCATAAGCC ATTCTCTGGC CCTCTGCACA AGACAGACTC AGCAAATCTG CGAGGTATGG GGATCTGCC AACTCCCCAC CTCGCCTCAC CTTCCCTAGG TCTGCGCGTT AGGAGATTCT GGAGCCACAG GGAGACACCC CAGAAACTCC CCGGTCGGCG ACCCAGCCCG AGACGCCTGG GGTCCCAAGG GAAGCTGAAC GCCCGCAGAA TGGGGAAATG GAGAGAGAC CTGAAAGAGC CCCTGTAACT CGAG  (2) INFORMATION FOR SEQ ID NO:355:	60 120 180 240 300 360 414
(A) LENGTH: 443 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GAATTCGGCC ATCATGGCCT ACTCCCGAGT AGCTGGGACT ACAGGCATGT GCCACCACGC CCAGCTAATT TTTTGTATTT TTTTTAGTAG AGATGGGGTT CCACCATGTT AGCTAGGATG 60 120

PC1/US98/00950	
ATTTCGATTT CCTGACCTTG TGATCCGCCC GCCTCGGCCT CCCAAAATGC TGGGATTATA	180
GGTGTGAGCC ACCACGTGGC CTCATTTCAT TCTTTCATGT GGATAGGCAG TTGTTCCAGA	240
AGTATATAGT GAGGAGCTTC TTCTTTCTCT AATGATCTGC AATGTCACCT TCATCATTTA	300
TGAAGGTTGC ACATATACAT GGGAATTTTT TAGTCTGGCA TTAAATGTTC TTCAAAAGAG	360
TTCCTGCAAA CGTTTTTGTT TTTATTTCCT ACTGTTCCCT TCACGTACTC TCTACTGAAC	420
TAAACTCTCT AATGTGTCTC GAG	443
(2) INFORMATION FOR SEQ ID NO:356:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 286 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) 101020011 111Cd1	
(ii) MOLECULE TYPE: cDNA .	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:	
• • • • • • • • • • • • • • • • • • • •	
• •	
GCGATTGAAT TCTAGACCTG CCTCGAGCTC AAGAGCAGCC CACCTGTTCA GTATTCATAC	60
CCACATATCC ATAATAGAGC TCTTCTCTTC CCCCGGGTTC CTCTGCCTCA GCCTTTTCCT	120
CTTAGCAGAT GCCATCTGCA GGGCCACTTG GCTGCCCGTA GCAGTAACCG CACAGTCTTC	180
CACATTTACT CCCTCAGCCT CAGCTGCTCC TGCAGCCCAG GCACTGTCTC TGTCTCTGCA	240
TTGCTCAAGC CTCCACCATC TCGGTTACAC CCCACAGCCA CTCGAG	286
(2) INFORMATION FOR SEQ ID NO:357:	
(i) CECHENGE CHARACTERS	
(i) SEQUENCE CHARACTERISTICS:	*
(A) LENGTH: 269 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
12//	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:	
GAATTCGGCC TTCATGGCCT ACTGCCTTAG CCTCCCAAAG TGCTGGGATT ACAGGCGTGA	60
GCCACCATGC CCAGCCCTAT AGTAGTTCTT CTTTTGCCCC TTAATATCCT CACCCACATG	120
TCCTGTACCC TGCCTGAACC CTCCTCCTCT TTTTGTTCTG ATCTTTGAGC TCCCTAGAGC	180
CCATAATTCT TTAGAGCAGG TATGTCCCGA GTCTGAAACA TGCCCTTATT TGTCCCAAGC	240
TCTGGACATT TCTCACCCCA TCTCTCGAG	269
(2) INFORMATION FOR SEQ ID NO:358:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 250 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	**
(xi) SEQUENCE DESCRIPTION: SEO ID NO:358:	

GAATTCGGCC	TTCATGGCCT	ACCAAGGAAG	CCTTTCTGTT	TTTGGCCCAA	GGAGCGTCAA	60
TAAGATCTTT	GAAAATACTT	TGAAGTCATT	TTGTGTGTGT	GTATGTGCAT	ACACACCTGA	120
TTTGTTTTAT	TTTTTATTTT	TATTTTTTGA	GTTAGGGTCT	GGCTCTGTCG	TCCAGGCTAG	180
AGTGCAGTGG	TGTGGTCTCA	GCTCACTGCA	ACCTCTGCCT	CCCAGGCTCA	AGCCGCCCCC	240

CCACCTCGAG	250
(2) INFORMATION FOR SEQ ID NO:359:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 258 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:	
GAATTCGGCC TTCATGGCCT AATGGGAGAT TGGTGGGAGT AGGGAACACA AAAGGCATGG GAAAAGAAGA TAGGTTGTAT TTTGGTCATA CTGACACCAA CATGCCTAAA GGATAGCCCT GTGAAAAAAG CTAGCAGACA GTTGAACTGC GGCTGTGAAA CAGGAAGCCG TGAGGGCTAG ACTCATCGTT GTAGTCATTC GTAAAGAGTA AATACTTGGA GCTATTGTAG TAGATGGTAT CACCACGGAA CACTCGAG	120 180
(2) INFORMATION FOR SEQ ID NO:360:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 259 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:	
GAATTCGGCC TTCATGGCCT AGGAAGCCAC AGGTCGGCTC TGCATTAGCA GGAGCAGCCG CCCTCGCTGG CCGGGGGCTC CTGGGGTTTG TCCAGCTTGA TGTCGATCAT CCCTTCTTTG CTTTTCTCCT GGACATTCTC CATTCCGGGT AGAGCCGACG CCACACGTCG AAAAAGCTGC TTCACGTTGT AGCCAGTCTT CGCACTGGTC TCAATGAACA TGACGCTCAG TTCTTTGGCG CGCTGCCCCC CCCCTCGAG	120 180
(2) INFORMATION FOR SEQ ID NO:361:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 422 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:	
GAATTCGGCC TTCATGGCCT AAAGATTAGC CTGGGTAACA TAGTGAGACC CTGTCTCTAT TAAAAAATAA TAATAAAAAT AACATTCACA TTGGTATTGT TCACTAAGGT ATTGGTTGTT AAGGCATTCA TTAAGGTATT GTTAAAACTT GTGTTAAAGCA TGTTAAAGTC TCAGTAACTT TGGGATAGAA ATAAAATGTG ATAAAAAAGCT GAAAGAAACC ACCACAAGGA AGAGTCCTTT TTGAAATATT AGAGACATAA TGCTGTCTAA TAAAAAACGA CATCAAAGAA AAACTACACT ACAGTGACTG CAGACTTAAT GTTGGCCAAC CATGCATCCT CCCTAGAAAT GCATTTGAAT TTGATTTACT AATCTTTTAT TTAGGAAATT TACATTTTTA CATTAGTGAG ATTGGCCTCG AG	120 180 240 300 360

(2)	INFORMATION	FOR	SEQ	ID	NO:362:
(2)	INFORMATION	FOR	SEQ	ΙĐ	NO:362:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 288 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GAATTCGGCC	TTCATGGCCT	AGTTATTCTT	CTAATAGCTC	AGCTACTTTT	CCTTAAAATA	60
TCTTTTTCTG	TGCAAAGCCT	TCATATAATT	GTTGTTATTA	TAACAGTGAT	GATGACTGCC	120
ACTCATTACA	ACTGCTGTTG	TTAATCTTTG	TTGTTATTTT	AAACCATATG	TTATTTAAAC	180
CATAAACTGC	ATCATAAAAG	CAGTTTCTTT	CTAATCCATG	ATGACACCTG	CTAGCCAGGT	240
ATCGTATCAA	TTCTTCACAG	GTCTATTGAA	TTCTAGACCT	GCCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:363:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 264 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

AAAAATTTCA	ACAAATCCTG	AAGTCTTTCT	GTGAAGTGAC	CAGTTCTGAA	CTTTGAAGAT	60
AAATAATTGC	TGTAAATTCC	TTTTGATTTT	CTTTTTCCAG	GTTCATGGTC	CTTGGTAATT	120
TCATTCATGG	AAAAAAATCT	TATTATAATA	ACAACAAAGA	TTTGTATATT	TTTGACTTTA	180
TATTTCCTGA	GCTCTCCTGA	CTTTGTGAAA	AAGGGTGATG	AAAATGCATT	CCGAATCTGT	240
GAGGGCCCAA	AACAGAGACT	CGAG				264

- (2) INFORMATION FOR SEQ ID NO:364:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 260 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

C	AATTCGGCC	TTCATGGCCT	AGACCCTCAT	CAATAGATGG	AGACATACAG	AAATAGTCAA	60
F	CCACATCTA	CAAAATGCCA	GTATCAGGCG	GCGGCTTCGA	AGCCAAAGTG	ATGTTTGGAT	120
C	TAAAGTGAA	ATATTAGTTG	GCGGATGAAG	CAGATAGTGA	GGAAAGTTGA	GCCAATAATG	180
7	CGTGAAGTC	CGTGGAAGCC	TGTGGCTACA	AAAAATGTTG	AGCCGTAGAT	GCCGTCGGAA	240
7	TGGTGAAGG	GAGACTCGAG					260

- (2) INFORMATION FOR SEQ ID NO:365:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 332 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GCGCCTATCA	CAAGCAGATC	ATGGGTGGCT	TCAAGGAGAC	GAAGGAGGCT	GAAGATGGCT	60
TCCGCAAGGC	CCAGAAGCCT	TGGGCCAAGA	AGATGAAGGA	GCTGGAGGCA	GCCAAGAAGG	120
CCTACCATTT	GGCTTGCAAA	GAGGAAAAGC	TGGCCATGAC	ACGGGAGATG	AACAGCAAGA	180
CGGAGCAATC	GGTCACACCT	GAGCAGCAAA	AGAAGCTGCA	GGACAAAGTG	GACAAGTGCA	240
AGCAGGATGT	GCAGAAGACA	CAGGAGAAGT	ATGAGAAAGT	GCTGGAAGAT	GTGGGCAAGA	300
CCACACCCCA	GTACATGGAG	AACAAACTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO: 366:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 330 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GAATTAACAG	AGTTTTCAGA	ATTAGAATAC	TCAGAAATGG	GATCATCGTT	CAGTGTCTCT	60
CCAAAAGCAG	AATCTGCCGT	AATAGTAGCA	AATCCTAGGG	AAGAAATAAT	CGTGAAAAAT	120
AAAGATGAAG	AAGAGAAGTT	AGTTAGTAAT	AACATCCTTC	ATAATCAACA	AGAGTTACCT	180
ACAGCTCTTA	CTAAATTGGT	TAAAGAGGTT	GAAGTTGTGT	CTTCAGAAAA	AGCAAAAGAC	240
AGTTTTAATG	AAAAGAGAGT	TGCAGTGGAA	GCTCCTATGA	GGGAGGAATA	TGCAGACTTC	300
AAACCATTTG	AGCGAGTATG	GGATCTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:367:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 200 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GCGATTGAAT	TCTAGACCTG	CCTCGAGTAC	GGAGCGAAAC	TCTGTCTCAA	АААААААА	60
AAAAAAAA	ACCGAGTATA	AAAGGCATTT	TTTTCCTTTA	AACTAAGTAA	AATATAATGT	120
TGAATAGTTC	TATTTTGCTT	AACGGGCTTT	TGTTATTTGT	TTTGTGTAGA	AATTGGCATT	180
TTTCACATAG	AAATCTCGAG					200

- (2) INFORMATION FOR SEQ ID NO:368:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 368 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GAATTCGGCC	TTCATGGCCT	AGAGAAATGA	GGAAAAAGAA	GGAAGAATAT	TTAACTTTTA	60
GTCCTCTTAC	AGTTGTAATA	TTTGTGGTCA	TCTGCTGTGT	TATGATGGTC	TTACTTTATT	120
TCTTCTACAA	ATGGTTGGTT	TATGTTATGA	TAGCAATTTT	CTGCATAGCA	TCAGCAATGA	180
GTCTGTACAA	CTGTCTTGCT	GCACTAATTC	ATAAGATACC	ATATGGACAA	TGCACGATTG	240
CATGTCGTGG	CAAAAACATG	GAAGTGAGAC	TTATTTTTCT	CTCTGGACTG	TGCATAGCAG	300
TAGCTGTTGT	TTGGGCTGTG	TTTCGAAATG	AAGACAGGTG	GGCTTGGATT	TTACAGGATA	360
TTCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:369:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GAATTCGGCC	TTCATGGCCT	ACATTCGGAG	AAGTTGAAAG	AATTACACCC	AGAACACCCA	60
TGTCTACCAT	GTTACTACAT	TTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GCGTGTGCAA	120
TTTTAATTAC	AATGGTCGAG	GAAGCTCTTG	CTGAGAAGGT	GATGTTGAAT	AAAGACTCTA	180
AAGACCCTAA	AGAGTTGAGA	GAGAGCTGTG	TGGAGTTCTG	GGGCCCAGGC	ACAGCAAGTA	240
CAAAGATCCT	GAAGCAGGAG	CATTCTTGGT	GTGTTCAAGG	AAAGCAGGAC	AACCTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:370:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 289 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GAATTCGGCC	TTCATGGCCT	ACCGCCTTTC	CATTATGCAA	CTGTGGTGGC	TTTTCTTTTG	60
TTATACGACG	ATTATTTGTC	AACCCCACTA	TCTTTGCACT	CAACCATGGG	CCCCCTGGGC	120
TCAGAGACCT	CGTGACAGTC	ATCTTCTCAT	CACCACATCT	GCAAATGTGT	GGGTGGATGG	180
GGCAGCAACA	GTCCACCTCC	TCCAAGAAGC	AGTCCCTGAT	TTTTCCTCCC	CAGACAAATC	240
TTCGTCTCTC	TGTTCTTGGA	AACTCAAAGA	ACTAAGCACC	TCCCTCGAG		289

- (2) INFORMATION FOR SEQ ID NO:371:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 540 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

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AATTCGGCCT TCATGGCCTA CAAGCTCGAT CATTATCCTT CTGTGAGTTA CCATCTGCCA
                                                                       60
AGTTCATCCG ACACCCTCTT CAATTCTCCC AAGTCGCTCT TTCTGGGAAA AGTTATAGAA
                                                                      120
ACAGGGAAAA TTGACCAAGA GATTCACAAA TACAACACCC CAGGATTCAC TGGTTGCCTC
                                                                      180
TCCAGAGTCC AGTTCAACCA GATCGCCCCT CTCAAGGCCG CCTTGAGGCA GACAAACGCC
                                                                      240
TCGGCTCACG TCCACATCCA GGGCGAGCTG GTGGAGTCCA ACTGCGGGGC CTCGCCGCTG
                                                                      300
ACCCTCTCCC CCATGTCGTC CGCCACCGAC CCCTGGCACC TGGATCACCT GGATTCAGCC
                                                                      360
AGTGCGGATT TTCCATATAA TCCAGGACAA GGCCAAGCTA TAAGAAATGG AGTCAACAGA
                                                                      420
AACTCGGCTA TCATTGGAGG CGTCATTGCT GTGGTGATTT TCACCATCCT GTGCACCCTG
                                                                      480
GTCTTCCTGA TCCGGTACAT GTTCCGCCAC AAGGGCACCT ACCATACCAA CGTTCTCGAG
                                                                      540
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- (2) INFORMATION FOR SEQ ID NO:372:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 527 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

TCGACCCCTG	GCTAATGACA	AACTATGTGA	CCTTCATGGT	GGGGGAGATT	CTGCTCCTCA	60
TCCTGACCAT	CTGCTCCCTG	GCTGCCATCT	TTCCCCGGGC	CTTTCCTAAG	AAGCTTGTGG	120
CCTTCTCAAC	TTGGATTGAC	CGGACCCGCT	GGGCCAGGAA	CACCTGGGCC	ATGCTCGCCA	180
TCTTCATCCT	GGTGATGGCA	AATGTCGTGG	ACATGCTCAG	CTGTCTCCAG	TACTACACGG	240
GACCCAGCAA	TGCAACGGCA	GGGATGGAAA	CGGAGGGCAG	CTGCCTGGAG	AACCCCAAGT	300
ATTACAACTA	TGTGGCCGTG	CTGTCCCTCA	TCGCCACCAT	CATGCTGGTG	CAGGTCAGCC	360
ACATGGTGAA	GCTCACGCTC	ATGCTGCTCG	TCGCAGGCGC	CGTGGCCACC	ATCAACCTCT	420
ATGCCTGGCG	TCCCGTCTTT	GATGAATACG	ACCACAAGCG	TTTTCGGGAG	CACGACTTAC	480
CTATGGTGGC	CTTAGAGCAG	ATGCAAGGAT	TCAACCCAGG	GCTCGAG		527

- (2) INFORMATION FOR SEQ ID NO:373:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GGCAAGAAAG	GATGTCCGCA	CAGCTGGCTG	CTGCTGAGAG	CAGACAAAAG	AAGCTGGAAA	60
TGGAGAAGCT	TCAGCTACAA	GCCCTTGAGC	AAGAGCACAA	GAAGCTGGCT	GCCCGCCTTG	120
AGGAAGAGCG	TGGCAAGAAC	AAGCAGGTGG	TCCTGATGCT	GGTCAAAGAG	TGCAAGCAGC	180
TCTCAGGCÁA	AGTCATAGAG	GAGGCCCAGA	AGCTCGAAGA	CGTAATGGCC	AAACTGGAAG	240
AGGAAAAGAA	AAAGACGAAT	GAATTAGAAG	AGGAACTCTC	CGCTGAGAAA	CGAAGAAGCA	300
CAGAAATGGA	AGCTCAGATG	GAAAAACAAC	TCTCTGAGTT	TGACACTGAG	CGGGAACAGC	360
TTCGTGCCAA	GCTGAACCGG	GAAGAAGCAC	ACACCACAAA	CCTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:374:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 322 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GAATTCGGCC TTCATGGCCT	ACTCTGTTTT	CTCCCTGGAC	TTATGTGCTT	CGTCTGGAAT	60
GTTACATCTC TTCCTCTCTT	TCTTTTTTT	TGGTCCCCAT	GTTGACTGTT	TTATTGGGGT	120
TTCTGGATAT CTCGGGGCCA	CCTCACAGGA	AGCGGTTTGC	AATGAGATCA	TAAACATTGC	180
CGAAAAATCT GTTCATTACT	GCAGCACTGT	TTCTCATCCC	CTTGACTTTC	ATCACAAGGT	240
ATCCCCTTCT GACAATAAAT	CATCTTTAAT	CATTTCTCAG	CAACCTCAAG	CCCAGCAGCG	300
AAGAGTCACC CCCTATCTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:375:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 480 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GAATTCGGCC	AAAGAGGCCT	ACCTAAACCG	TCGATTGAAT	TCTAGACCTG	CCCCAAAACC	60
AACAAGGAGA	ACAAGCTCAG	TCTTCTGTGT	CTTAATTTTT	GGCTTTACTC	TTAGCCCTGC	120
CCCATTTCCT	AGGCTCTCCA	CAGTCCAGCC	GCTTTGAGCT	ACTTTTCCTT	CCCTGATATG	180
TGCAGCTCTC	TCACCTCTGA	GCCTCCGCAC	CTGCTGTTCC	ACAGCACTCT	CCGCATTGCC	240
TTCTCCCACT	GTGGCTCACT	GCTGAGCTGT	GTTCAGGCCC	TTTGGGAAAC	CCTCTCTTTC	300
ACTCCTTTTC	CCTGGTCTGG	CTTGGGAGCC	CATGCTTACC	CCTGTCAGGA	CACCTTGAAA	360
CCCAGCAGTG	AAAACATGAC	ACTTCCTTGT	CTGGCTGATT	TTCTTAGTGA	AGCGAGTAGG	420
AGTTTCCTTT	GTCAGGACTT	CAGCAAGCAA	AATTCAGGAG	AGGTCATAAA	ATGTCTCGAG	480

- (2) INFORMATION FOR SEQ ID NO:376:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 283 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GAATTCTAGA	CCTGCCTCGA	GTAACCAGAG	AGTCTTGTCA	ACATTAACAC	TAGCAGTATT	60
TCCAACACTT	TATTTTTTA	ACTTCCTTTA	TTATACAGAA	GCAGGATCTA	TGTTTTTTAC	120
TCTTTTTGCG	TATTTGATGT	GTCTTTATGG	AAATCATAAA	ACTTCAGCCT	TCCTTGGATT	180
TTGTGGCTTC	ATGTTTCGGC	AAACAAATAT	CATCTGGGCT	GTCTTCTGTG	CAGGAAATGT	240
СРАТССРСР	AAGTTAACCC	ACCOMMOGGA	ΔΑΟΤΟΔΟΟΤΟ	GAG		283

- (2) INFORMATION FOR SEQ ID NO:377:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 324 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GAATTCGGCC	TTCATGGCCT	AAACAGCAAA	GAACAACTCA	TCACCGCTCA	CGTTCAGTAT	60
CTCCTCATCG	CGGCAATGAT	CAGGGAAAGC	CGCGTTCACG	TTTACCAAAT	GTGCCATTAC	120
AGAGGAGTTT	AGATGAAATT	CATCCAACAA	GAAGGTCACG	TTCTCCAACC	AGACACCATG	180
ATGCCTCCCG	AAGTCCAGTT	GATCATAGAA	CCAGAGATGT	GGATAGTCAG	TATTTATCAG	240
AACAAGACAG	TGAGCTTCTT	ATGCTGCCCA	GAGCAAAACG	AGGACGAAGT	GCAGAATGCC	300
TACATACTAC	CAGAATGTCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:378:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GAATTCGGCC	TTCATGGCCT	ACTGAAATTT	CAATAAAACC	AGCTTGAAAG	TTCCATTACT	60
AGAAAGATAA	GAGTGGTCAG	AAAACATTTT	TTATTAACCT	ATTTCATCTA	GTAAGAGTAT	120
CTTAAATGTT	TTTTCTCTTG	AGTACTGAAT	ACACATGCAG	GACAATGGAC	CTAAATACAG	180
TTAACTTTTG	TTTTTCACTC	CTTTGCTTTT	GCATTGTCAA	TAGTCCGGTA	AGGTTTAGGT	240
TCTATCAGAA	GTACTCAGAC	ATGCAGTGGG	CAATCGATAA	TTTCTACCTG	GGCCCTGGAT	300
GCTTGGACAA	CTGCAGGGGC	CATGGAGATT	GCTTAAGGGA	ACAGTACTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:379:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 271 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GAATTCGGCC	TTCATGGCCT	AGTCTGTGTG	TAGTGGAAAC	TCTATTGCCT	GCCCTGCACA	60
TCTGCTCCTT	TTCTTCTCTG	CACTCTGGGA	CAGCTTCTAA	AGTTTGTCCA	ACATGTCATT	120
GACTGAGTTT	TGTATCATTT	CAGTTCTGCT	CTTTACTGGT	TCCTATGTGG	ATGCTAATTA	180
TGCAAATGCA	TTTTCCACCT	CTTGCACTCC	TTTTTCTAAG	TCACCTCACT	TCTCATTTCC	240
TCATGTTTTT	CCNTTATCCT	CTTCTCTCGA	G			271

- (2) INFORMATION FOR SEQ ID NO:380:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 371 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

WO 98/45437

	PCT/US98/06956	
TTGGTTCCCC CCACATAGTA AGAACTGCTC AAAACTATGT AATGTATTAC GAAGTCTCGA		60 120 180 240 300 360 371
(2) INFORM	ATION FOR SEQ ID NO:381:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 277 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:381:	
ATACCATTTA GGGGGAGGG TAACATATGG CAGAAATGTA	GCAAATTAAT TATAGCTATC TTTAAGCTAT AAATGTGTTA ACATGTATAT TTATGTTCTA CTTTAGTGAT ATACCTTAAT TTAGTGGGCT TTGGCAGGGC GAACGTTCAT TAATCTCTGA GGAAAACAAA ACCTGTTTTC TACTTGAGTC TCCCAATTTA TTAATACTTC TGTTAAATTT GATGTCAGGT CAACATTTT TTTATTCTCA GAAACAGAAC ACTCGAG ATION FOR SEQ ID NO:382:	60 120 180 240 277
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 290 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:382:	
GGAGTAGAAC GTACAGGAAG AAACTCATAA	TTCATGGCCT AGTTGTTACT GGAGTTAAAG AGAGAACTGA GAAAGACAAA GTTTACTCAA ATAAGTAATA ACAGAAAACT TTCCAAACCA GAATATACAG GTCAAGGGTC ACCAATCCGA GTTAACTCAG ACAAGAATAC TCCAATTTAC GGGTCAAAGA CAAAGAAGAA ATTTAGAAAA CAGCAGGAGA ATAGAAGCAA AGATAGATCC AATATGCTTG GTAGCAGATT TCTCAGCAGG	60 120 180 240 290
(2) INFORMA	ATION FOR SEQ ID NO:383:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 241 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	٠
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:383:	

ATAATCCCAT G	AGCAATTTAT GGTAAGAACA AGACCCCTTT CCCTCACCAC CGAGTCTCGA	240 241
(2) INFORMA	TION FOR SEQ ID NO:384:	
(i) :	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 299 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:384:	
GACGAAAGAG TATTACTGTG CTTCAACTTA	TTCATGGCCT AGAAACACAA TAAAGCCCCA CAACAGCAAA CTTTTTAAAC AGCTCTAAAT AACAGCAAAA TGCTGCTCTT CTTGCTCCCA TTATGTTTAC CTCTAGTGAG AATAGCAAGG GGTCAAAGGA ATTTATAACA CTTCCTATAC CCAAGTCCCC TACCAAGTAA CAGTTTTCTG TCAGAGAGAA AGTTCTGCCC AAGGTGTCCA TGCCAACTAG ACTTCCCCTG TAGCTACCTG GGTCTCGAG	60 120 180 240 299
(2) INFORMA	TION FOR SEQ ID NO:385:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 546 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:385:	
TAAGCGATAT AAGGTGAAGA AATTAGGGGT AGGCAGGTCT AGCCTCGATA TCTAGTGCCA GCTCATGCAG	TTCATGGCCT AGAAAGAGGT GGCAGAAGGA ATGGTAGGAA GGGGAGGATG CATCAAGTCA GAATCATGAG TTCTTGGTGC CCGGATGTTA GAGGAGGGAA TGGCTGAAGC TGTACACTTT CATGATGGTG GAATGGAGGG GTCCCTTGGG GTCTCTAGGA AGAACCAGCT TAGGGTACAT TGAGAAAGAG GAGACAGGCT AGAATTCAAT CGCAGATCAC AGCTACAAGG ACCAGGCCTT TGATACTCTG GCTCTGATAG CATGGAGACC AGCATCTCTG CTTGCTCACC AGACAACATC GCACTTCAAA TATTGCTAGA ATAGAAGAAA TGGAGAGACT TTTGAAGCAG AAAAGACGCG GCTGCTCGAA TCCAGGGAAC GGGAAATGGA AGCCAAAAAA AAGAAGAAAAA ACGACCCCGG GAAATCCTGG AAAAACGATT ACAGGGATAG	60 120 180 240 300 360 420 480 540
(2) INFORMA	ATION FOR SEQ ID NO:386:	
(i <sub>.</sub> )	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:386:	
CAAAGTGGTT	TACATCATAG GTGTATGTTT AACTGTTCAA GAAACTGCCA AACTGTTTCC GTATTGTTTT ACATTTCCAC GAGCAGTGTT TGAGAGCTCC AGTTCTTGCA ACABAAGGT TCTGTTTTTT AAAGACAATT TTTTTTTTTTT TTGAGAGGTTT	60 120 180

CGCCCTAGTC GCCCAGGCTG GAGTGCAGTG GTAAGCGAAT CCCTGCTACA GGCCAGAGAC

TGTTCTCAGT TGGTTTTTAC ACCAAGTATC GCACTTCATT CTAACACTCC ACCATTTTAC

240

AAATGAGATT TCTCGAG	317
(2) INFORMATION FOR SEQ ID NO:387:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 234 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:	
GAATTCGGCC TTCATGGCCT AGGTCAGGTT AGTCAGCTAA TCGATAAGAG ACTTGAAATT ACTCTTTTGG GATTAGCAAA TAGAAGGGAA AAACATGATA AGGGCACAGA GCGGTGGGTC TGGGGGAAAA AGCAGAGGCA CAGTTTGAAA AAAATGTGTA AGAGACTGAC TAGGTAAGAT ATGGTCACAG TTCATAAGTC CTTTGAATTC TAGGATTAAA AAGGTGAACT CGAG	60 120 180 234
(2) INFORMATION FOR SEQ ID NO:388:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 294 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:	
GAATTCGGCC TTCATGGCCT ACTAGATAAG TGTCAATTCC ATCTGCTTCT GATTTCCCAC GTCACTGCCC TGGTCCACAC ACTGTGATCT TCTGCCCCCA TCTGAGTGCC GCATACTCAG CCTTGTCCCT GCATCAGACC CCGGCCCAGC ACAGTAACGA GAATGGGCTT CCTAAACACA AATCTGATTT GTTCCGCCTT CCACTTCCTA GTGGCTTCAT TCTCGTGCCC TCACTCAGGG CCCTCACACA TGCTGTTCCC TGCACCTCCG ACACCCTTCC CAGCGCCCCT CGAG	60 120 180 240 294
(2) INFORMATION FOR SEQ ID NO:389:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 215 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:	
GAATTCGGCC TTCATGGCCT AAGCAAAGCT AAGTGTAAAA CTAAAAAGCA GTTTGTTGCA ACTGGTCATA AAAGTGATTA AATCTAAAGC TGGCATTAAT AAGGAAGCAA GGTAATAAAA CAAAAATATA AACAGCTTTG AGAAAGTACA CCTAATAACA AAATCTTGTA ACACAACAAA TGAAAATCAC AAAAAATATA AGGAGACTCC TCGAG	60 120 180 215
(2) INFORMATION FOR SEQ ID NO:390:	
(i) SEQUENCE CHARACTERISTICS:	

- (A) LENGTH: 477 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCGGCC	TTCATGGCCT	AGAAAAACAC	TATAGTCACG	CAAGTAATGA	CCCTTCTTAT	60
CCTCAACCCC	CAGCATATAT	GCACAAGGAC	AAACAGTATA	CATACAATCT	CACCTGAGAG	120
ACGTCCTCAG	ACTTGTGTTG	AAACCTTATC	ATGCTGCATT	ATCTCCCTTA	CAACATCCTT	180
CCTGCCTTGT	TTCTCATTTT	CACACTATAC	GGAGTAAAAA	AATATACAAT	TTCTATATAT	240
TATATATATA	ACCTCCATAT	ATTTTATACT	ATTTCATATT	TTTATACTAT	CAGATTAATG	300
TTTTATATTT	TATCTATCAT	TTTAAATATG	CTATGTAAAG	CATCTACAAA	ATTGGTCACC	360
ATTCCTATGG	GAAGTATCTG	CAGAACTCTA	GAAATGAATT	CATCTTTTGC	TTACCCCTCC	420
CTTTTTGAGG	GGACAGGGAC	TTTCTTCTTT	TCCCTCATCT	TCATCTTCCC	CCTCGAG	477

- (2) INFORMATION FOR SEQ ID NO:391:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 247 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATTCGGCC	TTCATGGCCT	AGTTAGTCAG	AGTGAAATAT	TCAATAATGA	GTGGTGCAGC	60
CTTGGGACTT	GAGATTGTTT	TTGTCTTTTT	TCTGGCATTA	TTTCTGCTTC	ATCGATATGG	120
AGACTTTAAG	AAACAGCATA	GACTTGTGAT	TATTGGAACA	CTGCTTGCTT	GGTATCTCTG	180
CTTTCTTATT	GTCTTCATAC	TGCCTCTGGA	TGTTAGTACG	ACAATATACA	ACCGGTGCAA	240
GCTCGAG						247

- (2) INFORMATION FOR SEQ ID NO:392:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GAATTCGGCC	AAAGAGGCCT	AGTCATCTGC	ATTTATTATG	AGCAGCAGGT	GGGACACTTC	60
CAGCAACAGT	AAAAAAAAGT	AATTTACAAA	AGCAGGTTTC	AGTGAAGCCA	TCTGGTTGTT	120
ACCCTTGGGT	GCTCACACGT	AGATGCCAAC	CCAGAGCAGC	AGGAAGAGGA	CTCCAAAGCC	180
CATGAAGAGT	GAGGCCACTA	AGGAGATGAG	GAGCTCTTTA	TAGATATCAC	GAGTGTACTT	240
GGTAGAGGTG	ACCTCGTAAA	CGAAGAACCA	GGCGGTGAAG	AACATGCCAA	TGGCCAAAAG	300
CACCACGGTC	AGATGGGGGA	AGACAGCTGG	GTTCACTGGG	CTGGTATATC	TGCTCATGGC	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:393:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GAATTCGGCC	AAAGAGGCCT	ACCCTGGGTT	AACATTCAAG	ATGGTACATG	CTGAAGCCTT	60
TTCTCGTCCT	TTGAGTCGGA	ATGAAGTTGT	TGGTTTAATT	TTCCGTTTGA	CAATATTTGG	120
TGCAGTGACA	TACTTTACTA	TCAAATGGAT	GGTAGATGCA	ATTGATCCAA	CCAGAAAGCA	180
AAAAGTAGAA	GCTCAAAAAC	TCGAG				205

- (2) INFORMATION FOR SEQ ID NO:394:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 387 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GAATTCTAGA CCTGCCTCGA GCCGGAGATG GANAAGAAAG TCAGCCTACT CAAGGACAAT	60
AGCTCTCTGG AATTTGACTC TGAGATGGTG GAGATGGCTC AGAAGTTGGG AGCTGCTCTC	120
CAGGTTGGGG AGGCACTGGT CTGGACCAAA CCAGTTAAAG ATCCCAAATC AAAGCACCAG	180
ACCACTTCAA CCAGCAAACC TGCCAGTTTC CAGCAGCCTC TGGGCTCTAA TCAAGCTCTA	240
GGACAGGCAA TGTCTTCAGC AGCTGCATAC AGGACGCTCC CCTCAGGTGC TGGAGGAACA	300
TCCCAGTTCA CAAAGCCCCC ATCTCTTCCT CTGGAGCCAG AGCCTGCGGT GGAATCAAGT	360
CCAACTGAAA CATCAGAACT TCTCGAG	387

- (2) INFORMATION FOR SEQ ID NO:395:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 553 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GAATTCGGCC A	AAGAGGCCT	ATCGAGAAGC	CTTGTTTATT	TAATGTGAGT	TTGTGCCTTT	60
TTGTCTCAAT C	TTCCAATAC	AGGTATATTG	AGAAAAAAAG	CAGTCTAATA	AAATCCTAGA	120
CAGAACTTTC T	GGAGTCCAG	TTTGGTGATG	TCCATTTTCC	AGCTGTATGT	ATCCTCAAAC	180
TTGCACTGAT A	ACCGCCATT	TTACCAGGGC	AGGATTAGGA	AGAGGTACAA	AGGTGTGTCT	240
GAAAATTTTT G	CACGTGGAT	TTCTGCATAT	AATAGTCCCG	TGTCAGTTTA	CTTATGCAAA	300
CATTGCACAT C	TGAATTGTA	ATTCGGCCGT	TTCCTACTGA	CAGGATGTCC	TTTTGCTTTT	360
GTCTGCCTCC T	CTTCACATC	TTCCTCTTTA	TCCACCCTGC	AGCCGGGGGG	CGGGGGAGAC	420
CGGATCCCAG G	CAGGACAGT	GGCTAGGCTG	CGTGTCCCCA	CCCCCGACCC	TCGTTTGACC	480
CCTGGGAGCC G	GGGCGAAGA	CAGCACAAGG	ACGGAGCCCT	CGGATCCCTC	ACGAGTGGGG	540
CAGAGGCTGC G	igg.					553

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 472 base pairs(B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCGGCC	AAAGAGGCCT	ACAAGGTTAC	TTGACCAAGA	TGGTGACATT	GTAAGATTTG	60
AACAAAGGAA	ATGTGACTTC	AGAGTCATGG	TTGTTAACTA	TGCTATGAAG	TAGGAAAACT	120
TTATGAGGTC	TTTTTAACTC	AAACAGTCGA	GTTTTAAGTT	GAGGGTTAGC	AATGATGAAT	180
${\tt GAGTGGCCAA}$	AAAATGTATT	CATATTTTTA	${\tt GTCTTTCTTA}$	GAATTACTGG	TAGTTGTGCA	240
CAACTAGAGG	GTATTTATTT	GTGTGTGTAT	GTGTCGTGTG	TGTACGAGTG	CTGGAAATAC	300
TCTGCCAGTT	TACAGTAGAG	GCAGGCTTAC	ATAATTCAGT	CATGAAAGCT	GAGGCTTATA	360
GTTTAGAGGG	GATCGTCCTC	TTCTTAATGA	GTCTGTAAGT	TACAAAAATA	ACTTTTTTCT	420
TTATTTACTA	ACTGGTTGGT	TTTTAATATT	AAAATATTAG	GTGCTTCTCG	AG	472

- (2) INFORMATION FOR SEQ ID NO:397:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 548 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCGGCC AAAGAGG	CCT AGATTGGGGG	ACATTCTTCT	TTAGAAGGAA	AAGAGTCTAA	60
TTAGTGGATA TTAAGTA	ATT AAATAATACA	TACTATCAAA	TATTATGAGA	GTCACATGAA	120
CCATGAAGTC TTCACTT	AAT TTAGGAGAAA	TGGGGAATAT	TTTCTATCAT	TCCTGATAAC	180
AGAACTAGAT ATTTCAA	GAT CATAGTCATG	GAATGTAATC	CATAATACCA	AACAGGGTGC	240
TTTACTTTGA AGCCATTO	GAC CATTAAATTT	GATTGTTAGT	AGCACAGGCT	ACCAAAAAAT	300
AGCAAGGAAT ATGGTAT	CCA CACAGATCTC	GGCTGGCCTC	AAGTAATCAA	AAGTGAGAAT	360
GAAACATACA TGACACA	ACT GGGGACCTCT	GGGTTTCTGA	GACGTGGGCT	ACAAGATTAT	420
ATTAGGTAGA AAACTAA	AGG AAATGTATTC	CAAGCAAAAG	TGGCAAGGGA	ATTTCACAGA	480
ACTAATTTT TAAGGGA	GGT AATAAAAGCA	GCAGTTAAAA	TGCATGTCCA	TGTATCAGAT	540
TCCTGGAG				•	548

- (2) INFORMATION FOR SEQ ID NO:398:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 462 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

60	TGAAGACAGC	ACCGATTTTC	CCGGCACGAG	AGGCTAAATA	AAAGAGGCCT	GAATTCGGCC
120	CCGCCCTGCT	GAATGATAAG	AACACCTCTG	AGCGGAAAAA	CTGTTAATCC	AGATTTATCA
180	CTTCGTGTGC	CAGCCTTGAC	ATTGTGGTAT	CATCCCTCTG	TGGAGTGGAT	CCAGGGAGGA
240	GCACAAGGGC	AGCTGGAGAA	AAGGAGCTGC	GGAGAACTGC	TCTCAAACTC	CTCATCCACT
300	CACGGTGATC	CCATCCTGCC	GGCTGGGGCT	GGTGGAGTCG	GCGTGGTGGT	GAGATCCTGG

WO 98/45437

	PCT/US98/06956
CTGGCCAACA TGATGAATGG CGGCCCGGCT GCCCGCTCGG GG CAGATCATGT CCATCAATGG CACCAGCCTG GTGGGGCTGC CC ATCATCAAGG GCCTGAAGAA CCAGACACAG GTAAAGCTCG AG	CCTCGCCAC CTGCCAAGGC 420
(2) INFORMATION FOR SEQ ID NO:399:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 428 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39	9:
GAATTCGGCC AAAGAGGCCT AGGCCGGGCA CACAGAAAAA TG GCATACTCTT GATTTTTTT TTTTTTTTTG GTGTAAAAAA CA CAAAAAACAT CAAATTCCTT CCTTTTCCCC AAATCCCTGG AT CTTCCCCAAT CTGTCCTCAC CTCCTTCAGC CCATCCAAGT TA TTAGTGAGAA ATTTGGGGAT TTGCACAACA AAAAATTAGA TA TCTTCTATGC TGTGTCAAAA AAAGTTTCCT ACAGACTGAG GA CTGGGGGTTA AATGAGCCTT TATTAGAATG TTGTAGCAGT TG CTACAAAA	ACACCCTCC CCTCCCACCC 120 PCTTGGAAT GAAAGCCACC 180 ATGCACAAA AAAACAAAAA 240 AATGTTTTC CAAAACTAGG 300 ATATTCACA CGACAGGAGC 360
(2) INFORMATION FOR SEQ ID NO:400:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 269 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40	0:
GAATTCGGCC TTCATGGCCT AAGTTGAAAC TTACGAGTAA CA TTGTCATACT TTTCATTTTC CCTCCTTCA GATCCAATCC AT TTTTTCCTAG TGTACTGATT TCTGTTATGT CACTTTGCTG CT CTGTATCAGG TGTAAACACC TTTTGCTTAC CTTTCCAGGC CT CTTACTCCCA TGCTCCAACT CCCCTCGAG	TTCTACACA TTATACTGAT 120 TTAGGCTTC TTAATGCTTA 180
(2) INFORMATION FOR SEQ ID NO:401:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 236 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40	01:

- (2) INFORMATION FOR SEQ ID NO:402:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 292 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GAATTACCTT	ATACACATAG	CCTGAAGGTA	ATTTTATACA	ATATTTCCAA	TAGTTTTGTG	60
CTTCAAACAA	AGTTTGGGTA	CATTGAACCA	TCAGAAAGGA	AAGGTGTCAT	TGTCTCAGCC	120
ACCCATGTGG	ACAATCTCTG	GTTGTTTGGC	ATCACTGTTG	TTGCTGAGTC	TGAATGTGAG	180
GAACATGCCA	TTGGCATGTC	TTGCCCACAC	ACACACCATT	TTGTTATCTT	TTGTGGGTGT	240
GCTTATGTGG	GGGAATCTGG	GCGTGTGTGA	AAAAAATATA	TTGCAGCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:403:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 345 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GAATTCGGCC	TTCATGGCCT	ACTTGGGGTA	CTGAGATACA	TGGGGCCGAA	AAGGGGTAAT	60
ATGGCCATCT	TTTATCAGAA	AAAGTGACAA	AACGGGAATT	TAAAAAATGA	ATTTTCCATC	120
TGACTTTATT	TCCAAATACA	CTTTCTTTTT	TAAAAAACCA	ATACACTTTC	TTTGAGGATG	180
ACAGTATTAG	GAAATCCAAT	TATACAAAAA	ATACTACATC	TAGTCTGGGG	TAGATATATT	240
TATTTTTGGT	AACATACATT	AAGTGGCACT	AATTACACAG	TAACTATAAG	GTAACTAACA	300
TGAAACCACA	GAACTGTAAC	TCTGCCACAG	CTGCATGAAC	TCGAG		345

- (2) INFORMATION FOR SEQ ID NO:404:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 252 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

CAAGAATTTG GGTTCAGATA CCACCTTCAG TCTTACTAA GCTGCGTGAC TTTAGCAAAG TGCTTAGTCT CTCTAAGCTT CGGTTTCCTA ATCTATGAGG AGGGCCTAAG ATATCACCAC 24	GAATTCGGCC	TTCATGGCCT	AAAAAAAAA	AAGCCATTAA	TCTAATTAAT	TGTTTAATCC	60
TGCTTAGTCT CTCTAAGCTT CGGTTTCCTA ATCTATGAGG AGGGCCTAAG ATATCACCAC 24	TGCTTACAAG	ATTATCTTGA	AAAAATGTGC	TGGGGAGTAT	GGTATAATGA	ATTACGGGTC	120
Total Carlotta Control Manager Model Manager	CAAGAATTTG	GGTTCAGATA	CCACCTTCAG	TCTTTACTAA	GCTGCGTGAC	TTTAGCAAAG	180
CCATCACTCG AG 25	TGCTTAGTCT	CTCTAAGCTT	CGGTTTCCTA	ATCTATGAGG	AGGGCCTAAG	ATATCACCAC	240
	CCATCACTCG	AG					252

- (2) INFORMATION FOR SEQ ID NO:405:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 305 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GAATTCGGCC	TTCATGGCCT	AAGAATACGA	AATTTGAGAG	GATGAATTTG	ACCTTTAATA	60
TTGTTGGACT	TTGTATTGGA	TATCTTTCCT	CCATCACTTC	AAAATCGTCT	TGCTTGGCCT	120
CTTATTGCAA	CCACAGCTGC	AGTAGACAGT	TCCATACAAG	CTTCCAAGAA	CTTCATGGGT	180
ACATCTGGAG	AGCACCTCAC	CTGGGGCCAC	ATTCTCTACC	TTTCCTGTCT	TACTCTTCCT	240
CCTCTGGGCT	TCTTTCTGGT	GCATGGGGGT	GGGGGGAGAT	ATTAAGTATT	CCCCAACAGC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:406:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 250 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

GAATTCGGCC	TTCATGGCCT	ACACAGCAAC	AACCAACATA	GCTAATACAG	AAAGCAGTCA	60
GCAGACTCTA	CAGAATTCCC	AGTTTCTTTT	AACAAGGTTG	<b>AATGATCCTA</b>	AAATGTCTGA	120
AACGGAGCGC	CAGTCCATGG	AAAGCGAGCG	TGCAGACCGC	AGCCTGTTTG	TCCAAGAGCT	180
CCTTCTGTCC	ACTTTAGTGC	GTGAAGAGAG	CTCATCCTCA	GATGAGGATG	ATCGGGGGGA	240
GGTTCTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:407:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GAATTCGGCC TTCATGGCCT	AAAAGAAACT	AGGTGTGATT	GGÄAGGAAGA	ATCATGAAAG	60
ATCAGGGTAG ATACTGGTGG	GGCAGCTATT	AAAGGAGTTT	GAGCAGGGGC	ATGACATCTT	120
CACATTGAAA GCAATATGGG	AGTCGAATTA	AATTTAGTAC	CCAGTTGAGA	TAAAAGTCCA	180
TTGCCATATT CACAGTGAGG	TGGGACAAAA	GCAGAGTCAG	AGAGATTAAG	AGGCTGGGAA	240
AGATTGAAGT GATTTTTAGG	AATCAGAATC	CACATCAGTT	GATGACAAGT	ACAGAAGGGC	300
ACAATAGCAA GAAGAAGAAG	TAAATGATAA	TTCCTAGATG	CCATTAGTCA	CAATCAAGTA	360
CGGAAGAGAC ATTATTGACT	GAGGTTGAAT	CAGGGCAGAG	AAGATAATAT	ACCTGATTTT	420
GGAAGTGTTG CATGTAAGGG	GGCTTCGATT	TCAGCTACTT	ACATACTTGG	GAAGTCTCGA	480
G.					481

- (2) INFORMATION FOR SEQ ID NO:408:
  - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 308 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

GAATTCGGCT	TCATGGCCTA	CCCGGCAATT	GGCTGATCCG	CAGAAACATT	TCTGGGCTTC	60
TTTTCCATAT	CTCTGGAACT	GATAGTCAAA	CGTTAACTCT	GAGCCTGAAG	GAACCAGTTT	120
GGTGGTAAAA	AACCCAACCC	TCAGTTGTCC	GTTCACAGTC	CATTTTTGGG	TTTCACAATT	180
TGGTTCACAG	CTGTGATTCA	TGAAACGAGA	GCAATTTCCT	TTTTGAGTGG	CATCTATTAT	240
CTCATCATTC	TTCAGGGCCA	TGAAATAGTA	ATGGATGTTT	TTGTTTCGTG	CATACTCCTT	300
CACTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:409:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 337 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

C	BAATTCGGCC	TTCATGGCCT	ACAATGAGGA	TAATACAAAA	GAGCAATCTG	CCCCACTGTG	60
Į	AGCCTGAGCT	TCCCATACTG	ACTTCTCTCT	CTCCAGAGGG	ATCCACTCCT	ACCAGTCTGG	120
Į	AAGCACTGG	GCATACAAGC	GCACAAATGC	GTGGCACATA	CTACAAATCC	TTCTAAAGCC	180
7	CTGCTGTAC	ACCTGCCTCA	CTTAACCATG	CAGCCTCAAG	GCTGTCTCAT	GTCATTCTTT	240
(	CTACAGCTG	CAGAGTTTTC	AACATATGGA	CAGGTGTGCC	AGGATTTATT	TGACTAGTCT	300
(	TTACTGATC	TAGCTCACCT	CCTAAATACA	ACTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:410:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 315 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

GAATTCGGCC	TTCATGGCCT	AAAATGTGGG	GATTGGGAAC	CACTAGTTCT	TTCAGATGGT	60
ATTCTTCAGA	CTATAGAAGG	AGCTTCCAGT	TGAATTCACC	AGTGGACAAA	ATGAGGAAAA	120
CAGGTGAACA	AGCTTTTTCT	GTATTTACAT	ACAAAGTCAG	ATCAGTTATG	GGACAATAGT	180
ATTGAATAGA	TTTCAGCTTT	ATGCTGGAGT	AACTGGCATG	TGAGCAAACT	GTGTTGGCGT	240
GGGGGTGGAG	GGGTGAGGTG	GGCGCTAAGC	CTTTTTTTAA	GATTTTTCAG	GTACCCCTCA	300
CTAAAGGCAC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:411:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 277 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAATTCCCCC	TTCATCCCCT	ACCTGAACCC	CTTACTTCGA	ACCATCATA	CATTCACACC	60
						60
GGTGTTTGCA	TTTGGACTTT	TTGCTACTGA	CATTTTTGTA	AACGCCGGAC	AAGTGGTCAC	120
TGGGCACTTA	ACGCCATACT	TCCTGACTGT	GTGCAAGCCA	AACTACACCA	GTGCAGACTG	180
CCAAGCGCAC	CACCAGTTTA	TAAACAATGG	GAACATTTGT	ACTGGGGACC	TGGAAGTGAT	240
AGAAAAGGCT	CGGAGATCCT	TTCCCTCCAA	ACTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:412:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B' TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GAATTCGGCC	TCATGGCCTA	GTGGTAGGGC	TGAATTCGCA	CTATAGGGTT	AGATTTTCTA	60
CTGTAGGGTT	AGATTTTTTT	AATGGTGTGT	ATATAATAAT	ATAATATTAA	TAATAATCGG	120
AGAGGGTCAA	AGAGGAGGGA	AACTGGGTAA	CCCAAAAACA	TAAGGTCGAG	GTCCCTGTTC	180
TTCACCGGAA	AGAGGGTCAA	GGACCAAAGC	CATAGATTTG	ACTGGTAGTT	TAGTTTAGTC	240
CTGTCTACGA	AGAAGAAGAG	CGGTTGTTTG	TTTTAACAGA	TTCAAGAGCA	GGAAGCACTC	300
ATTTAGATAA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:413:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 249 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GAATTCTAGA	CCTGCCTCGA	GTCAGGCTTT	TAAAAACAAT	CTCATCTGTC	CCTCTAAAAA	60
TTAGCTTCCT	TTAGAACCTC	TTCTCCTTGG	CAATATATTA	GTGATACTAT	TGTTATCTTC	120
ACACTAAAGA	TTCAAAACTT	TAGTTTTTGT	TTTAGGAAAG	TTTTTTTTTT	TTACATTTCT	180
TTCATCCTTC	ATAATTACCC	AGTCATCATG	AACTTTGTAG	TTATCTATTT	CTTCATAGGA	240
ATCCTCGAG						. 249

- (2) INFORMATION FOR SEQ ID NO:414:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GAATTGATAC	TAGGGACCGA	AGGGAACTAA	GAGACTCCAG	AGACATGCGG	GACTCAAGGG	60
AGATGAGAGA	TTATAGCAGA	GATACCAAAG	AGAGCCGTGA	TCCCAGAGAT	TCTCGGTCCA	120
CTCGTGATGC	CCATGACTAC	AGGGACCGTG	AAGGTCGAGA	TACTCATCGA	AAGGAGGATA	180
CATATCCAGA	AGAATCCCGG	AGTTATGGCC	GAAACCATTT	GAGAGAAGAA	AGTTCTCGTA	240
CGGAAATAAG	GAATGAGTCC	AGAAATGAGT	CTCGAAGTGA	AATTAGAAAT	GACCGAATGG	300
GCCGAAGTAG	GGGGAGGGTT	CCTGAGTTAC	CTGAAAAGGG	TAGGCTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:415:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 529 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GAATTCGGCC	TTCATGGCGT	TAAAACTGTG	CCTAACAGAG	GTGTCCTCTG	ACTTTTCTTC	60
TGCAAGCTCC	ATGTTTTCAC	ATCTTCCCTT	TGACTGTGTC	CTGCTGCTGC	TGCTGCTACT	120
ACTTACAAGG	TCCTCAGAAG	TGGAATACAG	AGCGGAGGTC	${\tt GGTCAGAATG}$	CCTATCTGCC	180
CTGCTTCTAC	ACCCCAGCCG	CCCCAGGGAA	CCTCGTGCCC	GTCTGCTGGG	GCAAAGGAGC	240
CTGTCCTGTG	TTTGAATGTG	GCAACGTGGT	GCTCAGGACT	GATGAAAGGG	ATGTGAATTA	300
TTGGACATCC	AGATACTGGC	TAAATGGGGA	TTTCCGCAAA	GGAGATGTGT	CCCTGACCAT	360
AGAGAATGTG	ACTCTAGCAG	ACAGTGGGAT	CTACTGCTGC	CGGATCCAAA	TCCCAGGCAT	420
AATGAATGAT	GAAAAATTTA	ACCTGAAGTT	GGTCATCAAA	CCAGCCAAGG	TCACCCCTGC	480
ACCGACTCTG	CAGAGAGACT	TCACTGCAGC	CTTTCCAAGG	ATGCTCGAG		529

- (2) INFORMATION FOR SEQ ID NO:416:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 363 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GAATTCGGCC	TTCATGGCCT	ACTGAGCCTA	GTAATTCAAG	GCTGCAGTGA	GCTGCGATCA	60
CATCACTGCA	TTCCCGCCTG	GGCAACAGAA	GTAGACTCCA	TCTCTAAAAA	GAAGGAAAGA	120
AAAAAAGGAA	GAAATATACA	GTAATTTTAA	ACTGGGAGAT	GAAATGCTAA	TTTCTAGAAG	180
TCCATTTGGT	TTTGAAGGGT	CTCATGTCAA	AAAAAAAAA	AAGTAAGTAA	AATAAGACCC	240
ATCCTACTGT	TTTATATACT	AAAATAGTAA	GTTAATTAAA	TGAAAATGAA	GTACATTTGG	300
GCTTTCATTT	ACCAATCCTG	GAATGTTGAA	AAGTTGCCCA	AAAGACATTT	AGCAAGACTC	360
GAG						363

- (2) INFORMATION FOR SEQ ID NO:417:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 129 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

1111	MOLECUL	F TYPE:	CDNA

(xi)	SEQUENCE	DESCRIPTION:	SEO	ID	NO:417:
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GAATTCGGCC	TTCATGGCCT	ACCTGAAAGC	CCATCTCCTC	CAACTTGCAG	CGCCGGTAGA	60
GCTCGTAGTG	CCGGCTGTGG	GTCTGCTCGC	GGAGGTCTTC	CATGTTCACC	CGGATCAACC	120
TGCCTCGAG						129

- (2) INFORMATION FOR SEQ ID NO:418:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 284 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

GAATTCGGCC	TTCATGGCCT	AGGAGGTGGG	TATAGGGAAC	ACTTGGGGAG	AAATAGTGAA	60
ATCTGAATAT	AGACTGTGCA	TTGTATCATT	TAGTATAAAT	GTTGACTTGC	CTGATTTTGT	120
TGTTGAAGGC	ACTGTGGTTA	CACAAGAGAA	CGTCTGTCTT	CCTAAGTGAT	GCATGCCAAG	180
GTTTGCAGGG	GCATCCTGTC	TGCAATTACT	CTCAAATAGA	TCAAAATAAT	AATAACGTGT	240
GTGTGCATGA	TGGAGACAGG	GAAGAAGAAA	GGAAAGGGCT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:419:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 292 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GCCAGCACAT	TGTGGAACAG	AAAAATGGCA	AAGAAAGAGT	GCCCATCCTC	TGGCATTTCC	60
TGCAGAAGGA	AGCAGAGCTG	AGGCTGGTAA	AGTTCCTGCC	TGAGATTTTG	GCCTTGCAAA	120
GGGATCTAGT	GAAGCAGTTC	CAGAACGTCC	AGCAAGTTGA	ATACAGCTCC	ATCAGAGGCT	180
TCCTCAGCAA	GCACAGCTCA	GATGGGTTGA	GGCAGCTGCT	TCACAACAGG	ATCACAGTCT	240
TTCTGTCCAC	ATGGAACAAA	CTGAGGAGAT	CGCTTGAGAC	GAACAGCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:420:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GGAACCAACA GAACAACCTG TGAGGAAGAA CAAAATGGCC TCTAATATCT TTGGGACACC 60
TGAAGAAAAT CAAGCTTCTT GGGCCAAGTC AGCAGGTGCC AAGTCTAGTG GTGGCAGGGA 120

AGACTTGGAG TCATCTGGAC TGCAGAGAAG GAACTCCTCT GAAGCAAGCT CCGGAGACTT CTTAGATCTG AAGGGAGAAG GTGATATTCA TGAAAATGTG GACACAGACT TGCCAGGCAG CCTGGGGCAG AGTGAAGAGA AGCCCGTGCC TGCTGCGCCT GTGCCCAGCC CGGTGGCGCT CGAG	180 240 300 304
(2) INFORMATION FOR SEQ ID NO:421:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 256 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:	
TAATTTAGAT TATACAGAAC TTGGCCTGCA GAAACTGAAG GAGTCTGGAA AGCAGCACGG CTTTGCCTCT TTCTCTGATT ATTATTATAA GTGGTCCTCG GCGGATTCCT GTAACATGAG TGGATTGATT ACCATCGTGG TACTCCTTGG GATCGCCTTT GTAGTCTATA AGCTGTTCCT GAGTGACGGG CAGTATTCTC CTCCACCGTA CTCTGAGTAT CCTCCATTTT CCCACCGTTA CCAGAGACAA CTCGAG	60 120 180 240 256
(2) INFORMATION FOR SEQ ID NO:422:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 216 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:	
GCGATTGAAA TGGATCCTCC AGCTCTTCCA CCAAAGCCAC CTAAGCCAAT GACTTCAGCA GTTCCAAATG GAATGAAGGA CAGTTCTGTT TCTCTTCAGG ATGCAGAATG GTACTGGGGG GATATTTCAA GGGAGGAGGT AAATGACAAA TTGCGGGATA TGCCAGATGG GACCTTCTTG GTCCGAGATG CCTCAACAAA AATGCAGAGA CTCGAG	60 120 180 216
(2) INFORMATION FOR SEQ ID NO:423:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 389 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:	
GAATTCGGCC TTCATGGCCT AAAATTAATG AGTTGAACCT GTGACCACTG CATTCAAGAA GAGTCACCCA AGAGAGGT GGGGATCGA ACAGAGCTCC TTTACTTTCT CCCACAGAGG AAAAGGTGGA ATTCTGGCT GGCTTTCCCT CACCAGAGGG TATCCCAAAT CTATGACAAA AGAAAAATGC CAGTCTCTT TGGAAAGTAG GGAATCCCA AGTGATGCTG TATGAAGAAG CAAGCCTCCA TCTTCCCGG GGAAATTGA AACCAAGATG GGGTCCTGTC AATGACCTC TAGCATTTAT TGAGTGCCTA TTAGACAGGT GGCCTTGGGC TTTGAAATGC AATATCTTAT TTAACTTAAT TCTGAGAACG TATCTCGAG	60 120 180 240 300 360 389

- (2) INFORMATION FOR SEQ ID NO:424:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 411 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GCCCGTGCTG	ATGTCTTTGA	AAGAAGGCTA	TAAGAAGTCC	TCAAAAATGG	TATTTAAGGC	60
TCCCATCAAA	GAAAAGAAGA	GTGTTGTGGT	CAACGGAATA	GATTTATTAG	AAAATGTCCC	120
ACCCAGGACA	GAGAATGAGC	TCCTTCGAAT	GTTCTTCCGG	CAGCAGGATG	AGATTCGACG	180
GTTGAAAGAG	GAGCTGGCCC	AGAAGGACAT	CCGCATTCGG	CAGCTCCAGC	TGGAACTGAA	240
AAACTTGCGC	AACAGCCCCA	AGAACTGTTA	GCTCCCCAGC	TGGGCTGTTT	TCTAAGCCGA	300
TCTCTCCGTC	GTTTCTACTC	ATCCCTTAAC	TTCTCCCTTA	CCAGTGACCC	CAGAGACAGA	360
GCCAGGACAG	GAGTGGGGGC	CAGCCTGAGG	ACCCCCGCCT	ACCACCTCGA	G	411

- (2) INFORMATION FOR SEQ ID NO:425:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 691 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GGTACCAACA GGACACCCCG	GTGGCCCCCC	GCTTTGACGT	CAATGCCCCG	GACCTCTACA	60
TTCCAGCAAT GGCTTTCATC	ACCTACGTTT	TGGTGGCTGG	TCTTGCGCTG	GGGACCCAGG	120
ATAGGTTCTC CCCAGACCTC	CTGGGGCTGC	AAGCGAGCTC	AGCCCTGGCC	TGGCTGACCC	180
TGGAGGTGCT GGCCATCCTG	CTCAGCCTCT	ATCTGGTCAC	TGTCAACACC	GACCTCACCA	240
CCATCGACCT GGTGGCCTTC	TTGGGCTACA	AATATGTCGG	GATGATTGGC	GGGGTCCTCA	300
TGGGCCTGCT CTTCGGGAAG	ATTGGCTACT	ACCTGGTGCT	GGGCTGGTGC	TGCGTGGCCA	360
TCTTTGTGTT CATGATCCGG	ACGCTGCGGC	TGAAGATCTT	GGCAGACGCA	GCAGCTGAGG	420
GGGTCCCGGT GCGTGGGGCC	CGGAACCAGC	TGCGCATGTA	CCTGACCATG	GCGGTGGCGG	480
CGGCGCAGCC TATGCTCATG	TACTGGCTCA	CCTTCCACCT	GGTGCGGTGA	GCGCGCCCGC	540
TGAACCTCCC GCTGCTGCTG	CTGCTGCTGG	GGGCCACTGT	GGCCGCCGAA	CTNATCTCCT	600
GCCTGCAGGC CCCAAGGTCC	ACCCTGTCTG	GCCACAGGCA	CCGCCTCCAT	CCCATGTCCC	660
GCCCAGCCCC GCCCCCAACC	CAAGGCTCGA	G			691

- (2) INFORMATION FOR SEQ ID NO:426:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 321 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GCAGACCATA TATCGAAAGT TCTTTACTTG TATCAAGGTG AGAAAAAATT AGAAGAGATA
TTACCTCTGG GACCAAACAA AGCTCTTTTT TATAAAGGAA TGGCATCATA TCTTTTACCA
120

GGACAAAAAT	CTCCATGGTT	TTTCCAAAAA	CCCAAAGGTG	TAATAACTTT	GGACAAACAA	180
GTAATATCCA	CGAGTTCAGA	CGCCGAATCC	AGGGAAGAAG	TTCCCATGTG	TTCAGATGCT	240
GAATCCAGGC	AAGAAGTTCC	CATGTGTACA	GGCCCTGAAT	CCAGGCGAGA	AGTTCCCGTG	300
TATACAGATT	CTGAACTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:427:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 190 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTCGGCC	TTCATGGCCT	ATATACTATC	AAATGAAAAT	AGCAAGATGC	TACCATTTAT	60
ATTAAAAAGA	GGACAAAATA	TTAATATATT	CATGGTTGCT	TGTCTATGTG	GAATATTTCT	120
GGATATATAC	ATAAGAAGTT	ACATTGGTTA	CCTATGGGCA	GGTTACTACT	GGGTGGCAGG	180
TGGGCTCGAG						190

- (2) INFORMATION FOR SEQ ID NO:428:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 670 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GAATTCGGCC	TTCATGGCCT	AGGCAAAGCT	GGCCCTGACG	CCTGGGTTTC	TTGGCCCCAG	60
CTGCCCAGCA	GGTGCCTCGA	TTCCCTGCCC	TTGTGACCTC	CCAGGAAACA	GAACTGATCT	120
GGGACACTAT	GTCACCTCTC	CTCTCATCTG	GGGTCAGTCA	GGGTTCGGGG	GCTGCAGCAG	180
CCAAGCGCAT	GAGAGGTGTT	TCCTTGGCCT	TCCAGAAGGC	CCACTGTGGA	GCCAGCCTCC	240
CTATGGGAGG	CAGAGCGGCA	AGGACAGGGC	TTTGGAATCA	GCCAGGTCGG	CTCCTGGGCT	300
GTGGCCGTGG	AGAAACACTG	CCCCCAGGAT	GACACAGGCA	AGAGCCCCTG	AGGCATGGGA	360
GGCCCAGGGA	AGACCATGGG	CTGTAGGGGA	GAGTGTGGCA	GGTGACCCAA	AGGCCCAAAG	420
AGGGCCGTGG	GGCCTGAGGA	GGTCATAATC	TCTTCTGAGT	GGGGGCAGGT	CGATTCTTGC	480
ACAAGGTGGG	CTCTTCACTG	AGCCATAAGG	GACAGGGAGG	TATGGGAGAG	CGCTGGGGGC	540
CCATCCCCCT	GTCCACCCAG	TGTCCACTGG	CCTGTCCTTC	AGGGAGCAGA	GCAGAGCAGG	600
TGGTGGACGG	GCCCAGTGCT	GGGTGTTTTC	ACCACCATCC	CCCCATCCCC	CATCTAAGTC	660
GCTCCTCGAG						670

- (2) INFORMATION FOR SEQ ID NO:429:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 278 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

101/00/0/00/0	
GTAAGGATTG GCGATTCCTA CAGCGAATGA TCACCGCTCC CTGCATCCTC TTCCTGTTTT ATGGCTGGCC TGGTTTGTTC CTGGAGTCCG CACGGTGGCT GATAGTGAAG CGGCAGATTG AGGAGGCTCA GTCTGTGCTG AGGATCCTGG CTGAGCGAAA CCGGCCCCAT GGGCAGATGC TGGGGGAGGA GGCCCAGGAG GCCCTGCAGG ACCTGGAGAA TACCTGCCCT CTCCCTGCAA CATCCTCCTT TTCCTTTGCT TCCCTCCCCA ACCTCGAG	60 120 180 240 278
(2) INFORMATION FOR SEQ ID NO:430:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 299 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:	
GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TCTGTTCATC TTTAAATGCT GTTTTCTCTG TTCAAAATGC CCTTTCCTAC CTTATCTACT TGTGCCACTG CATATTCCTA AGGCTCAACT CAGGGTATCT TCCCTCGGAA ACCTTGTCTG ATCATCCTGG CCCCTCTGGC GGACAGTAAT TTCTGCCTCT GTGCTCCCAT CACCTGAGCA CACCTGTATG GTGCTGCTGA GCCCGCTGAA TTGGCATTAT GGGCACGTGC GTCTCCTCCA TTCCATGGAG CTCCTCGAG	60 120 180 240 299
(2) INFORMATION FOR SEQ ID NO:431:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 350 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:	
GTTACATGAC ACTGTTAATG ATTGCATTTG GCTTGCTGTG GGGGCATCTC TTGCGGATCA AACCCACGCA GAGCGTCTTC ATTTCCACGT GTCTGTCCTT GTCAAGCACA CCCCTCGTGT CCAGGTTCCT CATGGGCAGT GCTCGGGGTG ACAAAGAAGG CGACATTGAC TACAGCACCG TGCTCCTCGG CATGCTGGTG ACGCAGGACG TGCAGCTCGG GCTCTTCATG GCCGTCATGC CGACTCTCAT ACAGGCGGGC GCCAGTGCAT CTTCTAGCAT TGTCGTGGAA GTTCTCCGAA TCCTGGTTTT GATTGGTCAG ATTCTTTTT CACTAGCAGC GGCTCTCGAG	60 120 180 240 300 350
(2) INFORMATION FOR SEQ ID NO:432:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 305 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:	
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GCAGAAGGTC GAGGAGGAGC AGATGCTGGA CATGTGGATT AAGGAAGAAG TCTCCTCTGC TCGAG	300 305
(2) INFORMATION FOR SEQ ID NO:433:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 273 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:	
GAATTCGGCC TCATGGCCTA CTCCTCAGCC CCTCATCTTG CCTCCACCCA GCTGCTCCAT TTTTGCCACA TCGTGGCCCG CAGCCCCAGA GTCACTGTCC ATGTCACCAT CCTCCTCCTC CTTTGGAATC CTCTCCGCAC ACTGTGGCCC TTGTCTCAGG GCCCACAAGC TGAACTGTGG CATAGCTCTC TCTTCTTCTC CAAGAAGACT CAGCAGCCTA CATTCCCATT CCTGGTATGT GCCATTGGGT TGGATGTCCC CACTTATCTC GAG	60 120 180 240 273
(2) INFORMATION FOR SEQ ID NO:434:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 324 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:	
CGAGTGAGCG GGCGGACAG TGCTTGTGAA ACTGAACACA ACAAAAGTAT GGATATGGGA AACCAACATC CTTCTATTAG TAGGCTTCAG GAAATCCAAA AGGAAGTAAA AAGTGTAGAA CAGCAAGTTA TCGGCTTCAG TGGTCTGTCA GATGACAAGA ATTACAAGAA ACTGGAGAGG ATTCTAACAA AACAGCTTTT TGAAATAGAC TCTGTAGATA CTGAAGGAAA AGGAGATATT CAGCAAAGCTA GGAAGCGGC AGCACAGGAG ACAGAACGTC TTCTCAAAGA GTTGGAGCAG AATGCAAACT ACCCACACCT CGAG	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:435:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 548 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:	
GAATTCGGCC TTCATGGCCT AAATGATCAA ATTTTGGCTT ACATATTTTG CAACAGTGGT ATAACACAAA GAAGTAAGCA AATATGGCAG AAGTGTGGT GCTTTGGGGT CTACTTTTGA CCATAGTGGT GGCCCTGTTA TTCGTGGCTC CCGGGGGTTCC TACACATCCT TCCCGATGGA AGAAGGGGTT GGCCAAAAAAG GTCAGCCAGC TGATGGGTTG GACCAAGAA GACGAGTGA TAAGAATGAG TGACACCATG TTCTATCATT TTGTATTAGA TGCACCAAAA AACTATTCTG TTATTGTGAT GCTTACTGCT GCTCTCCACG CGTTCAGTTC ATGTGTCATG TGCAAAGGTG CTGCTGAAGA ATTTCAGATC TTGGCAAATT CCTATCAACG CCCTGGTGCA TTCACCACAA	60 120 180 240 300 360 420

GTCTCGAG

AGGTATTTTT TGCAATGGTG GATTATGATG AAAGCCCTGA GGTCTTTGAA GCGCTCCAGG TAACGTCAGT TCCGAGTTTC TTCCACTTTT CTGCCCAATG GAAATTTACA ACAGATGACA

480 540

(2) INFORMATION FOR SEQ ID NO:436:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 308 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:	
GAATTCGGCC TTCAT.GCCT AAAATGAAAT TCAGACAAAA TCACTGGCAC CAAAAATGGT TTATTCTGAG CTGTCTTCAC TTTGACTATT TGGGGGGCTT CTCTCAAGTA CAGATGTGGG TTGGGGTCCC CTGGAGCAGG CAGGATTGGC AGTAAGAGAT ATTGGCCACT CAAGTCTACT GTGTGTGTGT GCCTCTGGAA GAGTGAAGAA TGGACTTCAA AAGTAACATC AAAAATCTAA CTGCCACCAT CCTGGAGACA TTTTGCAGGG CTTTCCTTTC	60 120 180 240 300 308
(2) INFORMATION FOR SEQ ID NO:437:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 420 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:	
GAACAGAAGA GATCCCCTCG GCCCCCACGC CATATGACCA AAGTCACACC AGGTTCAGAG CTGCCCACTC CCAATGGAAC CACCTTATCA TCTAACCTCA CTGGTGGCAT GCCCTTCATT GATGTGCCCA CTCCCATCTC CTCTGCAAGT TCAGAAGCTG CCTCAGCAGT GGTCAGTCCC TCTACAGACAC GTGGCCTGGA ATTCTCCTCC CAAACCACTT CCAAGGAAGA CCTTACTGAT CTAGAGCAAC CTGGCTCTCC AGGGTACAGC ACAGCTACAG AGCCTGGAAG CAGTGAGCTA GGTGTTCCCG AGCAGCCTGA CCTCCAGGAA GGGACCCATG TGGAAAAGTC CCAGTCAGCA TCTGTGGGAGT CCATCCCTGA AGTGTTAGAG GAGTGCACGT CCCCTGCCGA CCAACTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:438:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 279 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:	
GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCT TCTCACTGCA CCTGGATGGC AACGTGCTGG ACCACTTCTC GGAGCTGCGC AGCGTCGAGG GGCTGCAGGA GGGCTCTGTG CTGCGTGTGG TGGAAGAGCC GTACACGGTG CGTGAGGCCC GCATCCACGT GCGCCATGTC CGAGACCTGC TCAAGAGCCT GGACCCATCC GATGCCTTCA ACGGGGTTGA CTGCAACTCC	60 120 180 240
236	

TTGTCCTTCC TG	AGTGTCTT CACCGACGGC GACCTCGAG 2	79
(2) INFORMATI	ON FOR SEQ ID NO:439:	
(i) SE	QUENCE CHARACTERISTICS:  (A) LENGTH: 351 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) Mo	DLECULE TYPE: cDNA	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:439:	
TATAACCTTT AT AATATTCTCC AT TACATGTTAA TG TGCTTATATT TA	ACCACAGT AAGCTGTTGC ATCATTCAAA TGACTCTGCA TCCTATATTG  TATTCTCT AATATCTTTG GGGGTACCCA GGATTACAGG GTTCTGGGCA  CTTTTTGCC AGGACTTTC TTTTTATTCA TTGTCGTGAC CCATTGTCTT  AAGTTTTT GCTCTTGATA TCATTGGTTC TTTCCTAAGT CACTTTTTCT  3	60 20 80 40 00
(2) INFORMATI	ON FOR SEQ ID NO:440:	
(i) SE(	QUENCE CHARACTERISTICS:  (A) LENGTH: 412 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) Mo	DLECULE TYPE: cDNA	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:440:	
TTTCACAGTT CA TTTCTTAAGC CT - CATATCTCCT TA GTTGTGGAAG AA GAATGTGATT TA	GGAATCAC AGTCCTATTT CATCTTTTGA AATAAAAGTT AAAGTCCATT TATTATAC CATTATCCAA AAACACTACC TAGCATTCAT CTTAGTTTTT GCAGATAG TTTAGTATAT TCCATTTGTC TTATTTGAGG TTTAAAAAAAA GTTTCTCA GGAGTTCAGC AAGCCTTTCC ATCTATCTTC TATTTTAAAA TTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATGATGTTC  3	60 20 80 40 00 60
(2) INFORMATI	ON FOR SEQ ID NO:441:	
(i) SE	QUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
, (ii) M	OLECULE TYPE: cDNA	
· (xi) S	EQUENCE DESCRIPTION: SEQ ID NO:441:	
GAAGATCGTG TO GGATACGCTG GG GAAGGAGAAG CT	CTGCCGCA TCTGCAAGGG CGACCACTGG ACCACCCGCT GCCCCTACAA 1 GCCCATGC AGAAGGAGCT GGCCGAGCAG CTGGGCCTGT CTACTGGCGA 1 GCCCGGGAG AGCTAGAGCC GGTGCAGGCC ACGCAGAACA AGACAGGGAA 2	60 20 80 240

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 222 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:	
GAATTCGGCC TTCATGGCCT ACCGCCTCGC TGCCTGGACA CCTGTCCGTG CCACCCTGGT CACTGAGCAG GACATCCGCG TCTGTGGCCC CTGGGACCCT GCCCCGACA GCCAGGCCTG GGTTTGTCCT TTTAGGTAGA GTGCCTGGTC CAGGTCATTG GAGGAGAGTC CACATGGCCA CCTCTGGCGT GTTCTAGAGA GGCCCTCCCG TCTAGGCTCG AG  (2) INFORMATION FOR SEQ ID NO:443:	60 120 180 222
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 205 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:	
CTTTATGACA GCCATGAGCT TTTTCCGGTG CATTGCAATT GTTTTTCCAG TCCAGAACAT TAATTTGGTT ACACAGAAAA AAGCCAGGTT TGTGTGTGTA GGTATTTGGA TTTTTGTGAT TTTGACCAGT TCTCCATTTC TAATGGCCAA ACCACAAAAA GATGAGAAAA ATAATACCAA GTGCTTTGAG CCCCCACTAC TCGAG  (2) INFORMATION FOR SEQ ID NO:444: ,	60 120 180 205
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 178 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:	
GAATTCGGCC TTCATGGCCT ACCTGCCTCC CTCCTTGCTT CTTGCTCTGC TAACTCAACT CTGCCTTCCT CTTTTCATT CTTCTACTCT GCCCTATATG GAGGACAAAT GGACACCAGG GGTGCTAACC TTATTGGTGC CTGCCCCAGC CTACCCCAGG TGCAAGCAGA CTCTCGAG	60 120 170
(2) INFORMATION FOR SEQ ID NO:445:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 251 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GAATTCGGCC TTCATGGCCT AGAAAGCCAC AAACTTTTTA GTTTTTAACT TCAAAGGCTT	60
CTTTCTCTTT AAAAAAAATT ATTTTTAATA TAGAGTCAAA AAATTGGATG TATTATTTTG	120
AGCTTCTAAT TGCTGCCACT TGGAGATGTC CAAGTAAGAA GGCCTTCTTT TTACATGGGA	180
TGAATTGTGC ACTTCTACTG ATGATGACTA CAGCAGAAGT GATGTTATAC GTACAGGCAC	240
TTGAACTCGA G	251
(2) INFORMATION FOR SEQ ID NO:446:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 301 base pairs	
•	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
1	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:	
(AI) DEGOENCE DEDOKTITION. DEG ID NO. 140.	
GAATTCGGCC TTCATGGCCT AGGGCTTATA TTTTAACTGA ACTATTATTA AATAAAAACA	60
AAATAAAATC TTATCATATA GGTGTAATCT GTTCTAAGGA AAAAATCCTT CTATCAAGAC	120
TAAACGTCTA ACTGAATACA GAATGACATT TCATGCCTTA AGGTCTCTGT CCATGTTGTT	180
CCTTCTTTCT ACTGTCCTTT ACTGTATTAG TTCAAAACAT TCTAATTCAC TCTCCAAAAC	240

- (2) INFORMATION FOR SEQ ID NO:447:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 150 base pairs

CCAATTCAAA CATCACCATC AGAAAGTCTT CCATGATGGG CCAGGTGTGG CGGCCCTCGA

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GAATTCGGCC	TTCATGGCCT	AGCTGAAATG	CTTTCTATTG	GATACTATCT	GGGCATATTA	60
CTTCCTGTGG	TTCACTGTCT	GGGTGACAGG	ATTCATAGAA	GCCCAAACTT	TAGCACCACG	120
CAGCATACCC	TTGTAACAAA	GCCACTCGAG				150

- (2) INFORMATION FOR SEQ ID NO:448:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 226 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GAATTCGGCC	TTCATGGCCT	AATTTGATTT	TATTAGGTTT	AAATTGTATT	TCTTCAAATT	60
TCATAAACTA	TAGCATTTAT	CTCCATATTT	TTAATAAATG	ATCACAAATA	AATCACTGTT	120
AATATCTCCA	TTTACACTTT	TACAACTCCT	GCTATTGCTG	GATTTTTCAT	CCTATGATAT	180

226

GTTAAACCAA TTTAAAATAC ATTTAAAGAA TCACAGCTGT CTCGAG

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 453 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) Torologi. Timeat	
(ii) MOLECULE TYPE: cDNA	
(II) NOBECOLE TIPE. CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:445:	
GAATTCGGCC TTCATGGCCT AAGACTGGGG GCATGTACCC CACCTACTTT CTGCACCTGG	
	60
ACCGTGAGGA TGGGAAGAAG GTAAGGTTGG TCTGGGCATG TTATCATCTA GGCTTTACAG	120
CCCTTTGAAA TCCTAGGGGC TGAAATGTGA CTGGAAGTCT CATATCTACC GCTGACCTCT	180
CAGTTCCTCA AAGAAACTGC CTTCGTGTCT GGTCTGTGCA CATCTTTGTG TTTTCCAGTG	240
CATTTGTGTG TGTGCACATA TGTGCGTTTG GGAGCTGACG CAACGGAGAG AGTCTGTGTG	300
AGTGGCTCTC ATGACTGTGT GCAGACCAGA GGCTGAGTCT GGAATATGAC CTCATTCCAC	360
TCCCCAAGGT GTTCCTCCTG GCGGGAAGGA AGAGAAAGAA GAGTAAAACT TCCAATTACC	420
TCATCTCTGT GGACCCCACA GACTTGTCTC GAG	453
(2) INFORMATION FOR SEQ ID NO:450:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 246 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
( ) And the state of the state	
(ii) MOLECULE TYPE: cDNA	
, ,, , , , , , , , , , , , , , , , , , ,	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:	
GAATTCGGCC TTCATGGCCT AAAAGCAAAT TAACTTGTTC TGAAAAGAAA GTATAGATTA	60
ATTTTGTTTT CTGTTTAAAT TTTATCTCCT TGGTAAAGAT TTTTTTTTCC TGGGCAGAAA	120
ACTTGGCATT TTTAGGCGTA GATACCTTAC CTTACAATGC CAAAATGAAT TTAATTCCAG	180
TACTCAGGTT TTTCCCTTTA ACAGACTCTA TGTGTACCAG GCATTGAATT CTAGACCTGC	240
CTCGAG	246
(2) INFORMATION FOR SEQ ID NO:451:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 414 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:	
GAATTCGGCC TTCATGGCCT AGTTTGGTGG GGTTGAAGTT GATGGCAAAC TCATGGGAGA	60
CCTTCCAGTC TGGGGGTAAC TGGGCCCCGA ATCCCAGAGC TGGAAACATC TTATCACTGT	120
CGTAGTCCTG AATGATCTGC CCAACAGCCC AGATGGCCGA CAGATATTCG TTGGTGCCCA	180
TAGGGTTGAT ATAGTGCAAA GAGGAAGGGT CGAGGGGATT CCCGTTGGAG GCTGTAAAGT	240
CTATTCCAAC GGTGAACATG AGCTGGCAGC CTCCCAGGAT GTAGTCAAGG AAGGAGTAGT	300
CTCGGTTTAT CTTGCAGGAT CGCAGGATGA TGATGCCCGA GTTTTTATAG TTCTTCTTCT	360
Townson I and a country of the filter of the country of the	200
240	

TCCTCTGCTT CTTGGGGTTG ATGCACTCGA ACTCCAGCGG GACGCTGTCT CGAG

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: '374 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:	
GAATTCGGCC TTCATGGCCT ACACACTGAC TGACAGACCA CGGTATGCCT TGCACCACCC TGGCTGCTGG GGTCCAAAGA GGGATCTGGT AGACCTGGGC TGGAATCTCA GCTTCACCAT TTACCATCTG GGTGGCCAAT GGAGTGTTAC TTGGCCTCTC TGAGCCTCGG TTTTGCTCGT CTCTGAAACA GTAAGATACC TCCCTTTGGC TGTTGTGATG AGGATGAAGG TTAGCCTATG CCCAGTAGTA TGCCTGTCCC TTCATCGATG CCTGCTCATC TCACTCTTGC TCTGGAAACA CCCCTAGTAG AGGCGCAGAG GGGCAGGGCC CACCCCACCC	60 120 180 240 300 360 374
(2) INFORMATION FOR SEQ ID NO:453:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 288 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:	
GCGTCCGTCC GCCGCCACCA CCCACTCCGG ACACAGAACA TCCAGTCATG GATAAAAATG AGCTGGTTCA GAAGGCCAAA CTGGCCGAGC AGGCTGAGCG ATATGATGAC ATGGCAGCCT GCATGAAGTC TGTAACTGAG CAAGGAGCTG AATTATCCAA TGAGGAGAGG AATCTTCTCT CAGTTGCTTA TAAAAATGTT GTAGGAGCCC GTAGGTCATC TTGGAGGGTC GTCTCAAGTA TGAACAAAA GACGGAAGGT GCTGAGAAAA AACAGCAGAT GGCTCGAG	60 120 180 240 288
AGCTGGTTCA GAAGGCCAAA CTGGCCGAGC AGGCTGAGCG ATATGATGAC ATGGCAGCCT GCATGAAGTC TGTAACTGAG CAAGGAGCTG AATTATCCAA TGAGGAGAGG AATCTTCTCT CAGTTGCTTA TAAAAATGTT GTAGGAGCCC GTAGGTCATC TTGGAGGGTC GTCTCAAGTA	120 180 240
AGCTGGTTCA GAAGGCCAAA CTGGCCGAGC AGGCTGAGCG ATATGATGAC ATGGCAGCCT GCATGAAGTC TGTAACTGAG CAAGGAGCTG AATTATCCAA TGAGGAGAGG AATCTTCTCT CAGTTGCTTA TAAAAATGTT GTAGGAGCCC GTAGGTCATC TTGGAGGGTC GTCTCAAGTA TTGAACAAAA GACGGAAGGT GCTGAGAAAA AACAGCAGAT GGCTCGAG	120 180 240
AGCTGGTTCA GAAGGCCAAA CTGGCCGAGC AGGCTGAGCG ATATGATGAC ATGGCAGCCT GCATGAAGTC TGTAACTGAG CAAGGAGCTG AATTATCCAA TGAGGAGAGG AATCTTCTCT CAGTTGCTTA TAAAAATGTT GTAGGAGCCC GTAGGTCATC TTGGAGGGTC GTCTCAAGTA TTGAACAAAA GACGGAAGGT GCTGAGAAAA AACAGCAGAT GGCTCGAG  (2) INFORMATION FOR SEQ ID NO:454:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 383 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240
AGCTGGTTCA GAAGGCCAAA CTGGCCGAGC AGGCTGAGCG ATATGATGAC ATGGCAGCCT GCATGAAGTC TGTAACTGAG CAAGGAGCTG AATTATCCAA TGAGGAGAGG AATCTTCTCT CAGTTGCTTA TAAAAATGTT GTAGGAGCCC GTAGGTCATC TTGGAGGGTC GTCTCAAGTA TTGAACAAAA GACGGAAGGT GCTGAGAAAA AACAGCAGAT GGCTCGAG  (2) INFORMATION FOR SEQ ID NO:454:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 383 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	120 180 240

## (2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 409 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

AGAGCACGTC	AATGCCATGA	GGGGCCTGCA	AAGCAGCAAG	GAGCTCAAGG	CTGAGCTGGA	60
CGGGGAGAAG	GGCCGGGACT	CAGGGGAGGA	GGCCCATGAC	TATGAGGTGG	ACATCAATGG	120
TTTAGAGATC	CTTGAATGCA	AATACAGGGT	GGCAGTAACT	GAGGTGATTG	ATCTGAAAGC	180
TGAAATTAAG	GCCTTAAAGG	AGAAATATAA	TAAATCTGTA	GAAAACTACA	CTGATGAGAA	240
GGCCAAGTAT	GAGAGTAAAA	TCCAGATGTA	TGATGAGCAG	GTGACAAGCC	TTGAGAAGAC	300
CACCAAGGAG	AGTGGTGAGA	AGATGGCCCA	CATGGAGAAG	GAGTTGCAAA	AGATGACCAG	360
CATAGCCAAC	GAAAATCACA	GTACCCTTAA	TACGGCCCAG	AATCTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:456:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 317 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GAATTCGGCC	TTCATGGCCT	AAATTTCATG	AAAAACAAAT	GGCTTAAACC	CAGGGAAGCA	60
AGGATTATAA	TTGATTTTTT	TGAGCAATGT	CTCTTTTGGT	TACAAAGTAA	AAGGTAAAAT	120
AAAAGTTTAA	AAGCATTTGG	AAAGAATGTT	CTTTGGTTTT	TTCACTCAGT	AACCTAAAGT	180
TTAATGACCC	TTTACAGTGC	TGATAAACAC	TTAAATTTTT	GCAGTAGGCA	TTGCTAGTTC	240
AAATTGAAGG	AAGGTTGCCA	GGCTCATGCC	TATAGTCCCA	ACTACTTAGG	AGGCTAAGGC	300
AGGGGGACGC	CCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:457:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 510 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GAATTCGGCT	TCATGGCCTA	CTGCTCTTTG	GCTAAGGTGG	CAGTGTACCT	CTAGATCAAC	60
CTGGGCAACA	GTCACAAGGG	AGTGTGACTT	CTTGGCCATA	ATAAACTCAC	TTGATAGTGT	120
TTATGTTATT	AATCTGAATG	CAACAGAAGA	CAAAAGCACA	GGCATGCACA	CACACAGAAC	180
CCCAAACCAC	TAAAAACTAC	CTAAACACTG	ACTTAGTAAA	TAGTAAAAAG	GTAATGTTGG	240
GACTTTTAAA	CCTTGAATCC	ATTAGCCAGG	CTTGGGATGA	AAGGACCATC	TAAAATCATG	300
CTAGTCTAAA	CCATGCTCTT	CCACACAGCT	GTTTAAAAAC	CACTGGGTAT	GAGGAATATG	360
CTAGAAAGAA	ATGTTAAAAA	TAGATTGTTG	GCTCACACTT	ATTTTTCTAA	TAAATAGGAC	420
CATTATTACT	ACCAGGAAAG	TCTTATTTAT	TTTGCCTGAA	ATTGGCTTAA	AGAAAGTCTC	480

ATG	ACGGGAT GGGATGGGCC GGCACTCGAG	510
(2)	INFORMATION FOR SEQ ID NO:458:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 382 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:	
AAT AGAT GGCA AGAC CTGC	TTCGGCC TTCATGGCCT AGCGGAAACA ACTGAAACTA ATGGAAGATA TGGATACAGT TAAACCC CGTCCTCAAG TAGTAAAACA AAAAAAACAG CGACCAAAAT CTATTCACAG TCATATT GAATCCCCCA AAACACCAAT AAAGGGTCCT CCAGTCTCTA GCCTTTCTTT ATCGCTG AACACGGGTG ATAACGAGAG TGTACATTCA GGCAAGAGGA CGCCAAGATC GTCTGTA GAAGGCTTCT TATCTCCAAG TCGTTGTGGC AGTCGAAATG GAGAAAAAGA GGAGAAT GCATCAACAA CTTCTTCAGT GGCTTCTGGA ACAGAATATA CAGGACCAAA CTACAAA GAACACCTCG AG	60 120 180 240 300 360 382
(2)	INFORMATION FOR SEQ ID NO:459:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 433 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:	
GACT AGGC GGGC TTTC CCAT GTCA	TTCGGCC TTCATGGCCT ACTGAGTCCC AGGCCGGGC CCTGCCCCAG CCAGGGCTGG TCTGCAG TTGGGAGCTT GTCCAGCTGC CCCCTCTAAT GCTTTTCTCC TCCAGGACAC GAGCCTC CGGAAGCACA GTAGTCCCCG TGTGTCACCT TAGGCTGACC TCTGTCCCCA GTGACGAA AATGCTGTCA CTGTCTTGAA TTCTTCATCG TTTAACAGGG ACCCAGTGT CACCAAA AGCAGAATTG GATTTTTTT TTAAGTCGAT AAATTTTTAC TCAAGGAATT TGTTGTG ATTCTTCCA CTGTCCATCA AGGTCACTTT AGATCCTCTA AAGAGCTAGA AAAAGAT TTATCTTCAA GTTAGTCCTT TTTAATGAAA CCGATGCTTA TTTTAATCCA AGCCCTC GAG	63 120 180 240 300 360 420 433
(2)	INFORMATION FOR SEQ ID NO:460:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 305 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:	
CAA# GCC1	CGGCTAA AGTAATCCAG TCACCTGCTG CTGATACTAG AAGGGCTGAG ATGTCACAAA ATTTTAC CCCTGACACT CTTGCCCAGA ATGAAGGGAA GGCTATGTCT TATCAGTGTA FTTGTAA GTTTCTATCA TCATCCTTTT CCGTGTTAAA AGATCATATT AAGCAACATG AGCAAAA TGAAGTGATA CTGATGTGCT CAGAGTGCCA TATTACATCT AGAAGCCAGG	60 120 180 240

AGGAACTTGA AGCCCACGTG GTGAATGACC ATGACAATGA TGCCAATATC CACACCGAAC 300 TCGAG (2) INFORMATION FOR SEQ ID NO:461: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 563 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461: GAATTCGGCC TTCATGGCCT AAGAAATATC AGTCCAAGCA AGAGGAATTA CAGAAAGATA TGCAAGGAAG TGCACAGGCA TTGGCTGAAG TAGTGAAAAA CACAGAGAAC TTCTTAAAAG 120 AGAATGGTGA AAAGCTGTCA CAGGAAGATA AGGCTTTGAT TGAACAGAAA CTTAATGAAG 180 CTAAGATAAA GTGTGAACAG CTTAATTTAA AAGCAGAACA GTCTAAAAAG GAGCTGGATA 240 AAGTTGTGAC AACAGCAATC AAGGAAGAAA CTGAAAAAGGT AGCAGCAGTG AAGCAGCTGG 300 AAGAGAGCAA AACCAAAATA GAAAACCTTT TGGACTGGTT GTCAAATGTT GACAAAGACT 360 CAGAAAGGGC AGGGACAAAA CACAAACAGG TAATCGAACA GAACGGGACC CATTTTCAAG 420 AAGGTGATGG CAAGTCAGCA ATTGGAGAAG AGGATGAAGT TAATGGTAAC CTGTTGGAGA 480 CTGATGTTGA TGGGCAAGTT GGAACCACTC AGGAGAATCT GAATCAGCAA TATCAGAAAG 540 TTAAGGCCCA ACATGGACTC GAG 563 (2) INFORMATION FOR SEQ ID NO:462: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 477 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462: GCGGCTGTGA AGATGGCGGC GGCTGCGTGG CTTCAGGTGT TGCCTGTCAT TCTTCTGCTT CTGGGAGCTC ACCCGTCACC ACTGTCGTTT TTCAGTGCGG GACCGGCAAC CGTAGCTGCT 120 GCCGACCGGT CCAAATGGCA CATTCCGATA CCGTCGGGGA AAAATTATTT TAGTTTTGGA 180 AAGATCCTCT TCAGAAATAC CACTATCTTC CTGAAGTTTG ATGGAGAACC TTGTGACCTG 240 TCTTTGAATA TAACCTGGTA TCTGAAAAGC GCTGATTGTT ACAATGAAAT CTATAACTTC 300 AAGGCAGAAG AAGTAGAGTT GTATTTGGAA AAACTTAAGG AAAAAAGAGG CTTGTCTGGG 360 AAATATCAAA CATCATCAAA ATTGTTCCAG AACTGCAGTG AACTCTTTAA AACACAGACC 420 TTTTCTGGAG ATTTTATGCA TCGACTGCCT CTTTTAGGAG AAAAACAGGA GCTCGAG 477 (2) INFORMATION FOR SEO ID NO:463: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 382 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

CTTCCACTCC	TOTO TO STORY	TTTTACACCT	GGAAAAGAGG	TO THE OTHER	CATCTAACAC	60
GIIGCACICC	IGIIGIACIC	TTTTAGAGGT	GGAAAAGAGG	IGGATACIGA	GATCTAAGAG	0.0
GAAAGGATAG	TCATTCACGT	TCTGAGATAT	GCGCTCTCTC	TATTGTTCTC	GAACACAAAG	120
GGATAGTCTC	TTTTCTGGAG	CTGATGTCCC	TGCTTGGAGG	TTAGCCCCAA	AACATGGCTC	180
TTGTATTGTT	CTAAGAGAAA	AGGCTTTCAT	TTTGGTTCTT	CTGATTGGTG	TTACCTACTG	240
CCTAATATGT	GTTCATTTTT	TGACAGAGAG	GCAGACTATT	GAAAAAGTCT	GTGTGAACAG	300
AGAGCAGTTC	ATTAAGCCCA	TTGCTTTCAG	TAATGTGGCC	TTGACCCCTT	CTGCTTCCCC	360
CTTCTCCCAT	GACGAGCTCG	AG				382

- (2) INFORMATION FOR SEQ ID NO:464:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 275 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GGACCTGCCT	CAAGGACATG	GGTGGACATA	TGGGCGGACT	CTCAGGGACA	ACCAAAGTGA	60
TGATCACACT	GACCGATGTC	AATGACAACC	CACCAAAGTT	TCCGCAGAGC	GTATACCAGA	120
TGTCTGTGTC	AGAAGCAGCC	GTCCCTGGGG	AGGAAGTAGG	AAGAGTGAAA	GCTAAAGATC	180
CAGACATTGG	AGAAAATGGC	TTAGTCACAT	ACAATATTGT	TGATGGAGAT	GGTATGGAAT	240
CATTTGAAAT	CACAACGGAC	TCTAAAACAC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:465:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 488 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GTTCTAGACC	TACCCCGAAC	AGCCCCAAAC	AGTCAGAGTG	GCACAAAATG	ACAGTCTCCA	60
AAAACTGCCC	CGACCAAGAT	CTCAAAATCA	AACTTGCTGT	CCGAATGGAT	AAGCCTCAAA	120
ACATGAAGCA	TTCTGGGTAT	TTATGGGCCA	TCGGTAAGAA	TGTCTGGAAG	AGATGGAAGA	180
AAAGGTTTTT	TGTATTGGTG	CAGGTCAGTC	AGTACACGTT	TGCCATGTGC	AGTTATCGGG	240
AGAAGAAAGC	GGAGCCTCAG	GAACTTCTAC	AATTGGATGG	GTACACTGTG	GATTACACCG	300
ACCCCCAGCC	AGGTTTGGAG	GGTGGCCGAG	CCTTCTTCAA	TGCTGTCAAG	GAGGGAGACA	360
CCGTGATATT	TGCCAGTGAC	GATGAACAAG	ACCGCATCCT	GTGGGTCCAG	GCCATGTATC	420
GGGCCACGGG	GCAGTCACAC	AAGCCTGTGC	CCCCGACCCA	AGTCCAGAAA	CTCAACGCCA	480
TCCTCGAG					•	488

- (2) INFORMATION FOR SEQ ID NO:466:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 300 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GAATTCGGCC TTCATGGCCT AGCCGCTGCG GTGAGCCTTG AAGCCTAGGG CGCGGGCCCG

GGTGGAGCCG CCGCAGGTGC AGATCTTGGT GGTAGTAGCA AATATTCAAA CGAGAACTTT

60

AGAAATAGAA	TGAGCTAAAA AATAATGCTG ATTTGGCCTC ATCATATTTA TGAAGGAGGG GCATGTATAA TGTAGAAAAA CATATCTTAT CCTTATGTTT GCATATATTG ATAGTTTAAT GAATATGTTT TCTCACCTTT CTTTGCTTGC ACTTCTCGAG	180 240 300
(2) INFORM	ATION FOR SEQ ID NO:467:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 381 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:467:	
GGCCCGAGGC GTGTGTCCGC CTGCCTCCCA CAGAGGGCGG GGACCCCTCC	TGCCTCGAGA TATGCCGGAA GGTTGCATGG CTGGTCCCAG GGCCAGCACA CGGGCTGCCT GGTTTATTT TTATTTAACT TTATTTTCTG TTTTATGAGT CCACCCCCAC CCCCTCAGT GTTAAGTGGG GAGCCCTGGG GGAGTCTCTC GCCTCTCCCA AGACCTCCCC CCTCGTCACC AGCCATCCCT CTGGACCAGG ACCGGGTGGG CAGGGGCCTG AGGGTGGCTC GGGCCAGCCC ACCAGCCAAT TCAGGCCGCC AGTGTCGCCC TGCCCCTTTT TAAAACAAAA TGCCCTCGTT TAACGCTCGAG	60 120 180 240 300 360 381
(2) INFORMA	ATION FOR SEQ ID NO:468:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:468:	
TACTGGTCCC ATTAGAAATT ACCAGGCATG	TATACTGACC TGGCCATGAG CACGGTGAAG CAGACCCAAG CCATTCCATA TTTAATTTGC TCTGTTACCA GCTGCAGAAA TTGACAGGTG ATGTGGAAGA CAAGAAAAAC CTGCTCTGAA AGTGTTCAAA AATATTACTG TAATACAAGA GTGGTATTAG AATGGCTGGC AAACCCTTCT AATGATATGT ATGCAGATAC GTGATATTGG AAGTTCAGTC AAATCCCAAA ATAAGAAAAG GCGCAGAACT	60 120 180 240 300 304
(2) INFORM	ATION FOR SEQ ID NO:469:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 346 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:469:	
	TCTAGACCAC CCCGCACTCC AGCCTGGGCA ACAGAGCAAG ACTCTTTCTT AAAAAAAAAG GAGTACCCAT TGGGATAAAC CTCTTTGGAG GAGAGGACAT	60 120

AGTACAGAGG TTATACTGCA ACATGGACCC ACCAATAGCC ATGGATAACT TAGTTGGGAT

TACCCCTGCC TGCTGTTTAG ATACTTACAT GGACACTAAT TTCTGCCCAT CAACCTCCCT CTCTTTCTCC TTCAATGCCC ATCAACCTCC CCCTCTTTCT CCATCAATGC TATGTTGGTT

180

TTTTTTATTT GCCATCTTGG CAGGTTTAGG GCAGAGCATG CTCGAG	346
(2) INFORMATION FOR SEQ ID NO:470:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 321 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:	
GAATTCGGCC TTCATGGCCT AGGATTTCA GCAAGAATTA AATTATTCTG CATATTGGAC AGGGCCTATT TAGAGGCCTG CACATCTGTT TTTATCCATT TGTGTAACGA TACCGGTGTG CAAAGTAGGT TCATGGATCA GATGAGAAAA GTCAATTCTC TAAGATACCT TCCCTTGTGG CTGTGGATCC TACCCTTGAT GATTCAGCTT TGTGTGATGG AGGTGTCTGC CACAGAAATTC CTGGCCACCC AGCTCCTCAG CCCTCTGCC CCACCCCCAA TACACACACC TTTCTCCATT GTACCAGATG CTGGTCTCGA G	60 120 180 240 300 321
(2) INFORMATION FOR SEQ ID NO:471:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 417 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:	
GAATTCGGCT TCATGGCCTA CTTCATTCAC TGTAAAACCA ATAGCAAACA ACGGAAGAGA CGGGCAGAGT TGAAGCAACA AAGAGAGGA GAGGCAACAT GCAAGAGCA GGAAGCCCCT CGGAGAGACA CTCCCACCGA AAGTTCTTGC GCAGTGGCCG CCATTGGCAC CCTCGAAGGC AGCCCCCCAG GTATCTCCAC CTCCTTCTTT AGGAAGGTGC TGGGCTGCC CCTCAGGCTG CCGAGGGACC TGTGTAACTG GATGCAGGGA CTCCTGCAAG CTGCTGGCCT CCATATCAGG GACAATGCTT ACAACTACTG CTACATGTAC GAGCTCCTGA GCCTGGGCCT GCCACTCCTC TGGGCGTTC CTGAGGTCCT CTGAGGCCT TACAGGGAAT CTGAGGGCT CCTCGAG	180 240 300
(2) INFORMATION FOR SEQ ID NO:472:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 331 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:	
GAATTCGGCC TTCATGGCCT ACAAGAGGCA GCTTATAGAC AACCGCAAGC TCATTGAGAC GCAAATGGAA CGGTTCAAAG TTGTGGAACG AGAGACCAAA ACCAAAGCTT ACAGCAAAGA	60 120

GTGGCTCACG AATACCATCG ACACGCTCAA CATGCAGGTG GACCAGTTTG AGAGTGAAGT GGAGTCACTG TCAGTGCAGA CACGCAAGAA GAAGGGCGAC AAGGATCAGA AGCAGGACCG GATTGAGGGC TTGAAGCAGC AGCATCTCGA G	240 300 331
(2) INFORMATION FOR SEQ ID NO:473:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 260 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:	
GAATTCGGCC TTCATGGCCT AGAGGTGCTT CAGTGGTACA ATCAGTTAGC ACACAGTACG TATACAGCAG TATGTGTGT AGAAATTATT TTAAATATAA GAATTATCAA AAATTATAAG AAGACCATCC CTTTAACTGA ATAGTTTCAC CAAAAATCAG AAAAATATGT AAGTGATACA TTTTGTTTCT TGGATATAGC AATGTACCAC CTTGCATAAA TGAGACTATT AAAATGATCA CCTGAGGTCA GAAGTTCGAG	60 120 180 240 260
(2) INFORMATION FOR SEQ ID NO:474:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 511 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GAATTCGGCC TTCATGGCCT ACAAAGATTT GAGGAAAAGA GGTTCAAATT GGACCACTCA GTGAGTAGCA CCAATGGCCA CAGGTGGCAG ATATTTCAAG ATTGGTTGGG AACTGACCAA GATAACCTTG ATTTGGCCAA TGTCAATCTT ATGTTGGAGT TACTAGTGCA GAAGAAGAAA CAACTGGAAG CAGAATCACA TGCAGCCCAA CTACAGATTC TTATGGAATT CCTCAAGGTT GCAAGAAGAA ATAAGAGAGA GCAACTGGAA CAGATCCAGA AGGAGCTAAG TGTTTTGGAA GAGGATATTA AGAGAGTGGA AGAAATGAGT GGCTTATACT CTCCTGTCAG TGAGGATAGC ACAGTGCCTC AATTTGAAGC TCCTTCTCCA TCACACAGTA GTATTATTGA TTCCACAGAA TACAGCCAAC CTCCAGGTTT CAGTGGCAGT TCTCAGACAA AGAAACAGCC TTGGTATAAT AGCACGTTAG CATCAAGACT GAAAACTCGA G	60 120 180 240 300 360 420 480 511
GAATTCGGCC TTCATGGCCT ACAAAGATTT GAGGAAAAGA GGTTCAAATT GGACCACTCA GTGAGTAGCA CCAATGGCCA CAGGTGGCAG ATATTTCAAG ATTGGTTGGG AACTGACCAA GATAACCTTG ATTTGGCCAA TGCAACTCT ATGTTGGAGT TACTAGTGCA GAAGAAGAAA CAACTGGAAG CAGAATCACA TGCAGCCCAA CTACAGATTC TTATGGAATT CCTCAAGGTT GCAAGAAGAAA ATAAGAAGAG GCAACTGGAA CAGATCCAGA AGGACTAAG TGTTTTGGAA GAGGATATTA AGAGAGTGGA AGAAATCAGT GGCTTATACT CTCCTGTCAG TGAGGATAGC ACAGTGCCTC AATTTGAAGC TCCTTCTCCA TCACACAGTA GTATTATTGA TTCCACACAGA TACAGCCCAAC CTCCAGGTTT CAGTGCAGT TCTCAGACAA AGAAACAGCC TTGGTATAAT	120 180 240 300 360 420 480
GAATTCGGCC TTCATGGCCT ACAAAGATTT GAGGAAAAGA GGTTCAAATT GGACCACTCA GTGAGTAGCA CCAATGGCCA CAGGTGGCAG ATATTTCAAG ATTGGTTGGG AACTGACCAA GATAACCTTG ATTTGGCCAA TGCAACCCAA CTACAGATTC TACTAGTGCA GAAGAAGAAA CAACTGGAAG CAGAATCACA TGCAGCCCAA CTACAGATTC TTATGGAATT CCTCAAGGTT GCAAGAAGAA ATAAGAGAGA GCAACTGGAA CAGATCCAGA AGGAGCTAAG TGTTTTGGAA GAGGATATTA AGAGAGTGGA AGAAATGAGT GGCTTATACT CTCCTGTCAG TGAGGATAGC ACAGTGCCTC AATTTGAAGC TCCTTCTCCA TCACACAGTA GTATTATTGA TTCCACAGAA TACAGCCAAC CTCCAGGTTT CAGTGCCAGT TCTCAGACAA AGAAACAGCC TTGGTATAAT AGCACGTTAG CATCAAGACT GAAAACTCGA G	120 180 240 300 360 420 480
GAATTCGGCC TTCATGGCCT ACAAAGATTT GAGGAAAAGA GGTTCAAATT GGACCACTCA GTGAGTAGCA CCAATGGCCA CAGGTGGCAG ATATTTCAAG ATTGGTTGGG AACTGACCAA GATAACCTTG ATTTGGCCAA TGCAATCTT ATGTTGAGAT TACTAGTGCA GAAGAAGAAA CAACTGGAAG CAGAATCACA TGCAGCCCAA CAGATTC TTATGGAATT CCTCAAGGTT GCAAGAAGAA ATAAGAGAGA GCAACTGGAA CAGATCCAGA AGGAGCTAAG TGTTTTGGAA GAGGATATTA AGAGAGTGGA AGAAATGAGT GGCTTATACT CTCCTGTCAG TGAGGATAGC ACAGTGCCTC AATTTGAAGC TCCTTCTCCA TCACACAGTA GTATTATTGA TTCCACAGAA TACAGCCAAC CTCCAGGTTT CAGTGGCAGT TCTCAGACAA AGAAACAGCC TTGGTATAAT AGCACGTTAG CATCAAGACT GAAAACTCGA G  (2) INFORMATION FOR SEQ ID NO:475:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 610 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	120 180 240 300 360 420 480
GAATTCGGCC TTCATGGCCT ACAAAGATTT GAGGAAAAGA GGTTCAAATT GGACCACTCA GTGAGTAGCA CCAATGGCCA CAGGTGGCAG ATATTTCAAG ATTGGTTGGG AACTGACCAA GATAACCTTG ATTTGGCCAA TGCAATCTT ATGTTGAGT TACTAGTGCA GAAGAAGAAA CAACTGGAAG CAGAATCACA TGCAGCCCAA CTACAGATTC TTATGGAATT CCTCAAGGTT GCAAGAAGAA ATAAGAGAGA GCAACTGGAA CAGATCCAGA AGGAGCTAAG TGTTTTGGAA GAGGATATTA AGAGAGTGGA AGAAATCAGT GGCTTATACT CTCCTGTCAG TGAGGATAGC ACAGTGCCTC AATTTGAAGC TCCTTCTCCA TCACACAGTA GTATTATTGA TTCCACACGAA TACAGCCAAC CTCCAGGTTT CAGTGGCAGT TCTCAGACAA AGAAACAGCC TTGGTATAAT AGCACGTTAG CATCAAGACT GAAAACTCGA G  (2) INFORMATION FOR SEQ ID NO:475:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 610 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	120 180 240 300 360 420 480
GAATTCGGCC TTCATGGCCT ACAAAGATTT GAGGAAAAGA GGTTCAAATT GGACCACTCA GTGAGTAGCA CCAATGGCCA CAGGTGGCAG ATATTTCAAG ATTGGTTGGG AACTGACCAA GATAACCTTG ATTTGGCCAA TGCAATCTT ATGTTGAGT TACTAGTGCA GAAGAAGAAA CAACTGGAAG CAGAATCACA TGCAGCCCAA CTACAGATTC TTATGGAATT CCTCAAGGTT GCAAGAAGAA ATAAGAGAGA GCAACTGGAA CAGATCCAGA AGGAGCTAAG TGTTTTGGAA GAGGATATTA AGGAGTGGA AGAAATGAGT GGCTTATACT CTCCTGTCAG TGAGGATAGC ACAGTGCCTC AATTTGAAGC TCCTTCTCCA TCACACAGTA GTATTATTGA TTCCACAGAA TACAGCCAAC CTCCAGGTTT CAGTGGCAGT TCTCAGACAA AGAAACAGCC TTGGTATAAT AGCACGTTAG CATCAAGACT GAAAACTCGA G  (2) INFORMATION FOR SEQ ID NO:475:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 610 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	120 180 240 300 360 420 480

CCTCCCTATG	CTGCACCTGA	ACTCTTTGAA	GGAAAAGAAT	ATGATGGGCC	CAAAGTGGAC	240
ATCTGGAGCC	TTGGAGTTGT	CCTCTACGTG	CTTGTGTGCG	GTGCCCTGCC	ATTTGATGGA	300
AGCACACTGC	AGAATCTGCG	GGCCCGCGTG	CTGAGTGGAA	AGTTCCGCAT	CCCATTTTTT	360
ATGTCCACAG	AATGTGAGCA	TTTGATCCGC	CATATGTTGG	TGTTAGATCC	CAATAAGCGC	420
CTCTCCATGG	AGCAGATCTG	CAAGCACAAG	TGGATGAAGC	TAGGGGACGC	CGATCCCAAC	480
TTTGACAGGT	TAATAGCTGA	ATGCCAACAA	CTAAAGGAAG	AAAGACAGGT	GGACCCCCTG	540
AATGAGGATG	TCCTCTTGGC	CATGGAGGAC	ATGGGACTGG	ACAAAGAACA	GACACAGAAG	600
GCGGCTCGAG						610

- (2) INFORMATION FOR SEQ ID NO:476:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 409 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GGAGATTGGC	CACCTCCAAG	ATATGGTAAG	GAAAAGTGAA	CAAGGTCTTG	GCTCTGCAGA	60
AGGACTTATT	GCTAGTCTTC	AGGACTCCCA	GGAAAGGCTT	CAGAATGAGC	TTGACTTGAC	120
TAAAGACAGC	CTAAAGGAGA	CCAAGGATGC	TCTATTAAAT	GTGGAGGGTG	AGCTAGAACA	180
AGAAAGGCAA	CAGCATGAAG	AAACAATTGC	TGCCATGAAA	GAAGAAGAGA	AGCTCAAAGT	240
GGACAAAATG	GCCCATGACT	TAGAAATTAA	GTGGACTGAA	AATCTTAGAC	AAGAGTGTTC	300
TAAACTTCGT	GAAGAGTTAA	GGCTTCAACA	TGAAGAGGAT	AAGAAGTCAG	CAATGTCTCA	360
ACTTTTGCAG	TTGAAAGATC	GAGAGAAAA	TGCAGCAGAG	AAACTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:477:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 272 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GTATGCCTGT	TCCAGACCAG	CCTTCATCAG	CCTCAGAGAA	GACGAGTTCC	CTGAGCCCCG	60
GCTTAAACAC	CTCCAACGGG	GATGGCTCTG	AAACAGAAAC	CACCTCTGCC	ATCCTCGCCT	120
CAGTCAAAGA	ACAGGAATTA	CAGTTTGAAA	GGCTGACCCG	AGAGCTGGAG	GCTGAACGGC	180
AGATCGTAGC	CAGCCAGCTG	GAGCGATGCA	AGCTCGGATC	CGAGACTGGC	AGCATGAGCA	240
GCATGAGTTC	AGCAGAAGAG	CGGATACTCG	AG	•		272

- (2) INFORMATION FOR SEQ ID NO:478:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 284 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

	TTCATGGCCT ATGCGTGGGG GTGGGGGGGC AGGCTA		60
	TGTCTAGGGT GTGCTGGCCA CTGGAAGATT GGAGTC		120
	CTTGGCTGGG TCCACTCTGC AGACTCCACC TGAGGA		180
	GCCCAGGCCT GAACTGAGCC CGGCCGGGTG CAAGGGCCTCTTCCCAG GCCTGAGGGT GGCTACAGCT CGAG	CTGA GGTGTGAGGT	240 284
(2) INFORM	ATION FOR SEQ ID NO:479:		
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 352 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:479:		
GAATTCGGCC	TTCATGGCCT ACTAAATTTT CCAAAACGTT GATTTGG	CATA ATACAGTGGT	60
	GATAAATTGC CGTTATTTCA AAAATTAAAA TTCTCA		120
	GCTCCACACT TCAAAACTCC CGTTAGATCA GCATTC		180
	CTAACAGATC TGTCCTAGTG ATTTTACCTT TGTTCT		240
	GGTATTCTTA GGTTAGCGGA GCTTTTTCCT CTTTTCC CATTATTAAT TAACCTCTTT CTTTGGTTGG AACGAC		300 352
		LICG AG	352
(2) INFORM	ATION FOR SEQ ID NO:480:		
(i)	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 263 base pairs		
	(B) TYPE: nucleic acid		
•	(C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:480:		
	•		
GAATTCGGCC	TTCATGGCCT ATTAAAAGAA TGTTCTTTCA TTAAAA	GACC AAAAAGAAGT	60
	ATTGGGTGAT TTGTGGGCAG CTAAATGCAG CTTTGT		120
ACTTTCAATT	ATGAAATCTG TGGAGCTTGA CAAAATCACA AAAGGA	AAAT TACTGGGGCA	180
	TCAAGTCTGC CTCTACTGTG TCTCACATCA CCATGT	AGAA GAATGGGCGT	240
ACAGTATATA	CCGTGTTCTC GAG		263
(2) INFORM	ATION FOR SEQ ID NO:481:		
(i)	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 379 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:481:		
GGAGCAGGAA	GAAATGCAAG AGGAGATGGA GAAGCTGCGA GAGGAA	AACG AGACTCTCAA	60
	GATGAGCTGA GAACCGAGAT GGACGAGATG AGGGAC		120
	CAACTGCAGG AAATGCGCCA CGAGTTGGAG AGAGCC		180
GATCCTGCAG	TACCGCCTCC GCAAAGCCGA GCGCAAAAGG CTCCGC	TACG CCCAGACCGG	240

TGAAAACGAG AATCTCGAG

(2) INFORMATION FOR SEQ ID NO:482:

GGAAATCGAC GGGGAGCTGT TGCGCAGCCT GGAGCAGGAC CTCAAGGTTG CAAAGGATGT ATCTGTGAGA CTTCACCATG AATTAGAAAA TGTGGAAGAA AAGAGAACAA CAACAGAAGA

360

(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 301 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:482:	
	TTCATGCTTT CTAGGCAAGA GGTCATCAGA AGATTGAGAG AAAGAGGAGA	60
	CTATTTGGAG AGACTGATTA TGATGCTTTT CAACGTTTAA GGAAAATAGA CCAGAAGTTA ACAAGGGATT GAGGAATGAT TTGAAAGCAG CCTTGGATAA	120 180
	CAGTACCTCA ATGAAATCGT CGGCGGTCAG GAGCCTGGAG AGGAAGACAC	240
	CTGAAAGTTC ATGAGGAAAA CACCACAATT GAAGAGTCAG AGGCCCTCGA	300
G		301
(2) INFORM	ATION FOR SEQ ID NO:483:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:483:	
TGGTCTCCAG	AAATGCTTTG GGTTCATCTT TCATTGCTGC AAGGAACTTC CATGCCTCTA	60
ACACTCATCT	TCAAAAGACT GGGACTGCTG AGATGTCCTC TATTCTTGAA GAGCGTATTC	120
TTGGAGCTGA	TACCTCTGTT GATCTTGAAG AAACTGGGCT ATCTCGAG	168
(2) INFORM	ATION FOR SEQ ID NO:484:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 452 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	MOLECULE TYPE: cDNA	
,		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:484:	
GCAAGCTCTC	CATGGAAACC CCTGCCAAAA CAGAAGAGAT AAAACTGGAA AAGGCTGAGA	60
CAGAGTCCTG	CCCAGGCCAA GAGGAGCCTA AATTGGAGGA ACAGAATGGT AGTAAGGTAG	120
AAGGAAACGC	TGTAGCCTGT CCTGTCTCCT CAGCACAGAG TCCTCCCCAT TCTGCTGGGG	180
	CAAAGGAGAC TCAGGGAATG AACTTCTGAA ACACTTGTTG AAAAATAAAA	240
	TCTTTTGAAT CAAAAACCTG AGGGCAGTAT TTGTTCAGAA GATGACTGTA	300
	TARACTAGTT GAGAAGCAGA ACCCAGCTGA AGGACTGCAA ACTTTGGGGG	360 420
	AGGTGGTTTT GGATGTGGCA ACCAGTTGCC AAAAACAGAT GGAGGAAGTG ACAGCGAAGC AAAGGACTCG AG	420 452
AAACUMMUMM	POURCOUNCE WURRANTICA NO	4,72
	251	

- (2) INFORMATION FOR SEQ ID NO:485:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GTTTGTAAAT	CACCTGATGA	TGGTGATATA	GCTGTGGCCA	ACGAAATGTC	AAGGGAAGTC	60
TGCTGGGGAA	GGTAGACGTA	GGATAGGAGT	ATGGGAAAAA	ATTATTCACT	CAAAAGCATG	120
ATGCACAGAG	GAGCTATGAT	CTTTTCTTGT	TTTCCTCACT	GGATGTTGTC	ATGTCTGTAT	180
GTACTTCCTG	GAACTGTGGC	ACCATCTTAC	AACCATGAAA	GGAGCTCACA	TGAAATCATG	240
TTGAACATAG	CAGAGCGGGA	AGATGGAAGG	AATCCGAGAT	CTATGTTTGA	TGTTAAGCGA	300
TGATGTTAAA	AACTTAAAAA	ACTCCAGAAC	TCTCTTACCC	CTGGTGCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:486:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 420 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GAATTCGGCC	TTCATGGCCT	ACTCAGCTGG	AAGCTTTACT	CCCTCCTCGA	CAGAAAGTGA	60
GGATTACAGA	TGACATGGAT	CAGGTGGAGC	TGAAGGAGTT	TTGTCCCAAT	GAGCAGAACT	120
GGCGTCAGCA	CAGGGAGGCC	TACGAGGAGG	ACGAAGACGG	GCCCCAGGCT	GGAGTGCAGT	180
GCCAGACGGC	ATGACGTGGT	GCGGGGCAGC	GTGGCCCCAC	CGGACTAGCA	CATGATGAAT	240
GTAAAGTTGG	CACAATGAAA	ATGACATCGC	TTTAATGGCC	TTGTGTTTTGG	GATGTCCTGT	300
GTATGTGTTC	AGCATTCTTA	ATTGCTGAGT	GTCTTTTTGG	CTTTTCTTTT	GGTTGTAACT	360
TAAGTTATAG	CTTAATTTAT	ATTTAAATGT	TTTAAGTATA	AATCACCTCT	AGGCCTCGAG	420

- (2) INFORMATION FOR SEQ ID NO:487:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 318 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GGAGTGTCAA	GAATAACCGC	TCAGGTTGAG	TGTAAAAATA	TTTTATGGTC	CCATCAGCAT	60
CAACCTGCCT	TAATGCTTCT	TTGGTTGTCT	CTTCAGCTAG	TTCTTATTTT	ACAGCACATG	120
ATATATGAAG	TGATTTCACA	CCATGCCCAA	GATACGGGCC	ACCCACCAGC	TACATGGCAT	180
GATGACTCTG	CAGGCCGAAC	GGCAGCCTTG	ATAATTATAA	GGCCATGGGT	AATAGCCCCC	240
CAGGGGTTCA	CAGATCTTCT	GGCAGTGGGT	GTAGCTCCGC	CTACATTCTA	TACAACAGAT	300
TCCTTCGCCT	GCCTCGAG					318

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 487 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:	
GAATTCGGCC TTCATGGCCT AGGTGTTTGC TTTAAGGAGG AATAGAAAAA TCAGGTGGTC ACTACTACAAA GGGAAAGGGG AATGTGGTTT CAAAAAAGGGT TTTGCCTTAT TTATTTTAT AGTAGATACT TATTAATCAA ACATTTAAGA GCAACTCAGT AAGTATTTGT CCAGAATGAA CTGTTCTCAA GACTAGGTTT ACTGCTTGAC ATTAGAGGTT AAGGTGTTGC AATTCTGAGT CTGTTTTTTT ATTACTACCA ACCCCCACCC CCGCCGATAT TACTTCATCT CCCTCCAAGG TACTCATCTT GCTGGGCATG TCAAAGTGTT TTCTATATT ACAGATAATG CTGCAATGAA TCTTTATTTA TATAATACAC TTTTATCCAG TTGTCATTTT TTCTTTGTCT TATATTCTCA CATGGAA	60 120 180 240 300 360 420 480 487
(2) INFORMATION FOR SEQ ID NO:489:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 149 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:	
GCGATTGAAT TCTAGACCTG CCTCGAGACA AAAACTGTGA ATAGTGAGTG ATTTAAAAAA AAAAAATAAA CTGAAAGGAA AATTGTTGAA TGTTTGAATC TTGCCTAGTC CCCTCACCCC CAAGGCTGGC TTCTAGAGTT AAGCTCGAG	60 120 149
(2) INFORMATION FOR SEQ ID NO:490:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 259 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi') SEQUENCE DESCRIPTION: SEQ ID NO:490:	
GCAAATTTTG GAAGATTTAG ACCATTATTT CTCAAAATAT TTCTTACCTG CTCTCCTC TTTCTCCCAC TCCTCCCCAT CACCTTCTGG CACCTTCCATT GTTCATATAT TGATATGCTT AATGATGTTT CTGAAGATTT ATTCATTTTT CCTTTATTCC TTTTTATTCT GTTCCTCAGC CCAGATCATT TCAATGCACA TATCCTCAAG TTTGCTGATT CTTTCATTTC CTGCTCAGAT CTGCTGCTGG CCCCTCGAG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:491:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 320 base pairs  (B) TYPE: nucleic acid	
253	

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GAATTCGGCC TTCATGGCCT	ACAAATGTTT	AATCAGAGAC	TCATATTCAC	CTTTAAGTAA	60
AAAACATACT TCTTTCCCCC	TAATAGTCAC	AGCATTCTGC	AGAGCTAAAG	AAGGAGACCA	120
GGAGTCTGTG GGAGCAAAGA	TCATTTTGTG	AAGCTAGAGG	TCCAATTTAA	AAGCAGTTGC	180
TGCTACAAAT TAAAACATAT	TTGCATTCTG	CCTAAAATAG	TTGTCTCTTT	GAACGTTGGG	240
TGCCTTTTTT AGGTTGCTTT	GTGAATAATA	TGCACAAAAT	GAAAATGTTA	AAAAAAACAT	300
GTAGCCTGCT AACCCTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:492:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 224 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

GAATTCTAGA	CCTGCCTCCA	GCCACTTCAA	ACCTTTGGTG	ACCAAAGTGG	GGTAAAAACA	60
AGCACCTGCG	TGCGTTGTGG	TTATTCTATG	CTCTCCAATA	TATATAAATT	TTAAGAAGTT	120
TTTCTTGAGG	TGGTCAGTTC	TTAAACCAAG	AAAGTGGTAG	TAGTTGATTT	TAATTAGTGT	180
AAAGTTGTCT	TCGTAACTTC	CGTGTTGGTT	GGAAATAGCT	CGAG		224

- (2) INFORMATION FOR SEQ ID NO:493:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

CAATTCCCTT	CATCCCCTAC	CCAATCACAC	AGAAGAAAGC	CCNCCCCTCC	>	
GWWIIGCCII	CAIGGCCIAC	CGAATCAGAC	AGAAGAAAGC	CCAGGGCTCC	ACTICITCIA	60
CAAGGTTGCA	TGAGCCCGAG	AAGAATGCCA	GAGAAATAAC	ACAGGACACA	AATGATATCA	120
CATATGCAGA	CCTGAACCTG	CCCAAGGGGA	AGAAGCCTGC	TCCCCAGGCT	GCGGAGCCCA	180
ACAACCACAC	GGAGTATGCC	AGCATTCAGA	CCAGCCCGCA	GCCCGCGTCG	GAGGACACCC	240
TCACCTATGC	TGACCTGGAC	ATGGTCCACC	TCAACCGGAC	CCCCAAGCAG	CCGGCCCCCA	300
AGCCTGAGCC	GTCCCTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:494:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 504 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GAATTCGGCC	TTCATGGCCT	AGGTAGCTCT	ATGGTTTTCC	TCGCGTTCTT	GAGTCGGGAA	60
ATGGCCGCTG	TGTGGTTGCA	ACGGAGATAA	ATTCCCGGAA	CCGCGATTCG	GCGTGTCAGG	120
AATTCGAATT	TAGAGTTTAA	TTTCTCAGAG	CATTCTCTCC	AGGAAGAATT	TTTACAGTAT	180
CTCAAAGACT	TCACTTGACT	TCTTGATCCT	GCATAAAACC	AAGGAGAAAA	GAAATGGGTC	240
GCTCCAATTC	TAGATCACAT	TCTTCAAGGT	CAAAGTCTAG	ATCACAGTCT	AGTTCTCGAT	300
CAAGATCAAG	ATCTCATTCT	AGAAAGAAGC	GATACAGTTC	TAGGTCTCGT	TCCAGAACAT	360
ATTCAAGGTC	TCGTAGTAGA	GATCGTATGT	ATTCTAGAGA	TTATCGTCGC	GATTACAGAA	420
ATAATAGAGG	AATGAGACGA	CCTTATGGGT	ACAGAGGAAG	GGGTAGAGGG	TATTATCAAG	480
GAGGAGGAGG	TAGAAACCCT	CGAG				504

- (2) INFORMATION FOR SEQ ID NO:495:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 190 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

GAATTCGGCC TTCATGGCCT ACCAAC	TTAG TCATTTGAAG (	CCCAAGAGTC 1	ATATTTAA1	50
TGCCCTGCCA ATGTCCTCAT CTATTG	CAGA ATGNATAATT A	ATCTATTTGT T	TTTGGACTAT 12	20
ATGTTACAAA AATTTAAAAC ATAAGA	TCCT CTCTCTATAT T	TTCATTATTG (	GTGAACCCAC 18	30
ATTGCTCGAG			19	90

- (2) INFORMATION FOR SEQ ID NO:496:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 305 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

GAATTCGGCC	TTCATGGCCT	AGGTAAGAAA	ATCGTCAATG	AATTGTGGCA	TGACCAGGTG	60
GAGAGTAAGT	GTCATAAAGA	GGGATAGTGG	ATAGTATAAT	GTCAGGCACC	TCAAAGGAAC	120
TGGGCAGGGA	GTTAGGGAGT	AAAAAGGGCG	GTGGTCTGGA	AGCAGAAAGG	AGGAGCAGTG ·	180
GTCCAGTAGG	GGCTGCAGAG	CTGCAAGGCT	TTGCCTCAAT	CCTGTCAAAG	GCAACTTCAA	240
GCTTTCCAGG	AGCCATACTC	CTTCATTTGT	TCATTACTTT	CTAGATTAGG	AAATCACCAC	300
TCGAG				•		305

- (2) INFORMATION FOR SEO ID NO:497:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 334 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GAATTCGGCC TTCATGGCCT AGGTGGACCA ATGTACAGCA CTCAGGTTCA TGGCCAACTG GGTGGACTAT TTCAGTACTC TACAGGTGCC TCAGTGGAGG GAGAGCCCAT TGTCCAGGTG	60 120
CTTCCTGGGA CAATACCAGA GCGCTCTGGG AAAAGGGCTG CTTGCAGGCA CGAGGGCTCA	180
CAATGAGCCA TGGTGGGCCA CCGCCACGGC CCATGCAGCC TAATAGCAAG CCAAGGCAGG  AAGCTGTGAG AGCTGCTCAA CAGTGCCCCC TAGGGACTGG TTACTTCCTG ACCCTAACCT	240
CCGGAAATCT GCTGTCAAAG GCAGATTTCT CGAG	300 334
(2) INFORMATION FOR SEQ ID NO:498:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 160 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:	
FAATTAGGGG CTTTTTCATC CTTAGGAGAC CTGAGTCCTC AAGAAAACCC TTTTCTGGAA FTATCTGCTC CTTCAGAACA TTTTATAGAA AAGAATAATA CAAAACACAC AACTGCAAGA	60 120
ATGCCTTTG AAGAAAATGA TTTTATGGAA AACACTCGAG	160
(2) INFORMATION FOR SEQ ID NO:499:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 276 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:499:	•
SAATTCGGCC TTCATGGCCT ACTCGATCTC CTGACCTCGT GGTCCACCCG CCTCGGCCTC	60 .
CAAAGTTCT GGGATTACAG ACGTGAGCCA CCGCGCCCGG CCTTGTCCTG GATTTTTTAA	120
CAAGCACTA TTATTTATAG TTGCGTTAAA ATAAATAGGG ATGGGTTTGA TAAGTCACCA TTGGTGCTT TAAATTCTGC CATCATCTTT TCTAGGAGTG TAAGATATAG AGATACACAT	180 240
AGCAGAAAA TTTTTTTAA CATGAGGATA CTCGAG	276
2) INFORMATION FOR SEQ ID NO:500:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 256 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:	
SAATTCGGCC TTCTGGCCTA GACCTGCCTC TGATATGTAC TTGGTTTTTA AAAACCCATT	60
TGTTCTCTC TTGTTTCCTC TCTATTTCAG CCTAGTATCA GAAGGCCAGG CGAGACTGCA	120
CACTGCTCA TCACCCCGCG GCGTGATCCC TGCTCTTAGG TGCTGGGCAG AGGGGAAGGG	180
GGTCAGGGT GAGGATGGTG AGGGAGGGCT GGTGAGGGGC TCAGAGGAAT ACTTGGAACA	240

- (2) INFORMATION FOR SEQ ID NO:501:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 635 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GAATTCGGCC TTCATGGC	CT AGTGGTTTTG	TTGTTGTTGT	CGGAGACAGG	GCCTCGCTTG	60
GTCTCCCAGG CTAGAGTC	CA GTGGCATGAT	CACGACTCAC	TGCAGTCTCG	ACCTTCTGGG	120
CTCAAGTGAT CCTCCTG1	TGT CAGCCTCCCA	CACAGCTGGG	ACTACAGGCA	CATGCCACCA	180
CATCCAGCTA ATTTAAAA	AAA CATTTTTTT	GTAGAAATAG	GGTCTTACCA	TGTTGCCCAG	240
GCTAGTCTCA AATTCCGG	GG CTCAAGCAAT	CCTCCCACCT	CACCTTCCCA	AAGTGCTGGG	300
ATTACAGGCA TGAGTCAC	CA TACTTGGCCC	GAGTGAGCCA	AGATTGCACC	ACTGCACTCC	360
AGCCTGGGCT ACAGAGCA	AG ACACTATCTT	AGATCCNNAA	AGGAAAAAA	AAAAAGAAGG	420
AGAAAGAACC AGAGAAAC	CAT AAGGAAGAGT	GAGAGGAAGA	AAGAAAGATG	CAATTTGGGA	480
AGAAATGAAA AAGAAATG	SAA TAAAGAATAA	AATAATGTAA	CGGTCAATAA	ATAGGACTTG	540
TGAATGGAGG CCTTTAGG	SCC AAAGGCTATG	ATTAATTTCA	AGCTATGTTA	CTGAAGTCCA	600
TAAACAAAGG ACTCAGAT	CT AAATGGGTAC	TCGAG			635

- (2) INFORMATION FOR SEQ ID NO:502:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 452 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

GAATTCGGCC	TTCATGGCCT	ACCCGTAGAA	ATCCCCCTTT	CTCTAATAGC	GAGGCTCTAA	60
CCACACAGCC	TACAATGCTG	CGTCTCCCAT	CTTAACTCTT	TGCCTTTGCC	ACCAACTGGC	120
CCTCTTCTTA	CTTGATGAGT	GTAACAAGAA	AGGAGAGTCT	TGCAGTGATT	AAGGTCTCTC	180
TTTGGACTCT	CCCCTCTTAT	GTACCTCTTT	TAGTCATTTT	GCTTCATAGC	TGGTTCCTGC	240
TAGAAATGGG	AAATGCCTAA	GAAGATGACT	TCCCAACTGC	AAGTCACAAA	GGAATGGAGG	300
CTCTAATTGA	ATTTTCAAGC	ATCTCCTGAG	GATCAGAAAG	TAATTTCTTC	TCAAAGGGTA	360
CTTCCACTGA	TGGAAACAAA	GTGGAAGGAA	AGATGCTCAG	GTACAGAGAA	GGAATGTCTT	420
TGGTCCTCTT	GCCATCTATA	GGGGCGCTCG	AG			452

- (2) INFORMATION FOR SEQ ID NO:503:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GAATTCGGCC TTCATGGCCT ACAAAATTGT CTTGACATAA GTAATTTGGG TATGCTGTAT 60
AAAGGCTTCT AAGAATTAAG AAACATGGCC CGGGTTGCAA ATTTTAATGC ATGACTACCT 120

TTAAGAACCA	AGAATATAGC TTTTGTCAGA TTCTCTGGTCATGA GTGGTGATTT TCACCTCCTTATCT CACCTATACC ATCC	CTTTTT TGGTCTTAAC	CCACTTAGGT 2	80 40 86
(2) INFORMA	ATION FOR SEQ ID NO:504:		•	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 424 base pa:  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:504:		
AAGTAAACTA GTTCCTAATT AACACTAGCC AATCAATTAG CTATGAATAT	TTCATGGCCT AGAGGGGTTT AGGA CAAAATAATT GCTAAACTGA AAAT CTTATCCATG AAATATTTTC TGCC AAATTGTAGG TGATCAATCA GCAC AAATTCCACT GAAAATTCTT CTTA AGAGCTTACA TACATGTTAT ATAT TGTTGGATTT TTTATTGTTT TTGT	TGTATA AAGTGTACTG TTCTTA GAGGAAATAG TATGTCT AAATAAATTA AAATATA ACCAACTTCA TCAATAT GTGAGTAGAT	GACAGATGAT 1: CACCTGACAC 1: ATTAAAAAAG 2: TTATGACAAG 3: AAAGAATGAA 3:	50 20 90 40 00 50 20
(2) INFORMA	TION FOR SEQ ID NO:505:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 204 base pa:  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:505:		
TTCTTTCCCA TCTGCTTCCT	GTTTTCAGGT TCTTCCTAGC TCGC CCATCCTTTT TGACTGTTGA CCTT TACTTTTTTT CCTTTTTGAA TTCT ATATGGATCT CGAG	GGTTTT CTCTTCTAAG	TTTCTGTCCC 1: TGTTCACTTT 1:	20
(2) INFORMA	TION FOR SEQ ID NO:506:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 218 base pa  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:506:		
CAGAAATGTT	TTCATGGCCT ATAGGCCATG AAGGATTATTTT TGAAGATGTG GAGAATTACTAAA TGAATAACAG TTAT	AAACTAC TGTTATTTTT	GCTTATATTC 1	60 20 80

(2) INFORMATION FOR SEQ ID NO:507:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 352 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GAAGTTTAAC	ATTTCAACTG	TTGGTAAAAT	CTCCCTGGTG	CCACCTTGTC	GCACCCCCT	60
GTTATGAGGC	ACAGTTAGTG	GGTTTATGAG	AGGTTTGTTC	AGTGAAGCTC	CTGCCACTGT	120
AGACCTAAAT	GTTTCTCTCC	CTGTTGAAGT	GACCTGCCTT	CCTCTTTAGT	ACCTAACACA	180
GTTGGCAAAG	AGCATGGCTA	ACTCAAACCC	TTTTCTTTGG	GGGCAGGCTT	CCCTTTCTCT	240
CTGGCAGGTA	AAAAAAA	TTACAAAATA	GTAAATTTGC	CAAATTTTTC	TTGGTGTGTA	300
GCAAGGCATA	AAGACTGAAA	AATATCTTAT	GAATTAGTTC	ACTTCCCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:508:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 283 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GAATTCGGCC	TTCATGGCCT	AAAATGATAC	AGTGTGCAGA	ACTGGACCCA	GTAGGGAATG	60
ATAAAATGTA	CAGATGTGCA	GAACAGGACT	TGGTAGGACT	CAGCAGAGAA	AACAGGAGGA	120
GAGATGAAAA	TGATATGGTG	TGCAGAACTG	GACTCAGTAA	GGTGCGGAAA	GGGGAAGGAT	180
TCTGACAGAA	TCCAGCACAA	AAACAGAGAG	GGTGCAGAAA	AAGAGATTTG	GTCACTTAGA	240
CGTGTGGAGT	TGGAGGAGCC	TGTGGGAAAT	CCAGGATCTC	GAG		283

- (2) INFORMATION FOR SEQ ID NO:509:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 325 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

GAATTCGGCC	TCATGGCCTA	CTCTCCTTTC	TTAACTTGTG	TACTTGGGGG	CACTTTTGAT	60
TTTGGTCCCA	CATCATTGAG	GAAGCTGGCC	CAGAGTTCGT	CCTCCTTCTT	TTTCCTGGCA	120
TCCTCTGATC	CAATGCCTTT	TTCCTGCTCT	GCAGCGTCAT	CTTCCTCCTC	ACTACTGCTT	180
CCCTCAGATT	CTGAATTGGC	ATCCTCCTCT	TCCTCTTCTT	CTAATGAGAG	GCCACCTTGT	240
CTTCTCTTCC	TGGCTGGAAT	GCTCTGGGCC	TTTCTTTTTT	TCCCTTGGGT	TTTCTGTGTC	300
TGCTCTTCAC	CATTAGGCCA	TGAAG				325

- (2) INFORMATION FOR SEQ ID NO:510:
  - (i) SEQUENCE CHARACTERISTICS:

WO 98/45437

- PCT/US98/06956 (A) LENGTH: 281 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:510: GAATTCGGCC TTCATGGCCT AGACAGGAGG TCATTGGGGA TTTTAGAAGG TTACACTGGA 60 TACATTTCCA TTAAGCTTCA CGATATCCCA CAGGTCCATT CTGTGTGAAA TGGTCTAAAA 120 ATTTCCTGTT CTCATGCTTC ATTTTTTCT TTTAGTAATA TTCCTAATTG TGTAAAATAG 180 TATTTCTTT CATTTATCTT AATTATGTTA TATTAAGATA TCATGTGTAT GCTTAAATTA 240 TACTTTTGGG CTTCAAATGA GTGACCCCAC TCAGACTCGA G 281 (2) INFORMATION FOR SEQ ID NO:511: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 250 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:511: GAATTCGGCC TTCATGGCCT AATTCCCTTG ACTCAAGACA GCTAACTTCA TTTTCAGAAC TGTTTTAAAC CTTTGTGTGC TGGTTTATAA AATAATGTGT GTAATCCTTG TTGCTTTCCT 120 GATACCAGAC TGTTTCCCGT GGTTGGTTAG AATATATTTT GTTTTGATGT TTATATTGGC 180 ATGTTTAGAT GTCAGGTTTA GTCTTCTGAA GATGAAGTTC AGCCATTTTG TATCAAACAG 240 CACGCTCGAG 250 (2) INFORMATION FOR SEO ID NO:512: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:512: GAATTCGGCC TTCATGGCCT AATTGATTCT AATCTTTCCC AAACAGTGCT GTGGCAATGT ATGAAAGTAA TAAAAATAAT CCTTTTTCTG TTAAAAAAAA AATTGCTGTT ACTTGCTGTT 120
  - GAATCAAGCA AAACCATGGT GAAGAGATTC ATTTAAAGAG GACAAGTCTC GAG (2) INFORMATION FOR SEQ ID NO:513:
    - (i) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 358 base pairs

TTGTTATGCT TTTGCTGGAG ATTTTCCCAC CCATCTTAAA GCAGCAACTT CAGGATGGGG

180

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GAATTCGGCC	TTCATGGCCT	AGTCACCTTT	TGTGGGAACT	TCTCTCAGCG	AAGCGGAGCA	60
TGCGAATTTG	ACATCATGAT	TGTCTGAAAA	TTGGTAAGCC	ACTATCCCAG	AAAGAGCTCC	120
CTATGCCCAG	GGCTTGCAAT	GCTAAGAGAA	GGAGGCAGGA	GAGAGACAGG	GAGCGACACT	180
ACATTTGGTG	GGGTGAGGAT	ATGAGGTTCC	TTGGACATCA	TGGCCTCCAG	TGAATATGTG	240
GGTGATGGCT	TGGAACTTAA	GCTTTTTTGC	TAGTGCCCCA	CAAAAGAGTA	CCCTCCACAA	300
CCCATCTGTG	GACCACAGCA	GTGCCTCTCA	ACAAACATGT	GCCCCAAGGA	GTCTCGAG	358

- (2) INFORMATION FOR SEQ ID NO:514:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 337 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GAATTCGGCC	TTCATGGCCT	AGAATAGAGG	AAAATAGCCG	CCTGGTGGCT	AGACAATTTA	60
GGTGTAGAAA	ACACATTTAT	ATGGTTCTTT	GAATGTAACA	GTGGTAAAGA	ATATAGGTTT	120
AGTTGTTGCT	GCTAAGTAGG	GGGAAATGAC	ATTTTTATCT	GGTATGTTTG	AGAATAAAGT	180
AAATTTCAAA	ATTTGAGATG	ATCGAAGTTT	TTATTTATAA	ACTTAAGTAT	TATTATAATA	240
TGTTACATAT	TTTATTCTTT	AAAAATTGTA	ATTCAGAGAG	TGTAACAAAA	TGTACTTCCT	300
CACTTTCTTG	CTTTTTGTTT	CCCAGAAGTA	ACTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:515:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GAAAAGATGG	AAGAAAACCA	CCATAGCACT	GCAGAAGAAC	TACAGGCTAC	TCTACAAGAA	60
TTATCAGACC	AGCAACAAAT	GGTACAGGAA	TTGACAGCTG	AAAATGAGAA	GCTGGTGGAT	120
GAAAAGACGA	TTTTAGAGAC	ATCCTTTCAT	CAGCATCGAG	AGAGGGCAGA	GCAGCTAAGT	180
CAAGAAAATG	AGAAGCTGAT	GAATCTTTTA	CAAGAGCGAG	TAAAGAATGA	AGAGCCCACC	240
ACTCAGGAAG	GAAAAATTAT	TGAACTGGAG	CAGAAGTGCA	CAGGTATTCT	TGAACAGGGC	300
CGCTTTGAAA	GAGAGAAGCT	ACTCAACATT	CAGCAGCAGT	TGACCTGTAG	CTTGCGGAGA	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:516:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 329 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GCGAGTGAGC	CGGGGTAGCA	TCACCTCACT	CCAGCCTAGG	TGATGACAGA	GTTAGATTTT	60
GTCTCAAAAA	AGAAAAAGAA	AACAATTCCA	GGATTATTAT	TTCTACGTAA	ATGTGACATA	120
TTATTTCTAT	GATATTATTT	CTTTGATCTC	GTAGCCACAC	TGTTCCCAAT	AATGATTATG	180
AGAAAAGTA	CCCTCTGTTT	GAAGGCAATC	ATGGGGAAAA	TATAÁTTCAC	AAAGTATTTT	240
AAAATTAAAA	TCCTGTGTAT	TTCAAAAGAC	GATGGTCCTA	TTTTAAGAAA	AATAACCTTG	300
CAATTCATTT	GCTTTTTCAT	TGGCTCGAG				329

- (2) INFORMATION FOR SEQ ID NO:517:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 368 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GAATTCGGCC	TTCATGGCCT	AGTCCTTTCA	AGTACACAGA	GAAATTTTGC	TTGAATTTCT	60
GGAGGAAGAG	TCCAGGGTTC	GGGAAAAGGG	ACTGGGTGGT	ATCTATCTGG	GGCCCCAGAC	120
AGCGGCACTT	CTTTCTTCTG	TGCTGGAATT	CGGCGAACAA	TCATATCATC	TTTTTCCAAA	180
TCCGGAAGTA	CAAGTTCACC	TTCTCTACAC	TGTAAAATTA	TATCTCGCTC	TACAGAATCA	240
TCTTGCTCAG	AGAACTTTCT	AAAGTCTTCA	AAAGCTCGGA	GAACATATGG	ATTTGCATGG	300
AAAGCCCCAG	TCTTTCTGAC	AAAGAAATCA	TCATTCTCTA	AGTCAGGATC	CAGGGCTGCC	360
ATCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:518:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 397 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GAATTCGGCC	TTCATGGCCT	ACGCTGAGAT	CAAGATTCGG	AGTTTGGGCT	GCCTAATAGC	60
TGCAATGATA	CTGTTGTCCT	CACTCACCGT	GCACCCCATC	TTGAGGCTTA	TCATCACCAT	120
GGAGATATCC	TTCTTCAGCT	TCTTCATCTT	ACTGTACAGC	TTTGCCATTC	ATAGATACAT	180
ACCCTTCATC	CTGTGGCCCA	TTTCTGACCT	CTTCAACGAC	CTGATTGCTT	GTGCGTTCCT	240
TGTGGGAGCC	GTGGTCTTTG	CTGTGAGAAG	TCGGCGATCC	ATGAATCTCC	ACTACTTACT	300
TGCTGTGATC	CTTATTGGTG	CGGCTGGAGT	TTTTGCTTTT	ATCGATGTGT	GTCTTCAAAG	360
AAACCACTTC	AGAGGCAAGA	AGGCCAAAAA	GCTCGAG			397

- (2) INFORMATION FOR SEQ ID NO:519:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 640 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GAATTCGGCC	TTCATGCCTA	CTTTGGTAAC	AGAAGAGAAG	ACTGTGGAGC	CAGCTACCGT	60
CTCAGAAGAA	GCAAAGCCTG	CATCTGAACC	TGCTCCTGCC	CCTGTGGAAC	AGCTGGAACA	120
AGTAGACCTG	CCCCCAGGAG	CAGACCCCGA	TAAAGAAGCT	GCCATGATGC	CTGCGGGTGT	180
TGAGGAAGGT	TCATCAGGTG	ACCAGCCGCC	TTATCTGGAT	GCCAAGCCTC	CAACTCCCGG	240
GGCCTCGTTT	TCCCAGGCAG	AGAGCAACGT	AGATCCAGAG	CCTGACAGTA	CCCAGCCACT	300
TTCAAAACCA	GCTCAGAAGT	CTGAGGAAGC	CAATGAGCCA	AAGGCCGAAA	AGCCAGACGC	360
CACTGCAGAT	GCTGAGCCTG	ATGCAAACCA	GAAAGCCGAA	GCTGCTCCTG	AGTCTCAGCC	420
CCCAGCTTCT	GAAGATTTAG	AGGTTGATCC	TCCAGTTGCT	GCAAAGGATA	AAAAGCCAAA	480
CAAAAGCAAG	CGTTCAAAGA	CCCCTGTTCA	GGCAGCTGCA	GTGAGTATCG	TGGAGAAGCC	540
CGTCACAAGG	AAGAGTGAGA	GGATAGACCG	GGAAAAACTC	AAGCGGTCCA	ATTCTCCTCG	600
GGGAGAAGCA	CAGAAGCCTT	TGGAATTAAA	GACACTCGAG			640

- (2) INFORMATION FOR SEQ ID NO:520:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 469 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GAATTCGGCC	TTCATGGCCT	AGCAAGAGAA	AGAGAAGTGC	AAACACTCCC	ACGGCGAAGC	60
GCCCTCCGTG	GACGCGGATC	CCAAGTTACC	CAGTAGCAAG	GAGAAGCCCA	CTCACTGCTC	120
CGAGTGCGGC	AAAGCTTTCA	GAACCTACCA	CCAGCTGGTC	TTGCACTCCA	GGGTCCACAA	180
GAAGGACCGG	AGGGCCGGCG	CGGAGTCGCC	CACCATGTCT	GTGGACGGGA	GGCAGCCGGG	240
GACGTGTTCT	CCTGACCTCG	CCGCCCCTCT	GGATGAAAAT	GGAGCCGTGG	ATCGAGGGGA	300
AGGTGGTTCT	GAAGACGGAT	CTGAGGATGG	GCTTCCCGAA	GGAATCCATC	TGGATAAAAA'	360
TGATGATGGA	GGAAAAATAA	AACATCTTAC	ATCTTCAAGA	GAGTGTAGTT	ATTGTGGAAA	420
GTTTTTCCGT	TCAAATTATT	ACCTCAATAT	TCATCTCAGA	ACGCTCGAG		469

- (2) INFORMATION FOR SEQ ID NO:521:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 202 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GAATTCGGCC	TTCATGGCCT	ACCCGTTTCC	TCTAGTTTCT	TCCTGTAGTA	CTCCTCTTTT	60
AGATCCTAAG.	TCTCTTACAA	AAGCTTTGAA	TACTGTGAAA	ATGTTTTACA	TTCCATTTCA	120
TTTGTGTTGT	TTTTTTAACT	GCATTTTACC	AGATGTTTTG	ATGTTATCGC	TTATGTTAAT	180
AGTAATTCCC	GCGGCCTTCA	TG				202

- (2) INFORMATION FOR SEQ ID NO:522:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 492 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GAATTCGGCC	TTCATGGCCT	AAATTTAATG	AAGCAAAATT	CCATACATCA	TTTTGAAAAT	60
AGTGTTTCTT	TCCCTGATAG	GCCTGTTCTG	CATCATTCTT	TTAGCTTCCT	TCTGCCCTGT	120
TTATCACTTG	GTCCCACTTT	TATATTTTTC	CTCTTCGGTC	CAGAATTTCT	TATTTAGTTT	180
CTTGTATTTT	GCCTACTCCC	TCCCTTCTCC	ATGATTCAGC	CTAGTCTTTC	CGTCCTCTGT	240
GGACTTGGGT	GTGCCTTCCT	CTGGGCCACC	TCGTCTTTTG	CTGCTGTTAG	CCCTCCCGCC	300
TGCGCACCTG	CCACTTCACC	CTCGCCTGTG	GTCCACTTAC	GTTCCACTCA	GCCCGGTCAG	360
TCCTGCTTTG	TTCTTCTCCA	CCGCCTTGGT	CTCCCGTGTG	TCTTATCTAG	CTCTGGTTCC	420
TTCTCGTCTC	CACATTTATT	TTGTTTTCTT	CCTGTGCTTG	TTAGTCCTTG	TGCACTTGGC	480
CCTTTTCTCG	AG					492

- (2) INFORMATION FOR SEQ ID NO:523:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 394 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

GAATTCGGCC	TTCATGCCTA	GGAAATTTCA	CCATTTGGTC	TCCCCCTTTG	TGGGTCAGCA	60
GGTGGTCAAG	ACAGGGGGCA	GCAGTAAGAA	GCTACAGCCC	GCCAGCCTGC	AGTCTCTGTG	120
GCTCCAGGAC	ACCCAGGTCC	ATGGAAAGAA	ATTATTCCTT	AGATTTGATC	TAGATGAAGA	180
AATGGGGCCC	CCTGGCAGCA	GCCCAACACC	AGAGCCTCCA	CAAAAAGAAG	TGCAGAAGGA	240
AGGGGCTGCG	GACCCAAAGC	AGGTCGGGGA	GCCCAGCGGG	CAGAAGACCC	TTGATGGATC	300
CTCACGGTCT	GCAGAGCTCG	TCCCCCAGGG	CGAGGATGAT	TCTGAGTATT	TGGAGAGAGA	360
CGCCCCTGCA	GGAGATGCTG	GGAGGTGGCT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:524:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 600 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

CGATTGAATT	CTAGACCTGA	CCAAAGACCT	TCCGTACAGA	TTGACCGCAG	AATGTCAGGG	60
AAAGTTAGGA.	GAAGAAGTTC	TGAGAAGACT	GACTACAGAT	TGGCTGGCCT	GGCTGACCCA	120
GGAACTTCTG	AGCAGACTGA	CCTCAGATTG	TATGGCCTCG	TTGACCACAA	AACATCTGTA	180
AAGACTCACC	ACCAAGTGTA	CGGCCAAGCC	ACTGAACTAG	CTGAACACCA	GGCTATTGAC	240
CAAGCTCATA	GTAATGCTGA	TCAACCTCCA	GTTGACAATG	CTCACTACAC	TGAATCTGAC	300
CAGACTGACC	ACTTAGCAGA	CAGACAAGCT	AATCATAAAG	ACCAGCTGTC	TTACTATGAA	360
ACACGTGGCC	AGTCTGAAGA	CAGAATATTT	CCCCAGTTAG	GCAACAGCAA'	AGAGGACAAA	420
GAGGCTGACT	ACAGAGTACA	ACCCTGCAAA	TTTGAGGATA	GCCAAGTAGA	CCTCAATTCC	480
AAGCCTTCAG	TTGAAATGGA	AACTCAGAAT	GCAACCACTA	TCCCACCCTA	CAACCCAGTT	540
GATGCCAGAT	TCACCAGTAA	ATTCCAAGCA	AAAGACCAAG	CTCTTTTCCC	AAGACTCGAG	600

- (2) INFORMATION FOR SEQ ID NO:525:
  - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GAATTCGGCC	TTCATGGCCT	ACTITCTTCT	GCTGGCTTCC	ATCTTGCCAC	ACTTTCTTGC	60
TCTTCCTTCT	AACTGAAAGA	CTACTTCTCC	ATCCCCTCTG	CAGGCTCTTT	TGCTCCACCT	120
GATATTTAAA	TGTTGGAATG	CCTAGAGTTG	TTCTGACCCT	TCTTTATCTA	CCCCGATTTC	180
CTCAGTGATC	TTATGCAGAG	GTCTCCCAAA	GTTTACATGG	CTATCCTTGA	CCTCCTTCCT	240
GAACTGCAGC	TGGTGTCAGC	TGCCGTCACT	TGGATGTTTA	ATCAGCAACT	CAAGGTTTAC	300
GTGATGATTA	GACCGCAGTT	ACCCCCAGAC	TTCCTTATCC	CTTAGTTTTC	CCCATCTCAT	360
TAAGTTCACT	TCCATTCACC	TTCTTGATGA	AGCCAAGTAT	TTCAGAACTA	GCCTTGTTTC	420
TTCTTTTTCA	CTTTCCCCCA	TATCAATTCC	AGACTACCCA	CTCGAG		466

- (2) INFORMATION FOR SEQ ID NO:526:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 559 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GAATTCGGC	C TTCATGGCCT	ACATTGTAGA	AGAGATCACA	GAAACCACAA	AAGGTTTTCT	60
GAAGTATAT	G GATAATCAAT	CATTTGCAAC	TGAAAGTCAG	GAAGGAGTTG	GTTTGGGACA	120
TTCACCTTC	A TCCTATGTGA	ATACTAAGGA	AATGCTAACC	ACCAATCCAA	AGACTGAGAA	180
ATTTGAAGC	A GACACAGACC	ACAGGACAAC	TTCTTTTCCT	GGTGCTGAGT	CCACAGCAGG	240
CAGTGAGCC	r ggaagcctca	CCCCTGATAA	GGAGAAGCCT	TCGCAGATGA	CAGCTGATAA	300
CACCCAGGC*	I GCTGCCACCA	AGCAACCACT	CGAAACTTCC	GAGTACACCC	TGAGTGTTGA	360
GCCAGAAAC'	r GATAGTCTGC	TGGGAGCCCC	AGAAGTCACA	GTGAGTGTCA	GCACAGCTGT	420
TCCAGCTGC	C TCTGCCTTAA	GTGATGAGTG	GGATGACACC	AAATTAGAGA	GTGTAAGCCG	480
GATAAGGAC	CCCAAGCTTG	GAGACAATGA	AGAGACTCAG	GTGAGAACGG	AGATGTCTCA	540
GACAGCACA	A GGCCTCGAG					559

- (2) INFORMATION FOR SEQ ID NO:527:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 318 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

AATTCGGCC TTCATGGCCT AG	CGCAGTGGT TCAATTTTCT	TCGAAACGGT	GTGGTCCCTG	60
AAAAGGATG TTTCCTGTTT TO				120
ACATTTCAG ATGTTCAAGA A				180
ATTTGCTGT TATAGAAGTG G	· · · · · · · · · · · · · · · · · · ·			240
GCTAAAAAA TTGGAAGCCA A				300
CACTTGTGC CGCTCGAG	GACICAAGA AIIAAIGIAA	GCIGATCICC	WOOCHMINI	318

PCT/US98/06956 WO 98/45437

## (2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 276 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GGCACAGACT TACCGGACAC ACA	GGTCATG GGACACAGAG	TCATGGGGCA	CACAGGTTCA	60
CAGGGCACAC AGGCTCACGG GAC	ACAGAGT CATGGGACAC	ACAGGCTCAC	AGGGCACACA	120
GGCTCACAGG ACACACAGGT TCA	TGGGGCA CAGAGTCATG	GGGCACAGAC	TCACAGACTC	180
ACAGGTCATA GACGCTCATG GGG	CGCAGGC TCACAGGGCA	CACAGACTCA	GGGCACACAG	240
GCTCATGGGG CACAGAGTCA TGG	GGCAGGG CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:529:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 180 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GAATTCGGCC	TTCATGGCCT	ATTCTGTTCT	TTAAATTTGA	ATGAAAGTTT	GGCATTTTAA	60
AAAACTTTAG	GTGATTTAGG	AGTATAATTT	TAAGCAGATT	TTTAGAGTAC	GAGTGTCCAC	120
ATATTTAACT	AAACATTCAA	AAATTAGTTA	AAATCAATGA	ACTTGGGAAG	GATCCTCGAG	180

- (2) INFORMATION FOR SEQ ID NO:530:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 470 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GGGGACAGAA	GATGTGCTCC	AGGGTCCCTC	TGCTGCTGCC	GCTGCTCCTG	CTACTGGCCC	60
TGGGGCCTGG	GGTGCAGGGC	TGCCCATCCG	GCTGCCAGTG	CAGCCAGCCA	CAGACAGTCT	120
TCTGCACTGC	CCGCCAGGGG	ACCACGGTGC	CCCGAGACGT	GCCACCCGAC	ACGGTGGGGC	180
TGTACGTCTT	TGAGAACGGC	ATCACCATGC	TCGACGCAGG	CAGCTTTGCC	GGCCTGCCGG	240
GCCTGCAGCT	CCTGGACCTG	TCACAGAACC	AGATCGCCAG	CCTGCCCAGC	GGGGTCTTCC	300
AGCCACTCGC	CAACCTCAGC	AACCTGGACC	TGACGGCCAA	CAGGCTGCAT	GAAATCACCA	360
ACGAGACCCA	GGCCCTTCAG	CACCGTTCAC	AGTATTTTGA	AGGTGTTGTG	AAGTGCAATA	420
AGCTGGAAAT	ACTGGAGACC	ATCGTGGACA	GAATAGTAAG	AGCCCTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:531:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 553 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GAATTCGGCC	TTCATGGCCT	AGAAAATTCC	AGAAAGGATA	TTTAAGAAAA	TACAATAAAC	60
TATTGGAAAG	TACTCCCCTA	ACCTCTTTTC	TGCATCATCT	GTAGATACTA	GCTATCTAGG	120
TGGAGTTGAA	AGAGTTAAGA	ATGTCGATTA	AAATCACTCT	CAGTGCTTCN	TACTATTAAG	180
CAGTAAAAAC	TGTTCTCTAT	TAGACTTTAG	AAATAAATGT	ACCTGATGTA	CCTGATGCTA	240
TGGTCAGGTT	ATACTCCTCC	TCCCCCAGCT	ATCTATATGG	AATTGCTTAC	CAAAGGATAG	300
TGCGATGTTT	CAGGAGGCTG	GAGGAAGGGG	GGTTGCAGTG	GAGAGGGACA	GCCCACTGAG	360
AAGTCAAACA	TTTCAAAGTT	TGGATTGTAT	CAAGTGGCAT	GTGCTGTGAC	CATTTATAAT	420
			TCTCAAAGCA			480
		TTTGGAATCT	TCTCTTTGAC	AATTCCTAGA	TAAAAAGATG	540
GCCTTTGCTC	GAG					553

- (2) INFORMATION FOR SEQ ID NO:532:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 843 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GAATTCGGCC	AGAGAGGCCT	ACTTCTCTTA	GTGATTTCAT	GTTTCAACCA	GTACATTGTG	60
GTGAATACTG	AAATATCTTG	TTTAATTCAG	ATAATTAAAA	TGGTGGCAAA	GGAAGCTGTT	120
TAGCCAGAGC	CCTTCTTGAC	TTTGAGGAAC	AGTGGTAGTA	TAAGACTTGA	AGACAGACGT	180
GTAAAAAGTA	CTACTCACTG	GTAGGCTCAG	GTCTGGTTGA	TTGACTGATT	CTTGAGACGG	240
AATGTCGCTC	TGTCGCCTAG	GCAGGAGTGC	AGTGGCCCAG	TCTCGGCTCA	CTGCAGCCTC	300
CGTCTCCGGG	TCCAAGCGAT	TCTCCTGCCT	CAGCCTCCCG	AGTAGCTGGG	ACTACAGGCG	360
CCCGCCACCA	CACCGGGCTA	ATTTTTGTAT	TTTTAGTAGA	GACGGAGTTT	CACAATATTG	420
GTCTCGAACT	CCTGACCTCA	GGTGATCCAC	TCGCCTGGCC	CACCCAAAGT	GCTGGGATTA	480
CAGGGATGAG	CCCCTGCGCC	TGGCCTCGGT	TGAATTTATT	AAACAACTTT	TGTGGGCAGC	540
AAGCTGTACG	AGGTTAACTA	TGTGATGAGA	AGACTTAGAA	ATGGAGAAAA	GTTTTATCAG	600
TTCTACATAG	GACTTAGTTT	GGGAGTTTCT	GGAAACTACG	TTGGAAATCA	GTAGTTGCAC	660
ACTAGCTGAA	TTCAGCTGTG	TAATTTACAG	TGATTTGTTA	TTTACCAAAT	AAGTAGAAGA	720
GGGAATTAAG	AAGCTAAAAT	CTCTGGGTAC	TTGTTTGATA	TGAATTTGTT	AATTGTTTAT	780
ACTCAGGTAA	TAAGTGTTAC	CTCAGTCATA	GCATTTAATA	TTTTATCTGA	CTGTCCTCTC	840
GAG			•			843

- (2) INFORMATION FOR SEQ ID NO:533:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 525 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

•	
GAATTCGGCC AAAGAGGCCT ACATCCAGAA ATTTAGGGAC TCAGCCCTGG TCAGGGTGGC AAAGGGTCTG TTTGTCTTTC CCCATTAGAC AGAGGTCTTG TCCTGCTACC CTAATTGTAA AGGGGTGCCT GGGAAGGGGT GGTAGGGACA TGGTGGCGGT GGAGACTCCG GCCCCACTTC TCCAGGCTTT GCTGACAGGG GCCTGCTTTT AATTTTATT TTTATTCATA ACTTTTTAA AAAAGAATCC CGTAACTTCT TTTTCATAAC TTTTTTTGTA ACTTTTTAT CCCATAACTT TTTCACCCCA TAACTTTTTT AAATAAAGTT ATTTAATAAA ATAACTTTTT ATAAAACTTT AATAAAAGTT TTTTAATTAA CCCATAACTT TTTTATTTTG GTTTTTAATAA AACACTTGCA TAGTTATATT ACAACTTTGT AAAAATGAAA CACATTATCT CAGGC	60 120 180 240 300 360 420 480 525
(2) INFORMATION FOR SEQ ID NO:534:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 268 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:	
GAATTCGGCC AAAGAGGCCT AGAAAACCCT TGAAGACATG TTGAAAATAC ATACTCCTGT TAGCCAAGAA GAAAGATTGA TTTCTTAGA CTCCATTAAG TCCAAATCCA AAGACTCTGT GTGGGAAAAA GAAATAGAAA TACTTATAGA GGAAAATGAG GACCTCAAAC AACAATGTAT TCAGCTAAAT GAAGAGATTG AAAAGCAAAG GAACACTTTT TCATTTGCTG AAAAAAACTT TGAAGTTAAC TATCAAGAG TACAAGAG	60 120 180 240 268
(2) INFORMATION FOR SEQ ID NO:535:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 224 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:	
GGCTTGCACC TCGGCGATCC CCGACTCCCT TCTTTATGGC GTCGCTCCTG TGCTGTGGGC CGAAGCTGGC CGCCTGCGGC ATCGTCCTCA GCGCCTGGGG AGTGATCATG TTGATAATGC TCGGAATATT TTTCAATGTC CATTCCGCTG TGTTGATTGA GGACGTTCCC TCACGGAGA AAGATTTTGA GAATGGCCCC CAGAACATAG ACATTCCTCT CGAG	60 120 180 224
(2) INFORMATION FOR SEQ ID NO:536:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 303 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:	•
GAATTCGGCC TTCATGGCCT ACCACTCTGG CCCCAGCGTC ACTGGCCTAG GGACACATGG GGGTGGGGAT TGTTTGGCCT TCCTGGCTTA GGTCTCTGGA AGAGAGAAGA ACCCCATGGG	60 120

GCAGACCCAG GCCACGGGCA GTACATGCCT CCCACACTAC TGACACCGCC AGTGTCTTCT GTGAAGCCAC CTTTGAGCAA CGGAAAGGAA GGGGGATGGG CAAGATCAGT GCAAGGTTGG CCAAAAGCCT GGGGCTGGCC TTCTGCTGGC ATGAGAGGGC CAGGCCGCCC CCAGCTCCTC GAG	180 240 300 303
(2) INFORMATION FOR SEQ ID NO:537:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 350 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:	
GAATTCGGCC TTCATGGCCT AGAACAAAAT CTGAAATTCA GAAATAAACA ACAGTTGGAA AATATTTTCC ATTTTTTCC CTATTAAATA TGATAATTC AGGTGCAAAG AGTGTTTTT TTTTTTTTTT TTTCTCCACA GTGCTTTTCA CGGTGGGAC TAATGGATAT AGAGGGTGGG AGGCCAGAAT AACCAAGTAC CTGGAAGTGA ATCTTTGTGG AGATAATGAA ATAATTTTAT TCGAAAGGTG CAAAAGGAAG TCTTCCATCA CTAGCTCAGC TGTTATGGTC CTTGAACTGC CCTTGCCCGT CTGTCTTTT ATTAATCCTT TTTACCTGTC GAGTTCCAGG	60 120 180 240 300 350
(2) INFORMATION FOR SEQ ID NO:538:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 344 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:	
GAATTCGGCC TTCATGGCCT AGAGTTGCAC AGATGTCTTT TGTTAGCTTT GGTGGCGGAG TCATCCTCAC AGACCGTTAC TCAGATAATT AAGTGCCTTG CAAATTTAGT ATCAAATGCA CCTTATGATC GTCTAAAACT CAGCCTGCTG ACCAAAGTCTT GGAACCAGAT AAAGCCTTAT ATTCGCCACA AAGATGTTAA TGTTCGTGTG TCAAGTCTCA CACTCTTGGG AGCTATAGTG TCCACCCACG CACCTTTACC TGAAGTCCAA CTACTTCTGC AACAGCCATG TTCTTCTGGA CTCGGTAATA GCAATTCAGC AACCCCTCAC CTCAGCCCCT CGAG	60 120 180 240 300 344
(2) INFORMATION FOR SEQ ID NO:539:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 343 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:	
GAATTCGGCC TTCATGGCCT ACAACTCCAT TAAACCACCA CCAGCTCCCC AAGCCACCCC TTCAGCCATG AAGTTCCTGC TCCTGGTCTT GGCAGCCCTC GGATTCCTGA CCCAGGTGAT CCCAGCCAGT GCAGGTGGGT CAAAATGTGT GAGTAACACC CCAGGATACT GCAGGACATG TTGCCACTGG GGGAGACAG CATTGTTCAT GTGCAACGCT TCCAGAAAAT GCTGCATCAG	60 120 180 240

CTACTCCTTC CTGCCGAAGC CTGACCTACC ACAGCTCATC GGTAACCACT GGCAATCAAG

GAGAAGAAAC	ACACAAAGGA AAGACAAGAA GCAACCCCTC GAG	343
(2) INFORM	ATION FOR SEQ ID NO:540:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 248 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	,
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:540:	
CAGCATCTCT TGACCCATCC	TCTGAAGACC TCTCAGCCTC TTATGACCAC TCCTGGCACC CTGTCAAGCA GGTCACTGGC CCTATAGCCG TACAGACTAC ACCTGGAAAA CAGCTCTCGC TGAAATACTA GTTCCTCAAA TCTCAACAGA AGGTGGCATC AGCACAGAAA GATTGTGGAT GCTACCACTG GATTGATCCC TTTGACCAGT GTACCCACAA	60 120 180 240 248
(2) INFORM	ATION FOR SEQ ID NO:541:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 433 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:541:	
GTTCTATAAA AAATTAAGGT AGAGTAAAAC GAGAATGAGA GGGGTAGCAG	TCATGGCCTA GATTGTCTTT ATAGGAAATG TCTTTAGCAA AATACTACGG ACCCATTAAC GGGTTATCAG TGTCTAGGAC ATAAATGGCT TCTGGTAAGA CTACTCTCCC TAAAATACTAT CATAATTACA AAGGTTAAGA AAAAAGAAGT ATGTGTCCCT TAAAAATCAA ACATGAGTGG TCACAAGGTC CTAAGAAGCA ACTCCAGTTG CTTGTTTATC TCTCAGGCTG AGCATGGTTG GTTACAATGA GAAGAGCACA GCCTTGGACT CCAGTCCAAG GAACTCCAGT CTCTCCTGCA GTTTGACCTT GGGCCACTTA CTGTTCCTTT CTCAGCCTCC ATTTTCATAT GAG	60 120 180 240 300 360 420 433
(2) INFORMA	ATION FOR SEQ ID NO:542:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 493 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:542:	
CTCAGAGCCC TCAATCAGAA TCTGCCAGTT	TTCATGGCCT AGACACGGGA CATAAAAACT TTTAATGAAG GAGGACACAG TTCCACATGC GGCCCAACCC TGCCCCACGG AGACCGGCCA TGGCAACCGC GGTGTTCTTG ATGCGGCCGG CCACCAGCCT AAGGATGTCC CCGATCTTCT GGCGATGTCC TTGGACACGG CGCACCACAG CTCCCCATGC CGAGGCTCTG GCGCTTCCTC ACCTCCTCCT GCTGCTCCTC AGTGCCATGC TGCAGCTCAA	60 120 180 240 300

WO 98/45437 PCT/US98/06<u>956</u>

ACCACTCCCT GGCCTTGGTG ATCTTCCGCT GACTCCAAAA CAGCTTGGCC ACGGCCAGGA GCACATGGGG GTCATGCTCA CACTTCTTCA GGGCATCCAC GCTCTTGGTC CTCCTCTGGG	360 420 480 493
(2) INFORMATION FOR SEQ ID NO:543:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:	
AGCAAAAAGC CCAAAGAAAA AAACATTTA TATTCATCTG TATAAAACATA TCCGCTAAGG CAAACGCAAT CCGGGTCCGA GGCTGCTGCG CTGGGCTCGG TGCCTCCTAA TTTCTGCAGA TTCTAAGGCC AAAAAATAAA ACCTCTGCAA GTCCGCGTAG CTTCCAGGAC TCCTGGGCAT TTTACTAAAA TAAAGAGTTA TCGAGTTTAA AAAGCAGTGA CGTCGTTATG ACACACACTG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:544:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 473 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:	
TGGATGAAGA GAGTTTAAAT AGATTACATA GAATTTTTAA TAATGTCGAT TGGTTATATA CTGGGCACTG ATAGCTGATT TTTCTTTGGG GAAAGGTATG TCAGCCTAGT CATTCAGATT CCTTTATTTT TTTAAATGTT TTTTCATTTT TTGCTTTGCA TTGCATTCAT TTGCTGAAGA GCTGGCTTGT ACTTTGGCAG GTGTCATACT TGGTTATTCT CCTTAGGATA TTGGCCCAAC AATCTGGGAT TTGTGAAAGG CGCTTCGCTT TTCAGACCTG GGCGTCTGTA TCATGACTAT CATAAATTTA GGATTAAGAC ACCTAGCCTC CTACCAGGAT GAATGAGGTG TCCATGTGAC	60 120 180 240 360 360 420
(2) INFORMATION FOR SEQ ID NO:545:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 120 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:	

60 120

GAATTCGGCC AAAGAGGCCT AGTCGAGAAG GAAGAGGGAA:GAAGAAAAAC TATAAAAGTG TGCTAAATGT TTTATTTTCT CTGGAAGAAT AGTTATATTC TACTCTTTGT GGCTCTCGAG

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(2) INFORMATION FOR SEQ ID NO:546:
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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 481 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GCTAGACCTG	CCCCCTTAGA	AATGGAAAAA	GCATGCAAGA	GAGATGTTAA	AGGAGACTAT	60
TGGAGCAACT	GTGTCCACAC	CCTCTGTGAT	AGAAATGGAA	AAAATATCCC	CAGAAGATCG	120
TGGTGAGAAT	ATTGGGAAAC	ACAAAGTGTT	ACCCGCAGTG	GTAGACATTG	AGAAAATACA	180
TGGAACAGGA	CTAGAATTGA	CCACTAAACA	AGGGGAGGCC	ATGCTTCCTG	CATTTGAAAG	240
TAAAACACCA	CAAGAGTATG	CTGAAGGGAG	TGTTGAAGAA	ACAATGGAAA	ATACTTACCA	300
AAAGGATGCT	GAAGGGGATA	TTGGAAAGGC	TGAAGTGATG	CCTGTGAGGT	TAGAAATGGA	360
AAATACTTAC	CCAAAGGATA	CTGAAAGAGA	CGGTGGCAAA	ACTGAGGTGA	TGCCCCTTGC	420
ATTAGAGGTA	GTAAATACTT	ACCAAAAAAA	TGCCAAAGGT	TTTACCGGGA	ACAATCTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:547:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 405 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GAATTCGGCC	AAAGAGGCCT	AGAAACCTGA	GGCTGCTGCC	CTTTATCTGC	CTTCACGGTA	60
CTGTCCCCTT	CCCCCAGCTC	CTCCCTGACC	CCATGGGCCA	GGCCTCAGAC	CTTCCAGCTA	120
ACCGCTTCCC	ATGAGCCACT	ACTCTGATGT	CAGCCTATAA	CCAAAGGAGC	TGGGGGGTCC	180
AGGCCTGGTG	ACCAACCTTT	CTCAGCCCAC	TCAATCAGGG	TGCTCCCCAC	CTGCAGGCAG	240
GAGGCAACAC	CCTATCTGCT	ACCATCAGCC	CCTTCCAGAG	CCCATCTGCC	CCGCCCAGCC	300
CTGCCCTGCC	CAGCCATACC	CTGCTCTGCC	CCATCTGGGG	GTGCCCTGCT	CAGGGATGGG	360
CTGGCAGGGC	TGTACCCAGC	CTCCCTGGTA	AGCAAAGAGC	TCGAG		405

- (2) INFORMATION FOR SEQ ID NO:548:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 142 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GCGATTGAAT	TCTAGACCTG	CCTCCCTGCT	TTCTAATAAA	TCTGACTAAC	CTTAGACATT	60
TTGTATCTTA	CTAAGAACAT	CCCTTCAATA	TCTACTTCAT	TATCCCATGC	CATTTCCCCA	120
CTGTCTCAAC	ACGAATCTCG	AG				142

(2) INFORMATION FOR SEQ ID NO:549:

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(A) LENGTH: 296 base pairs(B) TYPE: nucleic acid

(i) SEQUENCE CHARACTERISTICS:

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(C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:
GAATTCGGCC TTCATGGCCT ACTATGGTAT TGCTAAACAA GGGTGGGAGG AGAGAGAGT
                                                                       60
AATCAGGGAG GACTTCCCAC AGGAGGTGGC ATCTGCAGAT GTCTCAAAAA AGAAAAGAAT
                                                                      120
TAGCCTGGCA AGAGGTGAGG ATTGTGTAGA GGTCACTCAC TTTCCTTGTG GGTGGAGGAA
                                                                      180
ACCATTCCAG GAGCTGTAGG AAGCTTGGTG CTGGTGAAGG AGGCAGGAGA GGAGAAGA
                                                                      240
GGAGATGACC TTAGAAATCA CATCCAAGAG CCTCTGATCC CAGGAGGCAG CTCGAG
                                                                      296
(2) INFORMATION FOR SEQ ID NO:550:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 254 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:
GCAGGAGAA AAATTGAGGC TTAGGTTAAG AAACTTACCC AAAGTCAAAC AATTTAATTG
                                                                       60
GTTTGGGAAG ACCAGGAAGA CTTTAAGTTC CTAAGATCGT TTGAGATTCT GCATCAGGGA
                                                                      120
ACACTTGACA GCAGGTTTAT ACAAAGACAG ATTTGGTATC TTTGGAGGGA ATGAGTTTCC
                                                                      180
AGTCATTGCA GGTGGTCCAG CAGAGAGGGC CACTCTCCTT TTTTTCTTTC TTTACTCCCT
                                                                      240
TTTTGATTCT CGAG
                                                                      254
(2) INFORMATION FOR SEQ ID NO:551:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 278 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:
AGGCCATGAA GGCCCTTTCC ATTTCTTTTT GTTCCATCAC TCTTCTCTCA ACCTGTGTTT
CTTTTTTAC TGAGGAGTTA GTCCCCATTA GTTCTTGTAT CACATTTTCA TTTGCACGAC
                                                                      120
ATTACTCGCA GGTGGTGGGG AGCCTGGGCT TTTGGGGAAC CAGGCTGCTC TGGTCCCCAG
                                                                      180
CATTGCCTCC TCCTAGCCCC TCTAGTCCAG TTTGCCTCCC TTACCCTCAT TTTCCAAACC
                                                                      240
TCTTGTACCC TCCTCTCCT CCCCCAGCTG GCCTCGAG
                                                                      278
(2) INFORMATION FOR SEQ ID NO:552:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 322 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GAATTCGGCC	TTCATGGCCT	ATGCACTTCT	TCTTTCTCTC	CTCCTTTTGC	TGGGTGCTTA	60
CCGAGGCCTG	GCAGTCCTAC	CTGGCTGTCA	TTGGGCGGAT	GCGCACCCGC	CTCGTTCGCA	120
AGCGCTTCCT	CTGCCTGGGC	TGGGGTCTGC	CTGCCCTGGT	GGTGGCCGTG	TCTGTTGGCT	180
TTACCCGAAC	GAAAGGATAC	GGTACATCCA	GCTACTGCTG	GCTCTCCCTG	GAGGGCGGCC	240
TGCTCTACGC	CTTTGTGGGC	CCTGCAGCCG	TCATTGTCCT	GGTGAACATG	CTCATCGGAA	300
TCATCGTCTT	CAGCAGCTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:553:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 390 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

GCCAAAATCA AGCAAAGTAT	GAAGAAAGAT	AAAGAAGGGG	AAGAAAAAGG	GAAGCGAAGA	60
GGATTCCCCA GCATCCTGGG	ACCCCCACGG	AGACCAANCC	GTCATGACAA	CAGTGCAATT	120
GGCAGAGCCA TGGAACTACA	GAAGGCGCGC	CACCCTAAGC	ACTTATCCAC	ACCCTCATCT	180
GTGAGTCCTG AACCTCAGGA	CTCTGCCAAG	TTGCGCCAGA	GTGGGTTAGC	AAATGAAGGA	240
ACAGACGCTG GATACCTGCC	TGCCAATTCC	ATGTCTTCTG	TAGCTTCAGG	GGCCTCTTTT	300
TCCCAGGAAG GAGGGAAAGA	GAATGATACA	GGATCAAANC	AAGTTGGAGA	AACATCAGCA	360
CCTGGAGACA CCTTAGATGT	CACCCTCGAG				390

- (2) INFORMATION FOR SEQ ID NO:554:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 306 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

GACGGCTACA	CCATGGGCCG	GCTGCTGCGG	GCCGCCCGGC	TGCCGCCGCT	GCTTTCGCCG	60
CTGCTGCTTC	TGCTGGTTGG	GGGAGCGTTC	CTGGGTGCCT	GTGTGGCTGG	GTCTGATGAG	120
CCTGGCCCAG	AGGGCCTCAC	CTCCACCTCC	CTGCTAGACC	TCCTGCTGCC	CACTGGCTTG	180
GAGCCACTGG	ACTCAGAGGA	GCCTAGTGAG	ACCATGGGCC	TGGGAGCTGG	GCTGGGAGCC	240
CCTGGCTCAG	GCTTCCCCAG	CGAAGAGAAT	GAAGAGTCTC	GGATTCTGCA	GCCACCACCA	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:555:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GAATTCGGCC	TTCATGGCCT	ACCCTCTCAC	GCCACCCCCG	CCCCCACCGG	GCTGCAGGTG	60
CTGCTGATGC	GCTGGGATCT	GATTGAGGAT	AAAAAGGAAG	GAGAGATGAC	CCCTACCCCC	120
TCATCCCCCA	GTTTTGAAAA	GGTCTAAGCA	AGTGAGTCTG	GTGGAGGAGC	TGAGGGAGGG	180
AGCCATGGAA	GGTGCCAGAA	GGAAGGTTGG	CGGGGGCACG	TGTGGGCCGT	GGCTTGGGCT	240
GGTCAGAGTG	GCGTGAGCTG	CCCGGCGCCT	GCCCTGCCCA	AGTGACCAGG	GAAGTGTGTG	300
TGTGTCCATG	TGTATGCGTG	GCTCGAG				327

- (2) INFORMATION FOR SEO ID NO:556:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 272 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GAATTCGGCC	TTCATGGCCT	AGAGAAGGAG	CCAGCTGGGG	CCGAATCCAT	CCGCTTGAAC	60
ACCAAAGAAG	ACAAAAATGG	TGTCCCCGAC	TTAGTGGCCC	TGCTGGCTGT	GAGAGACACC	120
CCGGACGAGG	AGCCGGTGGA	CAGCGACACT	TCGGAGAGCG	ACTCGCAGGA	AAGTGGGGAC	180
CAAGAAACAG	AGGAGTTGGA	TAATCCTGAG	TTCGTGGCCA	TTGTGGCCTA	TACCGACCCG	240
TCGGACCCCT	GGGCCCGGAA	GGAGAACTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:557:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GAATTCGGCC	TTCATGGCCT	ATTTCCGATC	TATGTATCTG	TACTCATACA	GCCTCATCGG	60
GCTAAACAGC	CTTCTTTTCA	GAACAGTAGA	TCACTCAACT	GGGTTTTCAA	GTGACTGTTT	120
ACCTTTCAAG	GCTGGCTTTA	TAGGTCTTGC	CTCACTGTAT	CCAGCAATCC	AAACTTTACC	180
CTATCCCAGT	CAGGACTGCA	CACCTCATAT	TGAAAGACAT	ACCTTAGAAC	CAGACTCCCC	240
AAACCTTACA	AATATCCCAC	CCTTGACTCC	CGTTCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:558:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 474 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GCAATGGTCT CCAGGATGGT CTCTACCATG CTATCTGGCC TACTGTTTTG GCTGGCATCT

PCT/US98/06956\_ WO 98/45437

GGATGGACTC	CAGCATTTGC	TTACAGCCCC	CGGACCCCTG	ACCGGGTCTC	AGAAGCAGAT	120
ATCCAGAGGC	TGCTTCATGG	TGTTATGGAG	CAATTGGGCA	TTGCCAGGCC	CCGAGTGGAA	180
TATCCAGCTC	ACCAGGCCAT	GAATCTTGTG	GGCCCCCAGA	GCATTGAAGG	TGGAGCTCAT	240
GAAGGACTTC	AGCATTTGGG	TCCTTTTGGC	AACATCCCCA	ACATCGTGGC	AGAGTTGACT	300
GGAGACAACA	TTCCTAAGGA	CTTTAGTGAG	GATCAGGGGT	ACCCAGACCC	TCCAAATCCC	360
TGTCCTGTTG	GAAAAACAGC	AGATGATGGA	TGTCTAGAAA	ACACCCCTGA	CACTGCAGAG	420
TTCAGTCGAG	AGTTCCAGTT	GCACCAGCAT	CTCTTTGATC	CGGAAACACT	CGAG	474

- (2) INFORMATION FOR SEQ ID NO:559:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 290 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GAATTCGGCC	TTCATGGCCT	AATTTTTTTG	TTGTTGTTTC	CTTTTTGTAT	TTTACTGATA	60
TCACCAGGAT	AGTTTACTCT	CCTTCTAGCT	TTCTGCTTAC	CGCACACTGG	ATAACACACA	120
CATACACACC	CACAAAAATG	CTCATGAACC	CAATCCGGAG	AAGGTTCCAG	CAGGTCCCCC	180
ACCCTCCCCT	CCTCCTCCTA	CTTCTCCTCT	TGACAGCGAG	GACAGGAGGG	GGACAAGGGG	240
ACACCTGGGC	AGACCCGCCG	GCTCTCCCCC	CACCCCACCC	CGTCCTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:560:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 361 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GTGTATGTGG	GGGGTAAGTG	TGTGTGTGTG	CGTGTGCGTG	TATGTGCACG	TGTTGTGTGT	60
GTGCGCCTGC	ACACGGAGAG	CCCACTCATA	CGTAGCAGAA	AATCAAATGG	CCCCAAATCA	120
GAAACATGGC	GCATGTGAGC	ATGCCACTTC	TTGTGTGCCT	GTGACTGTTC	AGAATGTACA	180
CGGCCCTGCA	GCTCCCGAAG	GCCAGCTCTG	CTGCAACCCC	TCCTCTGTCC	AACACAGTCC	240
TCACTGGTGT	CTTTTCCTCT	TCAAATCTAC	AGCATTTCTG	ATCTCTGCAA	ACAATTTAAC	300
CCAAAACCAA	GTTCTGGCTG	ACAAGGCTAC	ATCTTGTTTC	TTGTGCGTGA	TTAGCCTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:561:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 381 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

GTTCTAGACC TGCCTCGAGA TATGCCGGAA GGTTGCATGG CTGGTCCCAG GGCCAGCACA

GGCCCGAGGC	CGGGCTGCCT	GGTTTTATTT	TTATTTAACT	TTATTTTCTG	TTTTATGAGT	120
GTGTGTCCGC	CCACCCCCAC	CCCCTTCAGT	GTTAAGTGGG	GAGCCCTGGG	GGAGTCTCTC	180
CTGCCTCCCA	GCCTCTCCCA	AGACCTCCCC	CCTCGTCACC	AGCCATCCCT	CTGGACCAGG	240
CAGAGGGCGG	ACCGGGTGGG	CAGGGGCCTG	AGGGTGGCTC	GGGCCAGCCC	ACCAGCCAAT	300
GGACCCCTCC	TCAGGCCGCC	AGTGTCGCCC	TGCCCCTTTT	TAAAACAAAA	TGCCCTCGTT	360
TGTAAACCCT	TAACGCTCGA	G				381

- (2) INFORMATION FOR SEQ ID NO:562:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 317 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GCACTCATAA	AAATCTTACT	CAGAAATCTT	CAGAGGTTTG	CTAAGGATAC	AATTTGATTC	60
TTACACATTT	AATGCTCACC	AGCTGCTTAG	GCCCACACCA	TTTATCCACC	CTGATTTGCT	120
ACTGCTCTTT	GAAATACAAC	CAGTGTTTCA	GCCAGACTGT	TTTCCTGCTT	CTGCTCCCCT	180
TCTCCTCCTC	CCAGCACATC	TGTGAATTCT	TTGACTGGTT	TACCACTCCC	ACACTCCTCC	240
CCAGCAATGC	AGATCTTCTA	CACCCTTTAG	GATCTAAGCT	AAGTCTGCTT	CCCAGATATC	300
CTCCCGAACA	GCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:563:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 472 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

	CAGGAAGGCT TACTTCTATT GCTGTTATCA AGAAGCAGCA TGGCAGCTGG AAAATGATGC	GGGTGTTCCT TCATCACTCT TTGAAACATT CTACCTCAAC TAGCTGTGGA GGTCATCCGT	CATGTACAGA CATTTTCTTC TGCAGAAATC AGCCACCACC TGTCAACAAG TTTCCACATG	GCAATTGACA CTCGCCTGGC AGAGTACAGT CAGATGTTTC CCCCAGGGAC TTCATCCTGA	GCTTTCCCCG TTGTGAAGAA TTCAACAAAT ATGAAGATGC GCGCCCCAGC GCATGGTGAC	60 120 180 240 300 360 420
CGTGGACGTG						472

- (2) INFORMATION FOR SEQ ID NO:564:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 411 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

TCATGCCCGG TACAAAGAGT TCCGCGAACA TCGCTGTGGC AGTCAGCTCA	TCCCCCTTCG GGCCCTGTGG TTGGTCTGGG CGCTTCTAGG AGTGGCCGGA AGCCGTGCGC CTGCGTGGAC AAGTACGCTC ACCAGTTCGC GGACTGCGCT TGCGTGAGGT GCCGGAGGA CTGCCTGCCA ACGTGACGAC GCTTAGTCTG AGATCACTGT GCTGCGCGC GGGGCCTTCG CCGACGTCAC ACAGGTCACG TGGCGCACAA TGAGGTGCGC ACCGTGGAGC CAGGCGCACT GGCCGTGCTG AGAACCTCGA TCTGAGCCAC AACTTCATAT CCAGCTTTCC GTGGAGCGAC TGAGCGCGCT GCAGCTGCTC AAAATGAACC ACCACCTCGA G	60 120 180 240 300 360 411
(2) INFORMA	TION FOR SEQ ID NO:565:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 270 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:565:	
ATTAATTAAG GTATTCATTA GCAACATTTA	CCTCAGACTT TCAAAGAGCC AGGAAATCGG TATAAAATTT TTGAGATAAC CTTTTTGCAG TTTTTCCTAG GACCAGATTA AACAGAAGTT TTCCTTTACA TGGTTGGTAT CTCCAGAGTT CATCCTTTTT TTGTGGTACT GGGAAAAGTT CCTTTGCAGG GACATGGATG GAGCTGGAGG CCATTATCTT TAGCAAACTA AAAGACAAAA ACCACTCGAG	60 120 180 240 270
(2) INFORMA	ATION FOR SEQ ID NO:566:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 272 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:566:	
CCATGTCACT TGGAAATTAC TTATACTGGG	ACTAACGGCT CATCTTTCC TTGTTTTTGT TTTTTTTTT TTCTTTTTTT  AAAGGCCAAA ACTGGAACCA AGGATTTAAT AACTATTATG ATCAAGGATA AATAGTGCCT ATGGTGGTGA TCAAAACTAT AGTGGCTATG GCGGATATGA TATAACTATG GGAACTATGG ATATGGACAG GGATATGCAG ACTACAGTGG ACTTATGGCA AGGCATCTCG AG	60 120 180 240 272
(2) INFORMA	ATION FOR SEQ ID NO:567:	
	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 306 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:567:	
AGAAGAGGTA	GAATTCGAAA TATTGGCATA TGGTTCTTTT GGATTAGATT ATATAAAATC GAACCAGGCC CCAAGCACTC CTTTTTCTCT GCATGATACT TCTGCTTATT	60 120

CTCGAG

CAAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCTT TCTGTGCCAA AGAGATGTGA TGCAGAAGGT CCTGAAGATC AGTGTACTGT TACCCGGACG

240 300

(2) INFORMATION FOR SEQ ID NO:568:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 253 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:	
GGTGTTTGGC CACAGTTCGG GACCTATGGT AGAAAAATAC TCAGTAGCTA CCCAGATTGT AATGGGTGGC GTTACTGGCT GGTGTGCAGG ATTTCTGTTC CAGAAAGTTG GAAAACTTGC AGCAACTGCA GTAGGTGGTG GCTTTCTTCT TCTTCAGATT GCTAGTCATA GTGGCTATGT GCAGATTGAC TGGAAAAAGA TTGAAAAAGA TGTAAATAAA GCAAAAAGAC AGATTAAGAA ACGAGCTCTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:569:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 544 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:	
CACAGTGCTG GCTCACAACA AGATGCTCAA GGTGTCAGCC GTACTGTGT TGTGTGCAGC CGCTTGGTGC AGTCAGTCTC TCGCAGCTGC CGCGGCGGTG GCTGCAGCCG GGGGCGGTC GGACGGCGGT NATTTCTGG ATGATAAACA ATGGCTCACC ACAATCTCTC AGTATGACAA CGAAGTCGGA CAGTGGAACA AATTCCGAGA CGATGATTAT TTCCGCACTT GGAGTCCAGG AAAACCCTTC GATCAGGCTT TAGATCCAGC TAAGGATCCA TGCTTAAAGA TGAAATGTAG CGCATAAA GTATGCATTG CTCAAGATTC TCAGACTGCA GTCTGCATTA GTCACCGGAG GCTTACACAC AGGATGAAAG AAGCAGGAGT AGACCATAGG CAGTGGAGG GTCCCATATT ATCCACCTGC AAGCAGTGCC CAGTGGTCTA TCCCAGCCCT GTTTGTGGTT CAGATGGTCA TACCTACTCT TTTCAGTGCA AACTAGAATA TCAGGCATGT GTCTTAGGAA AACAGAATCT CGAG	60 120 180 240 300 360 420 480 540
(2) INFORMATION FOR SEQ ID NO:570:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:	
GAATTCGGCC TCATGGCCTA CATTAAAGAA AAGCTTCCCA CACATCCATT TGAAGCTGAT CTCCTTGAGA TGGCAGAAAT GATTGCAGAA GATGAAGAGA AGAAGACTCT ATCTCAGGGA	60 120
,	

GAGTCCCAAA CTTCTGAACA CGAACTCTTT CTAGACACCA AGATATTTGA AAAAGACCAA GGAAGTACAT ACAGTGGTGA TCTTGAATCA GAGGCAGTAT CTACTCCACA TAGCTGGGAG GAAGAGCTGA ATCACTATGC CTTAAAGTCA AATGCTGTGC AAGAGGCTGA TTCAGAATTG AAGCAGTTCT CAAAAGGGGA AACCCTCGAG	180 240 300 330
(2) INFORMATION FOR SEQ ID NO:571:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:	
GAATTCGGCC TTCATGGCCT AAGGGAAAAC ATTTTGCATG TGTAAAGCTT CATGAAGTTC TCTTTAAAAA ATACCAAAGC TTGTTTATTT CTGATAATTA ACCTAAGCCC TTATGAAAAT AAACAAAATG AAGGGATTAT GACAGGTATT ACCAAAAACA CCAAAAGGAA CAAAGGGGCC TGCGTTAAAA CCTAATTGCT AATGCTTCAC AACTAGGAGA GCATGCCGTC TTGATGTTTA AAAAACCCAG GGTCTCCACC CTTCCTTTGA TTTGTGCAAT TCTGTCTTCC ACAGTTCCGG AGCTTACTCG AG	60 120 180 240 300 312
(2) INFORMATION FOR SEQ ID NO:572:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 391 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:	
GAAAATGTTC ATGGCCGCAG CAGGAGTAGA GGTCCTGAGC CTCCTATTTT TCTGCATCTA CTGGGGTCAA TATGCCACCG ATGGCATTGG CAACGAGAGT GTGAAGATCT TGGCCAAGCT GCTCTTCTCC TCCAGCTTCC TCATCTTCCT GCTGATGCTT ATCCTCCTGG GGAAGGGATT CACGGTGACA CGGGGCCGCA TCAGCCACGC GGGCTCCGTG AAGTTGTCT TCTACATGAC CCTGTACACG CTCACCCATG TGGTGCTGCT CATCTACGAG GCGGAATTCT TTGACCCAGG CCAGGTACTG TACACGTATG AGTCGCCGGC CGGCTACGGG CTCATTGGAC TGCAGGTGGC GGCCTACCGT TGGTTCTGCT ATGCTCTCGA G	60 120 180 240 300 360 391
(2) INFORMATION FOR SEQ ID NO:573:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 377 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:	
GAATTCGGCT TCATGGCCTA AAAAAAACTC CAGAAAAAAA CAACAGCGCG GTGGTGGGGT	60
TTTGTTAATT TCGCCTTTTT TTTTTTTTGC ACGCGCCACG AAATTCAGGC TGCGTTTAGC TCCTGAGAAA TATCCAAAGT AATTGCAGAT TGCGGAGACG CACAGCATTA GTTCAAAAAA	120 180

AGGAACCTGC	ATTGGGGCAG GGTTAGGTGG AGGGCACCGG AGGCTCTACA CAAGAAAAGC AAACCCACGT AGATTTCCAC TACAACCTTC CCTTTTCTTC TGGCTAGCCA TCCATGGCAC TGCATGGCAC AAGTTGCTTC TGATAGTCTT TTAAGTTTGC CCTCGAG	240 300 360 377
(2) INFORMA	ATION FOR SEQ ID NO:574:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:574:	
ATCCGGGGGC AACCGCAGAA CTCACGTGGG AACTATGACT	TTCATGGCCT ACAGCCTCAA GTCACTCCCA AGCCCCTCC TTGTCTGTGC AGCTCTGGAG GGGGTTTGCT GGGGAACTGG CGCCATCGCC GGGACTCCAG GCCTCCCCAG CTCACCCCTG GAGGACGGCC GGCTCTCTAT AGCACCAGGG AACCCCCCTC CCACCCTCGC GAGTCTGTTT CCAAGGAGGA GAAGGAGCAG TAACTGAAGT CTCAGAGAGC ATGAAAGCTT TCATATCCAA AGTCTCAACC CAGAGCTGCC TCGAG	60 120 180 240 300 325
(2) INFORMA	TION FOR SEQ ID NO:575:	•
(i) ;	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 438 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:575:	
CCACACCCG CGTGTGCTTT GAAAGATCCA CACAGCCTCC TTAAGTAAAA	TTCATGGCCT ACTCAGCCTC CCTAATAGCT GGGATTACAA GCGTGAGCCA CTGGGAAATA TCTTAAAAGA ATCAAAATAA GAAAGTTACT CTACTTAAAT TTCTGTGTGT GATTTATGGT AATCTTACCA TGGGGTATCT GATTACTTTA TTTAGCTTAT TTTTTCTTC TTTGGGTTAT TTTTTTCTTC CTTCCATTTG CCCCAAATAA AAAATAAAGA TATAAAGTCT ATCTTCTCC TCTTGTCAGT AGAACTTTTG CTTCCATTTT AATAATAGA TTTGTGTGTA TATAATATAG GGCCTCAAGC TGAGTTTAGA TTTGAAAAGA TGAGAATATT AAAGCTTGTC CTCTCGAG	60 120 180 240 300 360 420 438
(2) INFORMA	ATION FOR SEQ ID NO:576:	
	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 510 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:576:	

60 120

GAATTCGGCC TTCATGGCCT ACTGTNTTCC ATAAAGGCTG TACTAATTTC CATTCTCACC AACAGTTCAC TAGGGTTCCC TTTTCTCCAC ATTGTTGCCA ACATTCTTTA TCTTGTGTTT

NTTAATAACA GCTATCCTAA CAGGTATGAG GTGATCTCTC TCATTGCGGT TTTGATTTGC ATTTCCCTAA CGGTTGGTGA TACTGAGCAT TTTTGCATAC ACCGGGTCAT TTGTTCTTTG TTGTTGACTT GAGTCCCTTA TATAGTTTGG ATACTGCTGT GGCCTGAATG TTTGTGTCCC CCAAAAATTC GTATATTGAA CTCTCATCCC TAAGGTCAAC AGTTTAGGGA AGCGATTAGG TCCTGAGGAC TCTGCCCTCT TGCATAGAAT TAGTGCTCTT ATAAAAGATG CCCGAGGGAG CTCTTTTGCC CCTCCTCCCA TCTGAGGACA CAGCTAGAAG CTACCATCTG TGAACCAGGA AGCCCCCCTC ACCAGACACT GTATCTCGAG	180 240 300 360 420 480 510
(2) INFORMATION FOR SEQ ID NO:577:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 276 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:	
GAATTCGGCC TTCATGGCCT AAAAAATAAA AATAAAATAT ACAACCAAAG GCAGTATTCA CAGAGGTATT TCTTGGGAAT AAAAGAAGGA ATATGCATT TCTTTGGT GTCCAGAGTT ACTTAAAAAAT TCTTGGTGTT TATTGCCTTT TAGTCACAGG GATACACCTT TTATTCATTT ATTTATTTAT TTACCAGTCT CATTTAGCAG TAGGAATGCA TCTTAGCATT TTTATACTGC TGCTCAACAC AGTGCTTTCA CTCGAG	60 120 180 240 276
(2) INFORMATION FOR SEQ ID NO:578:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:	
GAATTCGGCC TTCATGGCCT AAATCCTTCC AGATGTCCTG TGAAAATGTT TGAATGCTAC TTGTCTAAAA GTCCACAGAA TCTTAATCAG AGGATGGATG TTTTTTATTT GCAACCAGAA TGCTCTAGTT CTACAGATAG CCCTGTCTGG TATACGTCTA CTTCACTGGA CCGAAACACC TTGGAAAATA TGCTTGTACG GGTTCTTCTA GTAAAAGATA TTTATGATAA AGACAATTAT GAACTGGAGG AAGACACTCG AG	60 120 180 240 262
(2) INFORMATION FOR SEQ ID NO:579:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 439 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:	
GAATTCGGCC TTCATGGCCT AATTTAGGAC CATTTAAGAG AGTTTGACTA AGAAAGAGCT GTTTGAAACC TCCTGGCTTA TGTATTTTTA GGGGTGTGGT GATCGAGGCT TTCTCCTCTG AGTAGAGTTT GTGCATTTGC AGTATAAGAT TATCATTATC AAACATTCCT ACTAGGCCTT	60 120 180

TCTCCTCAGC	CCCTAAAAAA	ATATGTATAG	TAATGAAGTA	GGAAGATCAT	GTTTATATTT	240
GACTTCACAA	ATTCCTCAGG	CTAAGTTGCT	TTCTACTGGG	GTGTGGCTGG	AGACAAAAAT	300
TACAGGTAAG	ACTTGACTTA	ATTTTTGATA	GGGAGGTTCT	TAAGAGGCTT	TTTCGGAATC	360
ACTCACCTCG	CCCACTTCCA	TGCAGGGATG	TGGTGAGAGC	CCTTCAGTCT	ACTTAGGAAA	420
ACCTGGCACA	TGACTCGAG					439

- (2) INFORMATION FOR SEQ ID NO:580:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 346 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAATTCGGCC	TTCATGGCCT	AGATATTCTC	AGGGTCATCA	AGACTCCTGA	GATAGCAAAC	60
TTGGCCTTGC	TTGGCTTTGG	AGATATCTTT	GCCCTGCTGT	TTGACAACCG	CTACCTGTAC	120
ATCATGGACT	TGCGGACAGA	GAGCCTGATT	AGTCGCTGGC	CTCTGCCAGA	GTACAGGAAA	180
TCAAAGAGAG	GCTCAAGCTT	CCTGGCAGGC	GAAGCATCCT	GGCTGAATGG	ACTGGATGGG	240
CACAATGACA	CGGGCTTGGT	CTTTGCCACC	AGCATGCCTG	ACCACAGTAT	TCACCTGGTG	300
TTGTGGAAGG	AGCACGGCTG	ACACCATGAG	CCACCAGCCG	CTCGAG	•	346

- (2) INFORMATION FOR SEQ ID NO:581:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 740 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GAATTCGGCC	TTCATGGCCT	AGACCTGCCT	CGAGATTGCC	ATCTTGGTTT	TGGTGGGTTT	60
CGGCCGACTT	CTTTGCCACT	TGCTATTTTA	TTTTCTAGGT	CTTTGTGCCC	CGTATTGTGT	120
GCTGAACTCC	NGTCTCATCC	TGTGACTAAG	ATTGCCTAAC	CTCCTGGGAA	TGCAGCCCAG	180
TAGATCTCAG	CCTTACTTTA	CCTAACCCCT	TTTCAAGATG	GAGTCACTCT	GGTTCAAACA	240
CCTCTGACAT	TCGCAGTGGA	ATCCATTAAA	AGATGTTAAG	GAGATATGAT	TATATTTCTA	300
AATTGTCACT	CCAGCATCCC	CTACGCCAGA	CATTATGCCA	GTCTCTATCC	ATACAGTATC	360
TCATTTAATC	CTCCCGTCAT	TAATCTCATT	TTACCAATGA	GTAAACTTGA	AGCAAATGAG	420
TGACTTTCTC	AAGGCTACCT	ACTTACGCCT	TACCAGGGCC	AGGATTCAAA	CCTAGACTTG	480
TTCAGCGACA	GAACACACAC	TTAACCATCA	CCCACTTAGG	CCATGAAGGC	CGGCCTTCAT	540
GGCCTAAACT.	GCTGTTATTT	TGGATTATAT	GGAGTTATGA	AAATCTAAAT	GTTTTACAAA	600
GTTAAAAAGT	ATTCTTTTTT	TGCTCACTTA	TAACTCAAAA	ATCACTAAAG	TCATTCTGCT	660
AAACATGCCA	CGAAGCCAAG	CTTCTTGCCA	TATGTCTGCA	TAATTTTATT	AAATCACTGC	720
TATTGACGTG	CAACCTCGAG					740

- (2) INFORMATION FOR SEQ ID NO:582:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 491 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GAATTCGGCT TTCA	TGGCCT ACAAAGGGG	AGCAAGGCAT	GTCTTACATG	GTGGCAGCAG	60
AGAGAGAGAG CAGG	GAAAAC TGTCATTTAT	AAAACCATCA	GATCAGTTGG	GTTGTGCAAA	120
TGGTGGAGAA GAAA	ACTTCA GGAAGAGTG	ATAGACTGAG	CAGAGAAGAG	GACCAGCTAC	180
CTCCGTAGAG GCAG	GGAGAG CAGCCAAGCT	GGAGCCTGAG	CAGCATTGCT	GGACATGGAG	240
AAGGTCTGGA ATCT	TGTCAA GGAAGCAAG	AAAGGGTTTC	TTTCTATTCA	ATGAAGTCCA	300
CTCCCAGGAC CCTG	GGCAGC AACGGGTGCT	GGACTGGGCC	ACCTGGCAGC	GTCACATCAA	360
CTGGCAGCTA GAAG	TCCTGG AGAATGACAA	CTTCCAGGAC	GACCCCCATG	TGGGACTCCC	420
TCAGCTCAGC AAGAC	GACTGC CACAGTTCGA	TGATGATGCA	GACACCAGAC	AGTAAAAGAA	480
GAAAACTCGA G					491

## (2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 566 base pairs

  - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GAATTCGGCC AAAGAGGC	CT AAACAGTCCA GA	GAGGCATA AATCAGA	CCC AGTTCCTAGC	60
TGGCTTGTCC TTATCAAG	TA AATGGAAAAG GG	GCCAGGCC AAAGCAG	GGC AAGATGACCT	120
TGGACTTGGG AGAGACTT	GG ACTCATGCCA CA	ATCCTAGG GTGCCCA	CTG GACCATTGCT	180
TTTCTGAGTT TTGTAGTC	AT TCGGTGTCTG AA	GTAAGGTA GATTGAA	GTG AGGCCTTCGG	240
TTTCCATCTG GACCCTTT	CT CTCCTGTTTT CT	TTTTTTCC GCCTTGT	CCT AGGGATGTTC	300
AATAGCCCAG AAATGCAA	GC CCTCCTCCAG CA	GATCTCTG AGAACCC	CCA GCTGATGCAG	360
AATGTGATCT CAGCACCC	TA CATGCGCAGC AT	GATGCAGA CGCTTGC	CCA GAACCCCGAC	420
TTTGCTGCTC AGATGATG	GT GAATGTGCCG CT	CTTCGCGG GGAACCC	CCA ACTGCAGGAG	480
CAGATCCGCC TGCAGCTC	CC AGTCTTCCTG CA	GCAGATGC AGAACCC	AGA GTCACTCTCC	540
ATCCTTACCA ATCCCCAT.	AC CTCGAG			566

## (2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 482 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GAATTCGGCC	TTCATGGCCT	AGTTGAAAAT	GATCATTACA	CAATATATTC	CTAAACATAA	60
ACTGAGTAAA	CTTGAAACAG	CTCACTGTGT	GGAGAGGACC	ATTCCCGTTT	TGCTCACCAG	120
AACTGGAGAT	TCTTCTGCCC	GCCTCCGCGT	CACAGCTGCA	AATTTTATTC	AGGAAATGGC	180
CTTGTTTAAA	GAAGTTAAGT	CTCTCCAAAT	TATTCCATCC	TACCTGGTGC	AGCCATTGAA	240
AGCAAACTCT	TCAGTTCACC	TGGCAATGAG	TCAGATGGGC	CTCCTGGCCC	GGCTGCTGAA	300
AGACCTGGGC	ACTGGCAGCT	CGGGCTTCAC	CATTGACAAC	GTGATGAAGT	TTTCAGTGAG	360
TGCCCTGGAG	CATAGAGTGT	ATGAGGTCCG	CGAGACGGCG	GTTCGAATTA	TTTTGGACAT	420
GTACAGACAG	CACCAGGCTT	CCATCCTGGA	GTACCTTCCT	CCAGACGACA	GCTAATCTCG	480
AG		-				482

(2) INFORMATION FOR SEQ ID NO:585:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:585: GAATTCGGCC AAAGAGGCCT AATAAAGGTG TGGAAACTTC ATTCATTCAT ATCTTCAACA CAAATTGTAG GTAGCCTGTT TTTTAAAACA TTTATTCAAC AAATATTTAG TCCAAGCCAC 120 TATTACTTAC TACCTTCTCT ACTATTGTAT GGACTTTTAA CTATCTCTGA CACTATTCAC 180 TATTCTTCCA CATTCTCTAT TATTTATACC TATGGTAAAA TTTGCCAGTT TGACCATACA 240 ACTAATACTC ACAGGGACAC TCGAG 265 (2) INFORMATION FOR SEQ ID NO:586: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:586: GAATTCGGCC AAAGAGGCCT ACTCGAGTTT GGTGCTTTAT TTAGCAAGTG AGTAAAAATA 60 TTGGAATATT TAAGTATTTG CATAAAAAAT CAAATGGTAG TGTTTTGTAA TCTCTACTGT 120 (2) INFORMATION FOR SEQ ID NO:587: (i) SEOUENCE CHARACTERISTICS: (A) LENGTH: 503 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:587: GAATTCGGCC AAAGAGGCCT ACTCGAGTCA GGTCTAGAAT TCAATCGACG GTTTAGGAAA 60 AAGACAATTT AAGAGAAGAA CTAAAGAAAA GAACAGAAAC TGAGAAGCAG CATATGAACA CAATTAAACA GTTAGAATCA AGAATAGAAG AACTTAATAA AGAAGTTAAA GCTTCCAGAG 180 ATCAACTAAT AGCTCAAGAC GTTACAGCTA AAAATGCAGT TCAGCAGTTA CACAAAGAGA 240 TGGCCCAACG GATGGAACAG GCCAACAAGA AATGTGAAGA GGCACGCCAA GAAAAAGAAG 300 CAATGGTAAT GAAATATGTA AGAGGTGAGA AGGAATCTTT AGATCTTCGA AAGGAAAAAG 360 AGACACTTGA GAAAAAACTT AGAGATGCAA ATAAGGAACT TGAGAAAAAC ACTAACAAAA 420 TTAAGCAGCT TTCTCAGGAG AAAGGACGGT TGCACCAGCT GTATGAAACT AAGGAAGGCG 480 AAACGACTAG ACTCACTCTC GAG 503
- (2) INFORMATION FOR SEQ ID NO:588:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 567 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GCCACTATGG	TACCAAAACC	TCAGTCTTCA	CATAGTCAAA	CTTGGACACA	AACAGCACCT	60
CCCACAAACA	TTCTTATCCT	CATCCCAGCA	TTGGTTACTG	ACCACACACT	CTAGCAGGTC	120
ACTCAAGCGC	TAATGCTGGG	AAGGACCTCT	GAATACTTCT	CTTTGTCTTG	TGCCACACAG	180
CCAGGGTCAC	CAAAGCCTGT	TAATGCTACC	TCCAAAAAAG	GCAAATCTGA	CCCCTCTTCC	240
TCAAAACCCA	GCCACATAGT	AAGTTCAAGG	ATTCAGTCAC	AGGTCTGCCT	TAGTGCACTA	300
GCCCTATAAC	AGTAAACTAT	TCACTTCCCC	TCCAGTCCCT	TGCCCCCTTT	CAAGCAATTT	360
CCTGTACTGC	CAAGGGAATT	ACTTTTCTAA	AATTAGCTAA	GAAACTTTTG	ATGGTATCTT	420
ACTGTCCCAA	AAATAAATTT	TAATTCCTTC	TTTAGCATGG	TATAAAAAGG	ACACAACAGA	480
GTTTGGTCTA	GTGTCCTTTT	AAAGACACTA	GATTTCTCAT	CACCATACCG	CATGTACCCT	540
ATACGACTTA	TCAATTCCCT	ACTCGAG				567

- (2) INFORMATION FOR SEQ ID NO:589:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 138 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC	AAAGAGGCCT	AGGCATGGTG	AGTTTTGATC	TTCTTCCCCT	TCTTTTCTTC	60
CCCTTCTTCT	TTCCTTCTTT	GATCTTCTTC	CCCTTCTTTT	CTTCCCCTTC	CCCTTCTTTT	120
CAATTTCTCC	CACGTCAA					138

- (2) INFORMATION FOR SEQ ID NO:590:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 420 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAATTCGGCC	AAAGAGGCCT	AGAGAGAATG	GAAAAGATAA	GGAACAGAAA	CAAACAAATA	60
CCGATAAAGA	AAAAAATAAA	AGAGAAAGGG	AGCTTCTCTG	ACACAGGCTT	GGGTGATGGA	120
AAAATGAAAT	CTGATTCTTT	TGCTCCCAAA	ACTGATTCTG	AGAAGCCTTT	TCGGGGCAGT	180
CAGTCTCCCA	AAAGGTATAA	GCTCCGAGAT	GACTTTGAGA	AGAAGATGGC	TGACTTCCAC	240
AAGGAGGAGA	TGGATGATCA	AGATAAGGAC	AAAGCTAAGG	GAAGAAAGGA	ATCTGAGTTT	300
GATGATGAAC	CCAAATTTAT	GTCTAAAGTC	ATAGGTGCAA	ACAAAAACCA	GGAGGAGGAG	360
AAGTCAGGCA	AATGGGAGGG	CCTGGTATAT	GCACCTCCAG	GAAAGGAAAA	ACCGAGGCAG	420

- (2) INFORMATION FOR SEQ ID NO:591:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 611 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

GAATTCGGCC	AAAGAGGCCT	ACATTGCTTT	TCAAATAACT	TAAAATAACA	CGTTATGTGC	60
CATGTGGCTA	CTTTAGTAAT	ATTGCCAAGA	AGAGCACAGT	TTTTACACTA	GTGGCATCTC	120
AGTGAAATTA	ACCAAAGATG	AAGCTTTGGC	TTTGCTGGTG	AGATCAGAGC	CCTCCTGAGC	180
				GGCAGAGATA		240
				GATTGTTTAC		300
				CAAAGTGGTT		360
				CATTTCCCCA		420
				GTTTGGAGAT		480
				TNCACTTTGT		540
		GGAGGGTCTG	CCAAGCTACT	GCAACATCTG	TCACCCACTA	600
NACCCAGACC	T					611

- (2) INFORMATION FOR SEQ ID NO:592:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 443 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

GAATTCGGCC AAAGAGGCCT	AATTGAATTC	TAGACCTGCC	TGAAACCTGT	CCCTCCTAGG	60
AAATTGAATA GCTTGAGTTA	CGAAGGAACT	GCATGGGACA	GACTGAGTTT	TGTTCCTCTC	120
TTCCCTGGAA GCTGGATGTC	CTTTACAGCT	TTGCCCAGTA	TGTCATGTGG	CCCCTGAAGT	180
ACATAATCCA GAGTGGACTG	CCTTTCAGGG	TCCCTCAGCT	GTGAAAGTGG	AGCATTCATA	240
TCAAGACTAC ATCTTTCCTG	TTCAGCTTTC	TTCAGCCTTG	GAGGAACCAC	ACACAATGGA	300
TCCAAGACTT CTGTCCCTTG	CTAATTATCT	ATAAGAAGTA	AACCCATTTC	ACATAACTTG	360
TGAATATGTT TTCTTTCACT	GGATTTTGGC	AAATAGGTAC	CCAGTGCATG	GTGGACCTAC	420
ACAGTTAGGC CTCTTTGGCC	GAA				443

- (2) INFORMATION FOR SEQ ID NO:593:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 441 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

GAATTCGGCC	AAAGAGGCCT	AAAAGCATTC	AGTATTGGTA	AAATGAGTAC	AGCTAANCGA	60
ACTTTAAGTN	AAAAGGAGCA	GGAAGAATTA	AAGAAAAAGG	AGGATGAAAA	GGCAGCTGCT	120
GAGATTTATG	AGGAGTTTCT	TGCTGCTTTT	GAAGGAAGTG	ATGGTAATAA	AGTGAAAACA	180
TTTGTGCGAG	GGGGTGTTGT	TAATGCAGCT	AAAGAAGAAC	ATGAAACAGA	TGAAAAAAGA	240
GGTAAAATCT	ATAAGCCATC	TTCAAGATTT	GCAGATCAAA	AAAATCCTCC	AAATCAGTCT	300
TCCAATGAAA	GACCACCATC	TCTTCTTGTG	ATAGAAACCA	AAAAACCTCC	ACTTAAAAAA	360
GGAGAGAAAG	AAAAGAAAAA	AAGCAATTTG	GAACTCTTCA	AAGAAGAATT	AAAGCAAATT	420
CAAGAGGAAC	GTCGACTCGA	G				441

- (2) INFORMATION FOR SEQ ID NO:594:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 562 base pairs
    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

GAATTCGGCC	AAAGAGGCCT	AAGAAAACCT	AGCTAATAAA	GAAAAAGCTG	TTGCTCAAAT	60
GAAGATAATG	ATCTCAGAGT	GTGAATCATC	TGTGAACCAG	CTGAAAGAAA	CATTGGTTAA	120
		GCCTCCGGCG				180
TGAAGTAGGA	AGATCTAGAG	AAATCGCTTT	TAAGGAAAAC	AGAAGACTGC	AAGATGACCT	240
GGCTACAATG	GCAAGAGAAA	ATCAAGAAAT	CTCATTGGAA	TTGGAAGCAG	CAGTGCAAGA	300
AAAAGAAGAA	ATGAAGAGCA	GAGTTCATAA	ATACATAACA	GAGGTGTCAC	GATGGGAGAG	360
CTTAATGGCT	GCCAAGGAAA	AAGAAAATCA	AGATTTGTTA	GATAGATTTC	AGATGCTTCA	420
		AGGTCAAAGC				480
TCGACTGGAA	CTTCTTTCTA	TTGACACTGA	GAGGAGACAT	CTTCGGGAAA	GAGTGGAGCT	540
ATTAGAAAAA	GAAAATCTCG	AG				562

- (2) INFORMATION FOR SEQ ID NO:595:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 426 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GGAAGAGCAG						60
AGATATCCCT	CCTGAAAATG	AACTGCTTTT	TTATTATAGC	CGAGATTATG	CTCAACAGAT	120
TGGTGTTCCT	GAACACCCAG	ATGTGCATCT	CTGTAACTGT	GGCAAGGAGT	GCAATTCTTA	180
CACAGAGTTC	AAAGCCCATC	TGACCAGCCA	CATCCATAAC	CATCTTCCTA	CCCAGGGACA	240
TAGCGGCAGC	CATGGGCCAA	GTCACAGCAA	AGAAAGGAAG	TGGAAGTGCT	CAATGTGCCC	300
CCAAGCTTTT	ATCTCTCCTT	CCAAACTTCA	TGTCCACTTT	ATGGGTCACA	TGGGTATGAA	360
GCCCCACAAG	TGTGATTTCT	GTAGCAAGGC	TTTTAGTGAT	CCCAGCAACC	TGCGAACCCA	420
CTCGAG						426

- (2) INFORMATION FOR SEQ ID NO:596:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

GAAAATCAG TCGACTGAAT	CACACCATCA	330000000			
GAAAAATCAG TCGACTGAAT	GACACCATCA	MAICITIGAA	ACAACAGAAG	AAACAAGTGG	60
AACATCAGCT GGAAGAAGAA	AAGAAAGCAA	ACAATGAGAA	ACAGAAAGCT	GAAAGGGAGC	120
TAGAGGGTCA AATCCAGAGA	TTGAACACAG	AGAAAAAGAA	ACTAAATACG	GACCTGTATC	180

PCT/US98/06956 WO 98/45437

ACATGAAACA TTCTCTCAGA TACTTTGAAG AAGAGTCCAA GGATCTGGCC GGCCGCCTGC	240
AACGTTCATC GCAGCGTATA GGAGAGTTAG AGTGGTCTCT CTGTGCTGTC GCCGCCACAC AGAAGAAGAA GCCGGATGGG TTCTCGAG	300
AGAAGAAGAA GCCGGAIGGG IICICGAG	328
(2) INFORMATION FOR SEQ ID NO:597:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 529 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:	
GAGAAGTGCG AGAGGGGCCA GTGTTGTTGT TACCTGAAAG GTAAGTGCAG CCCACAAAAA	60
TGCAGTGAAG AAGAAGATAT ATGCATATGT TTAAGTTAAT ACAATTGAGA TACATTTAGC	120
AGACAGAATC AATAGAGTTG ATGAGTGACT GACTGGATGT GTGGGGGAGTT TATATCACTC	180
CCAGGTTTTT GACTTGGGCC ACCGGGCACT CAAGAAGGAA AAAGAGGATC CAGGGAGAGG	240
AACTTTTCTG AGGACTGGGG TAGGGCTGAA CAGCTGCATT CGAGACTGGT GGAGGGTGGG	300
CTGGGCATGG GATGCACAAA TGGAAATTCC ACTGGGTCTG CAGCTCACAC ATAGGCATGA CCAGCATAGA GATAGAGAGG CCCCAGTGCT GCTGAGTAAC TGTGATTCCC CAGGTGATGG	360 420
CATCAGCTGA GAAGGGAAGG AAGCCCATGT GAGGACACTG AAGAAGGAGT GAGCAGACAA	420
TAAGAAGCCC ACAGAAGACA GAGAAGGAAC AACTAGAAGG AGGCTCGAG	529
•	
(2) INFORMATION FOR SEQ ID NO:598:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 454 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:	
,,	
CARARACAMO ARAMOMORANO CAMBACCARO AMOMOGRADA MOCACARA CARARACA	
GAAAAAGATG AAATCTGATG GATTAGGAGC ATCTGGACAT TCGTCAAGTA CCAATAGAAA TAGTATAAAT AAAACTCTGA AGCAAGATGA TGTAAAGGAA AAAGATGGTA CAAAAATAGC	60 120
ATCTAAGATT ACAAAAGAAC TTAAAACTGG GGGAAAAAAT GTTTCTGGAA AGCCCAAAAC	180
TGTAACAAAA TCCAAAACAG AAAATGGTGA TAAGGCACGG TTGGAAAACA TGTCACCTAG	240
ACAAGTTGTA GAAAGATCAG CAACAGCAGC AGCAGCAGCA ACTGGACAGA AGAATTTACT	300
AAATGGAAAA GGAGTGAGAA ATCAGGAAGG GCAAATTTCA GGTGCCAGAC CCAAGGTACT	360
CACAGGAAAC TTAAATGTGC AAGCCAAAGC AAAGCCTTTG AAGAAAGCTA CAGGGAAGGA	420
TTCACCATGC CTCAGCATCG CAGAACCCCT CGAG	454
(2) INFORMATION FOR SEQ ID NO:599:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 411 base pairs	

- (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GAATTCGGCC	TTCATGGCCT	AGGTCCTCAA	GCATTGCTTC	AATATCAATA	TCGTCTGCCA	60
TTTTCTCTAA	ACGCCTGTTC	CGGCCTTCGG	GCGCCTGTGG	TGCTCGTGTT	CGGGAAGAGA	120
TTGCTGCTGC	TGCTGCTGCT	GCTGCCGCCG	CCGCCGCTTC	TGTTGCTACT	GTTAAGCCCC	180
TAGGCCCAGG	CCGCGGAACC	GCCCAGCCCG	AATATCGGGT	TCCAAGGACG	GCTAGGCCCG	240
AGAGAATCTA	AAAAAAACAA	TGGAATTAGA	GAAGCCCACG	CGGGAGAGCA	GGACGGCGGC	300
TTCGGCAGCT	CAGGATCCAC	CCCNGCGACA	GCGTCGACAA	GTTCCCTGAA	ATGGCGGCCG	360
CTGCTTCCCT	GTACTCANAN	TCCACCCCCC	GAATTCTAGA	CCTGCCTCGA	G	411

- (2) INFORMATION FOR SEQ ID NO:600:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 306 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GAATTCGGCC	TTCATGGCCT	AATTAAGCCT	GCCTACTTCT	ACAATGCATT	CTGTTACCTA	60
TTTGAACAGT	ATGTTTGTAA	CTATGGCAAT	GAAGTCAGTA	GATAGGAAAC	CAGTTATTCC	120
TTCTACCTTT	AAAAATTTTG	AGAACTTGCC	AACCAGGGAC	TAAAGCTATT	ATCTTGAACA	180
GAGTCCCTAA	AGCTAGTCTA	GTTTTTGCCA	CATCTGCAAT	GATTATTGTT	TAATTTCAAA	240
AGAATCCTCA	GGCTCTACAA	TCTAGGGGTG	GTAAATGTGT	TTCCACTATA	CTTGGGACCG	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:601:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 443 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601: "

GAATTCGGCC TTCATGGCCT	AGGAATCTCC	TCTTAAACCA	GGTGAAGTGG	GAAAGCAGGG	60
ACCATACCAC CCTGAGTGAC	ATCTACCTGA	ATAATATCAT	TCCTCGATTT	GTACAAGTCA	120
GCGAGGACTC AGGAAGACTC	TTTAAAAAGA	GTAAAGAAGT	CGGCCAGCAG	CTCCAAGATG	180
ATTTGATGAA GGTCCTGAAC	GAGCTCTACT	CGGTCATGAA	GACATATCAC	ATGTACAATG	240
CCGACAGCAT CAGTGCTCAG	AGCAAACTAA	AGGAGGCGGA	GAAGCAGGAG	GAGAAGCAAA	300
TTGGTAAATC GGTAAAGCAG	GAGGACCGGC	AGACCCCATG	CTCCCCTGAC	TCCACGGCCA	360
ACGTTCGCAT TGAGGAGAAA	CATGTCCGGA	GGAGCTCAGT	GAAGAAGATT	GAGAAGATGA	420
AGGAGAAGCA CCAAGCCCTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:602:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 585 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GAATTCGGCT	TCATGGCCTA	CAACATGTCA	GTTTTTTTT	TCATTTTCCT	CAATATTTTT	60
CTTCTNGCTT	TCTCTTCTCC	TGGTTCCCAG	CCTCTACTCA	ATAGTCCCCC	CAGCTTTGTG	120
TGCTGGTCTC	GGGGCTTCAT	GGAGATGAAT	GGGCGGGGG	AGTTGGTGGA	GTCACTCAAG	180
AGATTCTGTG	CTTCCACGAG	GCTTCCCCCC	ACTCCTCTGC	TGCTATTCCC	TGAGGAAGAG	240
GCCACCAATG	GCCGGGAGGG	GCTCCTGCGC	TTCAGTTCCT	GGCCATTTTC	TATCCAAGAT	300
GTGGTACAAC	CTCTTACCCT	GCAAGTTCAG	AGACCCCTGG	TCTCTGTGAC	GGTGTCAGAT	360
GCCTCCTGGG	TCTCAGAACT	GCTGTGGTCA	CTTTTCGTCC	CTTTCACGGT	GTATCAAGTA	420
AGGTGGCTTC	GTCCTGTTCA	TCGCCAACTA	GGGGAAGCGA	ATGAGGAGTT	TGCACTCCGT	480
GTACAACAGC	TGGTGGCCAA	GGAATTGGGC	CAGACAGGGA	CACGGCTCAC	TCCAGCTGAC	540
AAAGCAGAGC	ACATGAAGCG	ACAAAGACAC	CCCACACATC	TCGAG		585

- (2) INFORMATION FOR SEQ ID NO:603:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 368 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GAATTCGGCC	TTCATGGCCT	AGTCTGGTAG	TAAGGTGGAG	TGGGTTTGGG	GCTAGGTTTA	60
GCTCGGGGGA	${\tt GGTGGTGTTG}$	GGGGCCGCAG	GCTGCGCGGT	GCCTGGGTAC	ATCTCCAGGC	120
CCACGCCCCG	GGCTTGGGAA	GTCACATCCA	TGTCTCTGCG	CCGTGCAGCT	TTCAAGATTT	180
GCCGAAAGGC	TCCCAGAGCT	CTGTTTTAAA	TGGTGAATCC	ATCTTTAGAA	AGAAGCGTGA	240
TTCTCCTTGA	AGTGAGCCTG	GCATTTGTCA	GACAGGAAAC	TCCCCAGGAG	GAGCACCTGT	300
GGTGGTTTGG	GTTGGGTTTG	TTAACTGCAG	AGAGTGGGAA	GAACAGATGC	TCCTCACACC	360
GTCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:604:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 604 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GAATTCGGCC TTCATGGCC	I AGGAAAGACC	ATCAGCCTGG	GAGTCAGTGA	ACCTGACTCT	60
GATCCCAGCT CTGCCTCCA	N TCAGCTGTGT	GATGACAGGT	AGGTCACCTT	CCCTCTCTGA	120
GCCACAGTTT ATCTGTCTG	T AAACAGGGGT	ATTGGACTGG	ATTCTCTGTT	ATCTCTCATG	180
TCTCTGTGAA AGGTCTGTG	TTTCAAATAC	TCCTTAGGGA	CATGACCTCA	CATAGAAAGA	240
GGGGGTGCCA CGAACTGGA	T TCCCAGCACT	CCCCCTTCCC	AGCTCTGCTC	AAGCTGAGGG	300
ACCTTGGAAC ATGGTACTT	G GACCTAAGTA	CTCTCTCTGG	GCTTCAGTGT	CCCCAGCTAT	360
AAAATGGGGG AAATGCCTA	A CTCAGGAGGT	TGAGGTAAGG	ACAAAAGGAA	TTAATACATG	420
GAAAGTGCCT GGAACAGTG	C CTGGCACAGT	CTGCTTTCAG	AAAAAGCTGC	AAGGTGGCTA	480
CTCTCAGCAG ATATAAGTT	A ATGCAGGAAC	AGCAACTAGC	AGCTCTTGGA	CATGCAATAT	540
ATTATATATT TTTTGCATC	TTTACCCTTC	ACGGCACTGA	GCCTCACAAT	CCGTTGACCT	600
CGAG			•		604

- (2) INFORMATION FOR SEQ ID NO:605:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 495 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GCGCAGCCAG	CGCCTGCCTC	CGACTCGACT	CCACACCTGC	TTGCTACAGC	GGGTGAGGAA	60
GCAGGAAAGG	GGGAGGGAGG	GATGTCGTCT	GGATTCCTGT	AATAATTTGT	TTCATTGTTT	120
CCAATCGACT	TAGTCACCAG	GTTAAATAGT	AGCATAGACC	TTTCAAAAAA	GTAGCTAGCT	180
TATAAGTAGA	TGTATTGAAA	ACACCTGCTT	GTTGAGTCGT	AGACAATTCC	TCATTTACTG	240
TGTGAACTCT	AGGGGGTGAA	ACACGGGCGG	AGAGCGGCTG	TGAGCTCACG	CGGCTCCATC	300
CCCACAGCGG	CCCAGGGTCA	CTCGGGGCCA	TTAATCAGGC	CGCAGAGCTG	CCCTCTGAGC	360
CGGGCCGCCA	GCGCCCACAG	GGCCCAGACC	AGGGCTCCCT	GGGCGGGATG	TTTTAAATCG	420
CACAGGGACA	AAGGAAAGGA	AAGACGCTGG	GGCCCAAGCC	CGAGCTTATG	AAACGTTATC	480
AAGGAGCGAC	TCGAG					495

- (2) INFORMATION FOR SEQ ID NO:606:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 331 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GAATTCGGCT	TCATGGCCTA	GACTTCCAAG	GACATGCTTC	GAACTCTGGC	CCAAGCCAAG	60
AAGGAATGCT	GGGATCGGTT	CCTCCAGGAG	AAGTTAGCTT	CAGAGTTCTT	TGTGGATGGA	120
CTTGATTCTG	ATGAGAGGTG	ACTACAATTG	CAAAGTAGAA	TTTGCTTTGA	CACCTGATGC	180
CAGGACAATA	GTATGTTACC	ATCCTTCTAT	AGACATTCCA	TATGAACGCA	CAAAACCTAT	240
CCCTTGACCA	GATCCTGTGT	ATAATAATGA	AGAAACACAT	GGTCAAGTGC	TGAAAACTAG	300
AGAAGAAAA	AGTGAACACC	TGGAGCTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:607:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 632 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GAATTCGGCC	TTCATGGCCT	ACTGCCTCGG	CCTCCCGAGT	AGCTGGGACC	ACAGACGCCC	60
ACCACCATGC	CCGGCTAAAT	TTTTGTATTT	TTAGTAGAGA	CGGGTTTCAC	CGTGTTAGCC	120
AGGATGGTCT	CGTTCTCCCG	ACCTCGTGAT	CCGCCCGCCT	CGGCCTCCCA	AAGTGCTGGG	180
ATTACAGGCG	TGAGCCAACT	CGCCCGGCCA	GGAATCCCTC	CTCTGTCTGA	CCTAACTGCC	240
CTCTGCCCTG	GAGCTGCTCA	GCCTCTATCA	ATTTTTCTGG	CTCTCAGCGA	ACGTTTTCAT	300
TCAGTTGCAA	GACACAGAAA	CTCAAATTCA	<b>AACCTGCTTA</b>	CACAAAATAG	TGAATGTACT	360
GGCTCATGCA	CTTTTTAAAG	AGATGAGGTC	TGTTGTGCTG	CCCAGGCTGG	ATGTGAACTC	420
CCGGGCCCAA	GAAATTCTCC	TGCCTCAGTC	TCCTGAGTAG	CTGGGACCAC	AGGAGCATGA	480
CTGTAAGTCC	TGGTGTGAAT	CAGGCTCCAG	AAACAGCTTG	ATCCTGGTTC	CCAACAGTAT	540
GGTCAAAACT	CATTCTCTCT	TCTGTCTTCT	TCTCTATGAC	AGGTGCTCCC	TAAGAAGTGA	600
CAAAGAAGGC	CACTAACAGC	TCTGGGCTCG	AG			632

- (2) INFORMATION FOR SEQ ID NO:608:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 531 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GTATNGNTGA	AAATAAGAAA	AAATATTTCT	GAAATTCGGG	AACTTGAGAA	CATAGAAGAA	60
CACCAGTCTG	TAGATATTGC	AACTTTGGAA	GATGAAGCTC	AGGAAAATAA	AAGCAAAATG	120
AAAATGGTTG	AGGAACATAT	GGAGCAACAA	AAAGAAAATA	TGGAGCATCT	TAAAAGTCTG	180
AAAATAGAAG	CAGAAAATAA	GTATGATGCA	ATTAAATTCA	AAATTAATCA	ACTATCGGAG	240
CTAGCAGACC	CACTTAAGGA	TGAATTAAAC	CTTGCTGATT	CTGAAGTGGA	TAACCAAAAA	300
CGAGGGAAAC	GACATTATGA	AGAAAAACAA	AAAGAACACT	TGGATACCTT	AAATAAAAAG	360
AAACGAGAAC	TGGATATGAA	AGAGAAAGAA	CTAGAGGAGA	AAATGTCACA	AGCAAGACAA	420
ATCTGCCCAG	AGCGTATAGA	AGTAGAAAAA	TCTGCATCAA	TTTTGGACAA	AGAAATTAAT	480
CGATTAAGGC	AGAAGATACA	GGTAGAACAT	GCTAGTCAAG	GAGACCTCGA	G	531

- (2) INFORMATION FOR SEQ ID NO:609:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 330 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GTGACTTTGG	AACCTTGAGA	GTTAGATGAA	TAAATCAGAA	AAATGGAATT	AAATGTATCT	60
ACTTTATTAT	TGGTAAATCT	GGTTAGGATG	TGCAGCCCTA	ATCAGGCTTC	CTTAATTCCT	120
TCTCCACTGA	GTCTGGACCA	GCACTCTCCA	GTAGAACTTT	CTATGATGAC	GGAAATCCTC	180
TGTGTCTGCG	CTGATCAGTG	TGGTAGTTAC	TGGCCACATG	TGGCTGTTGA	GTACTTGAAA	240
TGTGGCCAGT	GTGGTGATGG	AATTGTGTTT	TTAATCTTAT	TTAATTTAAA	TTTAAATAGC	300
CAAATGTGGC	TAGTGGCTGT	TGTACTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:610:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 345 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GTGGAGGCTT	TCTTGATCAT	GGATGGTGAA	GATATACCAG	ATTTTTCAAG	TTTAAAGGAG	60
GAAACTGCTT	ATTGGAAGGA	ACTTTCCTTG	AAGTATAAGC	AAAGCTTCCA	GGAAGCTCGG	120
GATGAGCTAG	TTGAATTCCA	GGAAGGAAGC	AGAGAATTAG	AAGCAGAGTT	GGAGGCACAA	180
TTAGTACAGG	CTGAACAAAG	AAATAGAGAC	TTGCAGGCTG	ATAACCAAAG	ACTGAAATAT	240
GAAGTGGAGG	CATTAAAGGA	GAAGCTAGAG	CATCAATATG	CACAGAGCTA	TAAGCAGGTC	300
TCAGTGTTAG	AAGATGATTT	AAGTCAGACT	CGGGCCGAAC	TCGAG		345

## (2) INFORMATION FOR SEQ ID NO:611:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 633 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GAATTCGGCC	TTCATGGCCT	AAATGACCAN	ATCGAGAGGG	AGGACTATGA	GGACTTTGAG	60
TACATTCGGC	GCCAGAAGCA	ACCCAGGCCA	CCCCCAAGCA	GAAGGAGGAG	GCCCGAGCGG	120
GTCTGGCCAG	AGCCCCCTGA	GGAGAAGGCC	CCGGCCCCAG	CCCCGGAAGA	GAGGATTGAG	180
CCTCCTGTGA	ACCTCTGCTG	CCCCCGCTGC	CCCCTGACTA	TGGTGATGGT	TACGTGATCC	240
CCAACTACGA	TGACATGGAC	TATTACTTTG	GGCCTCCTCC	GCCCCAGAAG	CCCGATGCTG	300
AGCGCCAGAC	GGACGAAGAG	AAGGAGGAGC	TGAAGAAACC	CAAAAAGGAG	GACAGCAGCC	360
CCAAGGAGGA	GACCGACAAG	TGGGCAGTGG	AGAAGGGCAA	GGACCACAAA	GAGCCCCGAA	420
AGGGCGAGGA	GTTGGAGGAG	GAGTGGACGC	CTACGGAGAA	AGTCAAGTGT	CCCCCCATTG	480
GGATGGAGTC	ACACCGTATT	GAGGACAACC	AGATCCGAGC	CTCCTCCATG	CTGCGCCACG	540
GCCTGGGGGC	ACAGCGCĠGC	CGGCTCAACA	TGCAGACCGG	TGCCACTGAG	GACGACTACT	600
ATGATGGTGC	GTGGTGTGCC	GAGGTCACTC	GAG			633

- (2) INFORMATION FOR SEQ ID NO:612:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 296 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GATTGACGTG CTAAAATAAG CATTGATGTT TTGAGTTTTT TTACACCTAG GATTTTTAGC TTGGGTGTGT AGGTGAAGGC CAAGACTCTC TGCAGGAAAA AGCTTATTTT CAAACTCAGA AAATAAAATG TCAATCATAA AAATCTACTT CAACTTTAGC AAAAAGAAAA AAAAAATCAA	60
	120
AAATAAAATG TCAATCATAA AAATCTACTT CAACTTTAGC AAAAAGAAAA AAAAAATCAA	180
	240
CAAAAAGTAT ACTCTGTATG CTGGGATTCC GAGGTTCCAA CACACTGTTA CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:613:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GATCCAGTGC	TGCAGCTTCC	TTACTATGAA	ATGACAGCTC	CACTTCCTAA	TAGTGCATCC	. 60
GTGTCTTCCT	CACTGAATCA	TGTTCCAGAT	CTTGAGGCTG	GACCCAGCTC	ATATAAATGG	120
ACTCACCAAC	AACCAAGTGA	CTCTGACCTT	TATCAGATGA	CAGCTCCACT	TCCTAATAGT	180
GCATCCGTGT	CTTCCTCACT	GAATCATGTT	CCAGATCTTG	AGGCTGGACC	CAGCTCATAT	240
ATAATGGACT	CGCCAACAAC	CCCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:614:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 272 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

AGG CCTTCTGAAT TCCT	CTGACA TATATTTGAG AAACTGGGCT	60
CAC TTGGCTGCAT TTTA	TTTGGT AACCAGTGAG GCAAACACCC	120
TCC ATCTTGATGT GGTT	CCTGCA CTGGACACTG CTTGGGTACG	180
GGA ATGTGGGCAG TGGC	TCCTCT GAAGCACCAG TGGGCAGAGG	240
CCC GGCACCCTCG AG		272
	CAC TTGGCTGCAT TTTA TCC ATCTTGATGT GGTT GGA ATGTGGGCAG TGGC	AGG CCTTCTGAAT TCCTCTGACA TATATTTGAG AAACTGGGCT CAC TTGGCTGCAT TTTATTTGGT AACCAGTGAG GCAAACACCC TCC ATCTTGATGT GGTTCCTGCA CTGGACACTG CTTGGGTACG GGA ATGTGGGCAG TGGCTCCTCT GAAGCACCAG TGGGCAGAGG CCC GGCACCCTCG AG

- (2) INFORMATION FOR SEQ ID NO:615:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 521 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GAATTCGGCC	TTCATGGCCT	AGTATTTTTG	TAGAGACGGG	GCTTCAGCAT	ATTGGCCAGG	60
CTGGTCATGA	ACTCCTGACC	TCAGGTGATC	CTCCTGCCTC	AGCCTCCCAA	AGTGCTGGGA	120
TTACAGGCAT	GAACCACTGC	ACCCAGTCAA	GGGTATAAAA	TTTCTACACA	GCACAGGCAG	180
ATTCTGGCTG	TGGAAGACCC	CAAGATTCTT	TGGAATTGTG	ATGCTTTATT	TAATTTAGAG	240
ATTATCTTCT	CTGTCCCACT	CTTCCCCTTC	CTAAAAAGGA	CTAGATGCTT	GCTGCTTAAT	300
TAGTAAAGCA	AATTTAAGAT	AATTTTCTGC	TTTGAGATTT	AGGGATAGAT	TTTTTAACAT	360
AGTCTTGCTG	ATAATGATAG	ACATCCTGGG	ATGTTGGAAA	TTAGGAAACT	TGAACTTITA	420
TTTGCACAGA	CTGAGAATTA	TGACTGAGGA	AAAGTTAGAG	GATCAGAAAA	AATAAATTTA	480
TAAATCACAA	GCTAGGCTTG	GCAATATGAG	TGGCGCTCGA	G		521

- (2) INFORMATION FOR SEQ ID NO:616:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 577 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GAATTCGGCC	TTCATGGCCT	AGATTGGAAG	GTGTGGTAGG	CAGAATTCTG	GCCCCCATGA	60
CTGCCCCTTC	CCCTCACACC	CCCCGGGTTG	CTCCAATGGT	TATGTCACGT	TGCTTGGCAA	120
AAGGGACTTT	GTAGATGTCA	TAAAAGGTGA	CTAATCAGCT	GACTTGAGAG	AGTTTATCCT	180
GGATTATCCA	AGGGGCCCAG	TGTAATTCCA	AGAGCCCTCA	AGAGCAGAGC	TGGAGAGATG	240
CCGCGCAGGA	GGCCTGGGTG	CCGTTTCGGA	GCAGGATGGA	AGGCGGTGAA	TCCCGCCTCC	300
AGCATGGAGC	TCGGGAGAGG	CCCTGACTGC	AGATGGAGAG	GCTGCCCTGG	CCGCAGCGCA	360
CGGGGCTCCT	GACCCACAAA	AATCGCGAGA	TAATGAGTTC	ATGTTGTTTG	AAAGTCCGTC	420

TGCCATGATT TACATTAAAA TTAGGAACAT ACTCGAG

ATTTCTGGTA ATTTGCTATA TAAAACTATT GCTATACGAT TAAAAACTAA TACAGAAGAA

TATTTCTTTA ACATTATGTT AAAAAGGAAA AAAGCTAACA TTTTCTTTAT AGCAAAACAC

480

540

577

(2) INFORMATION FOR SEQ ID NO:617:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 269 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:	
GAATTCGGCC TTCATGGCCT AGCACATACA GTATAAAAAA TAATCACCCA CCATAATTAT ACCAAATTCC TCTTATCAAC TGCATACTAA GTGTTTTCAA TACAATTTT TCCGTATAAA AATACTGGGA AAAATTCATA AATAACAGGT AAGAGAAAGA TATTTCTAGG CAATTACTAG GATCATTTGG AAAAAGTGAG TACTGTGGAT ATTTAAAATA TCACAGTAAC AAGATCATGC TTGTTCCTAC AGTATTGCGG GCCCTCGAG	60 120 180 240 269
(2) INFORMATION FOR SEQ ID NO:618:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 469 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:	
GAATTCGGCC TTCATGGATT CTGCTTTGAA TATAGCTACA GAAATAAAGG ATGGACTACA ATGTGGGACA GTGTCTTCTC AGAAACAACC AGCCTTGAAG GCTACAACTG ACCAGGAAGA TTCTGTTTCG AATATAGCCA CAGAAATAAA GGATGAGGAA AAATCTGGGA CAGTGTCTTC TCAGAAACAA CCAGCCTTGA AGGCTACAAC TGACGAGGAA GATTCTGTTT TGAATATAGCC CACAGAAATA AAGGATGGAG AAAAATCTGA GACAGTGTCT TCTCAGAAAC AACCAGCCTT GAAGGCTACA ACTGACGAGG AAGATTCTGT TTCGATTATA GCCACAGAAA TAAAGGACGG AGAAAAATCT GGGACAGTGT CTTCTCGGAA AAAACCAGCC TTGAAGGCTA CAAGTGATGA GAAAGATTCT TTTTCGAATA TAACCAGAGA AAAAAAGGAT GGACTCGAG	60 120 180 240 300 360 420 469
(2) INFORMATION FOR SEQ ID NO:619:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 448 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:	
GAATTCGGCC TTCATGGCCT AGTCCGTGTT GTGGTCAGTG TGTGAACTCC ACACTGGACA GTAGCTGAGT TTGGGCAGGG ATGAGGAGTG GAGGGGTGAG GTCTAAGGTT CAGAAAAAGT TTGTGTTTAA GAACTTGGTT ACACTGGAGT CAGTTGCAGA CCAGAATGGA GAAAAGCACT CCTGACTTGA GTTGGGTGTG CTTGGGACTG GATCACCTTT GACCTTCTTT ATTTACCTAA	60 120 180 240
296	

TTGGAGGGAA GAGCAGGGGA GGCAACACTA TTTCTCTTGG GTGTTAGAAG AAGATTCGAG

CTTATTTGGG CACTGGTCTC TATCTTTGCC TTCAGCTGAA TCAACATCTA AGATGTTTTA

GATGCTTAGC TAATTCCTCT TAAAAAAAGA ATAAGCAGAG GCCGGACGTG GTGGCTCATA

300

360

420

GCTGTAATCC	CAGCAGTGTG GTCTCGAG	448
(2) INFORMA	TION FOR SEQ ID NO:620:	
(i) S	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 457 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:620:	-
TGAACAGAAC ( GGTAATTTTA / AACTGTGAGA ( ACATGCATCG ( GCATACACTA ' TAATGACCTG ( ATCACAAAAC (	TTCATGGCCT ACTTAAATCC ATCAAGTTAC ACAATCGATC TGTTGTCAGC CACATTAAAT TTAAGCCAAA CACACCAATA GGAATGTTGG AGGTAGAGAA AAGCCAAAAA TGTTGGATAA GAAAAAAACCT ACACCTATAA TACCAGAGAA GTAGTGATTA ATTTAAGAA AACACAGAAG ACCATAGTGA GAGTGAGTCC CTTCAAAGAGC TTGCCCCTAT TATATGTAGC AAATGTGAGT TTGATCCGTT TGTTTGAAAGA ATTATCAATC GCAGGAGCCT CTTGACTTGA	60 120 180 240 300 360 420 457
(2) INFORMA	TION FOR SEQ ID NO:621:	
(i) S	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 287 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:621:	
AGTTTGGATT AGAGGGTTTTC AGACAGAAGT AGACAGAAGT AGACTATGAC	TTCATGGCCT ACTCTCTGAT TTACAGATTG CTAATTAAAT GGCTATTATT AATTAGACTT AAGAAAACAA CTAACTGAGG GTTTTTTTTG TTTGTTTTTT TTTGCATGAG AATTGTATGT AACCAGTGAT ATGATTATTC CTGAATGTAC AAGCCTGGAC ATTGTTAAAT AGTCCCTGCT TTAAGGGACT ACGATAATGT AAACGTGCTT TATTCTTCTA ACGCAGTAAG TCTCGAG	60 120 180 240 287
(2) INFORMA	TION FOR SEQ ID NO:622:	
(i) <sub>.</sub> s	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 328 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:622:	
CAGGAGTAAT	TTCATGGCCT AGTAGGTGTA TCACAGATTT CTAATGTAGA ATGGTCAGTC TGTAATTGTG GAAAAAATGGA GAATTATAAA ACAAGAATGA TGTGCAAAAA TGAATTCATC TGTGTTCCTC TAAACTATTT CATTTACTCA TTCATCCAAG	60 120 180
	207	

TTTTGAAAAA	TGTTGGGAGT	CTGAAAAATT	CCAGGCACTC	TGGATAAATG	AGTATGGAAG	240
AATCCTCCAA	AAGAACTTTT	AGTCTACAGG	GGAACATTAA	TAAGCAATCA	GGGACTTGAG	300
ACCTACAGTG	CTGTGGAAGA	TTCTCGAG			,	328

- (2) INFORMATION FOR SEQ ID NO:623:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 375 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GAATTCGGCC	TTCATGGCCT	AGGACGTTTG	GGTTGTTTCC	ATCTCAAATA	AATAAATAAA	60
TAAAAGTCTA	TAAAAACAGC	TGGGCCCAGG	CATTTAAAAA	AATGTTCGGT	CTTCTAGTTT	120
AGTCTTTTAT	TGTCTATGCA	AATTCTTTGG	CTATTGAACT	ATCCAAGCTT	TCTCTTTTTA	180
AGCTTTTGGG	GAATAGGTTG	CAATACATTT	CTTGTCTACT	GTTTCTCTTA	GTGTTTTCTA	240
ATTCTAACCC	ACTGTTTTTG	GAATTTCTAT	TAGATGGTTT	TGCAACTTCT	GCATCTATCC	300
TCCATGCACC	TTCACATTTC	CTTCACAGTT	TTCGTGCTGT	TTTCCTTGTG	TGCTACATTC	360
TGCACAGGAC	TCGAG					375

- (2) INFORMATION FOR SEQ ID NO:624:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 763 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GAATTCGGCC	AAAGAGGCCT	ACCTCAAAGG	ATTGGCTAAA	AGCAAGCAAC	TGGATTGAAC	60
ACCCTAAGAA	GAAAGATTCA	CACTGCACCA	GGAGACATCA	GAAAGAATGA	AAACTCTGCC	120
GCTGTTTGTG	TGCATCTGTG	CACTGAGTGC	TTGCTTCTCG	TTCAGTGAAG	GTCGAGAAAG	180
GGATCATGAA	CTACGTCACA	GAAGGCATCA	TCACCAATCA	CCCAAATCTC	ACTTTGAATT	240
ACCACATTAT	CCTGGACTGC	TAGCTCACCA	GAAGCCGTTC	ATTAGAAAGT	CCTATAAATG	300
TCTGCACAAA	CGCTGTAGGC	CTAAGCTTCC	ACCTTCACCT	AATAACCCCC	CCAAATTCCC	360
AAATCCTCAC	CAGCCACCTA	AACATCCAGA	TAAAAATAGC	AGTGTGGTCA	ACCCTACCTT	420
AGTGGCTACA	ACCCAAATTC	CATCTGTGAC	TTTCCCATCA	GCTTCCACCA	AAATTACTAC	480
CTTCCAAATG	TGACTTTTCT	TCCCCAGAAT	GCCACCACCA	TATCTTCAAG	AGAAAATGTT	540
AACACAAGCT	CTTCTGTAGC	TACATTAGCA	CCAGTGAATT	CCCCAGCTCC	ACAAGACANC	600
ACAGGTGCCC.	CACCCACACC	TTGTGACAAC	TACACNAGCT	CCACCATCTT	CCTCAGCTCC	660
ACCAGAGACC	ACAGTNGCCC	CACCCACACC	TTTTGCAACT	ACACNAGCTC	CACCATCTTC	720
CTCAGCTCCA	CCAGAGACCA	CAGCTGCCCC	ACCCATCTTC	GAG		763

- (2) INFORMATION FOR SEQ ID NO:625:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 476 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GAATTCGGCC	AAAGAGGCCT	AGTAGTTTCT	ATGTGCGGTC	TGGGGTGGGG	GCAAGGCCCT	60
TGTGTTCCAC	TGGTTTCCAC	CACGTTGACA	GCAGTCGCTG	GCAGCAGAGA	GCCATTTCCT	120
GTCATGCTGG	TCTGTTCCAG	GACTCTGTGG	AAGATTCTCT	ATCTCCACTG	GCACAGGAGC	180
AGAGGAAATG	GAAGGACTCA	CAGGCAGAGC	AGATCTCATC	CCCCAAGCCT	GTTGGGAGCC	240
ATTACTTTGG	GTCGAAACAT	TATTGTGAAC	ACTAAGTTCT	TCAGGTTTTG	TAGCACATGC	300
TTTCATTTGT	AGAGTTCGTC	TAGAATATCG	TTTGCTGGGC	CTTCTTTCAA	AGGATGTTGA	360
TCTTCTTGCT	TTATTGGTTT	TTGTGGTCTG	ATACTCTGTT	TTCCCACTAT	ATCTAAATCG	420
TGATCCTAGT	CGAATAAATC	CTGATCGATG	AGAACTCTTT	TGGACGGGGC	CTCGAG	476

- (2) INFORMATION FOR SEQ ID NO:626:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 234 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GCGATTGAAT	TCTAGACCTG	CCTCAACTGT	CTGGTTTCCT	GTAAAATAAA	CACATTGTTT	60
TATATTTTTA	GGGAACAAAA	AGTGCTGCTA	TAGGGTTCAA	AGTTTTCCTT	CTGAACACTT	120
TTCCGAAACA	AATTACCCCA	AAGACACATT	TTGAATATCC	TGGTCACATC	TTTGGATCTG	180
TAAAATATAC	CTTTTAGTAT	GGCACCTGTT	AAAATGCAAA	GCAAAAACCT	CGAG	234

- (2) INFORMATION FOR SEQ ID NO:627:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 583 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GAATTCGGCC TTCATGGCCT A	AGGCCTTGTG	AATCATTCAG	CATAAGGAAC	TGTCAATATT	60
TTTTTGAGCT GTCAGAAATC C	CATTTAGTGA	TTTTCGACAA	TTCAAAAAA	TATTTCTGAC	120
CGCTTGATTC AGTTCCTAGT G	GAATTAGGGA	AGAAGAGGAA	TAAAAGAAAT	ATATCAATCT	180
AAATTATGAA CCCAGAGTCT A	AGCTTCCTGA	ATTCTTCTCT	GTGCTTAAAC	GAACAACAGG	240
ATGTTGAGGT TCAAAAATAC T	CTCTTCTAT	TTCCCCCCCT	TCCTTCCCTT	TTCTTTCCTT	300
CTCTTCCATT CCTCGAAAAG A	ЭААААТААА	AGAATGTGCC	TAGAGCTTCT	GGAAAGAATA	360
CAGTCCTGCT GATACTAGAA C	CTCAGTGAAA	TTTGCACCAG	ATTTCTGAGC	TACAGAACTG	420
AAGATAATTC ATTTATTTCA A	AGCCACTGAG	TTTGTGGTAA	ATTTGTTACA	GTAGCAATAA	480
AAATCTAATA CATGCCTTCT A	ATACCAGAAG	TACACATCCA	CGTGACCATT	CCTGTCCTCA	540
CCCCACACAC ACATACACAC A	ACACACACAC	ACGCACACTC	GAG		583

- (2) INFORMATION FOR SEQ ID NO:628:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 295 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GAATTCGGCC	TTCATGGCCT	ACCTGCCTCG	AGTTCCTACT	GCCCCCGGGC	GGCCTGCACA	60
GAGCTGCTGC	CCTCCAGAGA	CTGTGAATCC	CAAGCCTGAC	TCAGTGGACT	GCTTCCTGTT	120
CCCCTCCCTC	CTCTTCCTCA	CCTTGTTCTG	CACCCTCAAG	CCTTTCTCCA	ATGCCTCCCA	180
GGAGGATTTG	GGGACTTTCT	CCCTGGGGCG	CCCAGATCCA	GCTCGGAGGC	CTCACTGGGA	240
CCTGGCAAGG	CCTGACCTCC	CGCCCAAACT	TGCTTCTGTA	GCCCCCTAC	TCGAG	295

- (2) INFORMATION FOR SEQ ID NO:629:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

GAATTCGGCC	TTCATGGCCT	AACCTGTTGC	TTCCCCTGGG	ACTGAAGGCA	GAAGTGACTC	60
CCGAAATTCT	CTTTCTGGAC	TCAGAAGGAA	ACCAAAGCAA	TTGATGACAC	CGCATCCCAT	120
ACTAAAAGCT	ATGGAAGAGA	GAGCAATTCA	ACGAGCTGAA	TGTAGGCGGA	TCTTGGCAGA	180
GAAGNAGAAA	AAACAAGAAG	AAGANAAATT	GGCCCAGTTA	AAGGCCCAAG	AGGAGGAACG	240
TCAGAAAAGG	GAGGCAGAAG	AAAAGGAGGC	ACAGCTTGAA	AGAAAACGAG	AAGAGAAGAG	300
ACTGAAGAAA	ATGAAAGAAC	TTGAGAAGCA	GAAGAGAACT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:630:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 257 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GAATTCGGCC	TTCATGGCCT	AGTTCTTCCT	TAGGAACAAG	GGCAGGACCT	CAAACAGTCC	60
AGAGGAGAAG	CCTGGGGTGG	TCAGGGAAGG	CTTCCTGGCT	GAGAGGACAG	GCTTAGGGGC	120
ACCTTGAAAG	TTCAGGCTGA	CTGGGGCTAG	GGGCATGTGG	GTAACAGGTT	AAAGGGGGGG	180
GGGCTGGAAA	ATGCAGACAC	CAAAGACCCT	TCAATATGAG	GCCAAGAAAG	GAAGGTTCAG	240
AACAGGGATC	ACTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:631:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GTTCCAAATC CATGGGAACC	AGCACAGGAG	CTACAGCAAA	TCATGGCACT	TCTGCAGTAG	60
CAATTACTAG CCATGATTAC	CTAGGACAAG	AAACTTTGAC	AGAAATCCAA	ACCTCACCAG	120
AAACATCAAT GAGAGAGGTG	AAAGCGGACG	GAGCTAGCAC	CCCCAGGTTA	AGAGAACAGG	180
ACTGTGGTGA ACCTGCCTCG	CCAGCAGCAT	CCATCTCCAG	ACTCTCTGGG	GAACAGGTCG	240
ACGGGAAGGG CCAGGCAGGC	AGTGTATCTG	AAAGTGCGCG	GAGTGAAGGA	AGGATTAGTC	300
CAAAGAGTGA TATTACTGAG	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:632:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 480 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GAAAAAATGG	AAGAATTTGT	TTGTAAGGTA	TGGGAAGGTC	GGTGGCGAGT	GATCCCTCAT	60
GATGTACTAC	CAGACTGGCT	CAAGGATAAT	GACTTCCTCT	TGCATGGACA	CCGGCCTCCT	120
ATGCCTTCTT	TCCGGGCCTG	TTTTAAGAGC	ATTTTCAGAA	TACACACAGA	AACAGGCAAC	180
ATTTGGACAC	ATCTCTTAGG	TTGTGTATTC	TTCCTGTGCC	TGGGGATCTT	TTATATGTTT	240
CGCCCAAATA	TCTCCTTTGT	GGCCCCTCTG	CAAGAGAAGG	TGGTCTTTGG	ATTATTTTTC	300
TTAGGAGCCA	TTCTCTGCCT	TTCTTTTTCA	TGGCTCTTCC	ACACAGTCTA	CTGCCACTCA	360
GAGGGGGTCT	CTCGGCTCTT	CTCTAAACTG	GATTACTCTG	GTATTGCTCT	TCTGATTATG	420
GGAAGTTTTG	TTCCTTGGCT	TTATTATTCT	TTCTACTGTA	ATCCACAACC	TATTCTCGAG	480

- (2) INFORMATION FOR SEQ ID NO:633:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GAATTCGGCC	TTCATGGCCT	AGCGGGATCG	TATCACTACG	CACGTGGCGT	CAATGACAAA	60
GACGCCTTCC	CCACGGGACA	GGCCCTGGGA	ACTGCGGGGC	AAGGTGTGGG	CACGGCGGGT	120
CGCCTTCCAA	CCCTCCAGGG	TCTCCGGTCC	TGCCCCCTCT	CCAAGACCCA	GAGATTCTCT	180
CCATCCGGTG	CCTCCGGGAG	CCCAGGGTCT	GGGGAGTGTC	TGGCTATGGC	GGGGCGGCTG	240
CTTTTTAGGG	GAGGGAATCC	AGCATTTGGG	AAACCAGATC	TGTTCTCCTT	CTTTCCCTTC	300
CCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:634:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 458 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

CCTCTGCAAG	AAATGCCTAA	GCGTATTATC	AGGAAGTGGA	ATTATAAAAT	GTTTCCAGAT	60
CAAATTAAGC	ATCTACAGGT	GAATTAATAT	AGAATTAAGC	TTAGAAAGCT	TAAGTAGAAG	120
TTGAATGAAT	TGTGTTCATT	CTTTGAAACC	CATTGATTTG	CAAAACCAAT	ATTCCACTGT	180
CTATAGGAGG	CAATTCAGAC	TGAAAATAAT	TTAGAAAAAA	AAATAGTCCA	GAAAAAAAA	240
TAGTTCTAGA	GATAAATAGG	TCATTTGAAG	ACTAACCTCT	GCCATTAGGG	GTTTCTAAAG	300
ATAGGCTGAC	TCTATCTATT	TATTAATTAT	TTTGTTCATT	AACTCCTTGC	ATATAGAATT	360
GTAACTGATA	CCAGCCAGGT	ACGGTGGCTC	ACGCCTGTAA	TCCCAGCACT	TTGGGAGGCC	420
AAGGCGGGCA	GATCACCTAA	GGTCGGGAGT	CTCTCGAG			458

- (2) INFORMATION FOR SEQ ID NO:635:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 343 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GAATTCGGCC	TTCATGGCCT	ACCCACTCTC	ACTTTGTACC	TCTGTCAGTT	ATCTCCTCTT	60
TACCCTTCTT	TCAACGAGCA	TACCACCGGC	CCTCCCAGCA	CCTATGGCCC	AAGCCAGTTG	120
TTTGCAAATT	${\tt TTATACTGTG}$	ACACAGGACA	ATTTACACAC	ACATACACAG	TTTCACTTGT	180
GACATACTTT	TTTTTTGAGA	TGGAGTCTCA	CTTCATTGCC	CAGGCTGGAG	TGCAGTGGTG	240
TGATCACACC	TTATTGCAGC	CTCAAACTCC	TGGGCTCAAG	TGGTCTTCCT	GCCTCAGCCC	300
CCCTAGTAGC	CAGGATTACA	GGCGTGCACC	ACCATTTCTC	GAG		343

- (2) INFORMATION FOR SEQ ID NO:636:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 402 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

GTGGATAACA	AACAAACAAA	TCTGATGCTC	CCTGAGTCAA	CTGTTTATGG	TGATGTGGAC	60
CTTAGTAACA	AAATCAATGA	GATGAAAACC	TTCAATAGCC	CAAATCTGAA	GGATGGGCGT	120
TTTGTCAATC	CATCAGGGCA	GCCTACTCCT	TACGCCACCA	CTCAGCTCAT	CCAGTCAAAC	180
CTCAGCAACA	ACATGAACAA	TGGCAGCGGG	GACTCTGGCG	AGAAGCACTG	GAAACCACTG	240
GGACAGCAGA	AACAAGAAGT	GGCACCAGTT	CAGTACAACA	TCGTGGAGCA	AAACAAGCTG	300
AACAAAGATT	ATCGAGCAAA	TGACACAGTT	CCTCCAACTA	TCCCATACAA	CCAATCATAC	360
GACCAGAACA	CAGGAGGATC	CTACAACAGC	ACAGAGCTCG	AG		402

- (2) INFORMATION FOR SEQ ID NO:637:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 290 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GCTTCCTCGC	AGCAAGCGGC	TGGAGATAGA	GAAGAGCTTA	CTGGTGCGAG	CGTCCGTCGA	60
CCCCGTCGCC	GCTGACCTAG	AGATGGCAGC	CGGTCTCACC	GACATATTTC	AGCATGATAC	120
ATACTGTGGT	GATGTCTGGA	ACACCAACAA	ACGCCAGAAT	GGCAGACTCA	TGTGGCTCTA	180
TCTCAAATAC	TGGGAACTCG	TTGTCGAACT	GAAGAAGTTT	AAGAGAGTAG	AGGAAGCCAT	240
ACTAGAAAAG	TAAGACAAGA	GTGAAATCAA	ACTGCTTTTA	GTGACTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:638:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 463 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

GTCGAGAAAA	TGGGGATAAT	GGAGAAATTG	TGGGCAAGCT	GGCTTCCTGG	GAAGGGACTA	60
ATTGAACAAG	ACAATGATTT	ATCTTTTCGG	GGTTCAGAGG	CAGCTTGTTA	ATTCGAATTA	120
TTTTCTTTAT	TTTTGCCCAC	AAGTGTTTGG	TTGTCCTTTT	CTCTGGCTTT	TTACCTGATC	180
AGGCTGCAAG	CTGCAAAGGT	GTGGCTTGTG	CTGCAGATTT	GTAATAAAAG	ATGACAGGTG	240
AGAGAGACAG	TGGTGGAACT	GGTAGAGCTT	GCACACCCAC	ACGGTGTGGC	TGCTCGGGAG	300
GCTGTCTAGT	GCACCTGCCA	ACAGAGCACA	GATATCCTCT	CTTCCTCATT	TCAGATTCCT	360
CCTTCCAGCT	GTTTACTAAA	CAGCAACAAA	AACACCCTCT	TGGCTGTAAC	TTGTCAAATA	420
AAGTCCCTGC	AAAGTGTATA	AGATTTTCCT	CCCCAACCTC	GAG		463

- (2) INFORMATION FOR SEQ ID NO:639:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 513 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GCGAGGGAGA	TGGCAGCCTG	GGCTTTAGCA	GCAGGGAGGA	AGGTGAANAA	AGAACCGGGG	60
CTTGCAGCAG	AGGTGGGTTC	TGCCTTAAAG	GCAGAGACCC	CCAACAACTG	GAATGCCACG	120
GAAGACCAGC	ATGAGCCTAC	CAAACCTTTG	GTTCGCAGGG	CTGGAGCTAA	TTCTCGCTCC	180
AGGAGAAAGA	AGCAGAAGAA	GAACTCCAGG	CAGGAAGCAG	TGCCCTGGAA	AAAACCCAAA	240
GGCATCAATT	CCAACAGCAC	AGCTAACTTG	GAGGATCCTG	AGGTGGGTGA	TGCTGAAAGC	300
ATGGCGATCT	CAGAGCCGAT	CAAGGGCAGC	AGAAAGCCCT	GTGTGAATAA	GGAGGAGTTG	360
GCTTTGAAGA	AGCCCATGGC	GAAATGTGCC	TGGAAGGGTC	CCAGAGAGCC	ACCTCAGGAT	420
GCCCGGGCAG	AAGCCGAGAG	CCCAGGAGGC	GCCTCTGAGT	CAGACCAAGA	TGGTGGCCAT	480
GAAAGCCCAC	CAAAGAAGAA	GGCCGAGCTC	GAG			513

- (2) INFORMATION FOR SEQ ID NO:640:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 510 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

GAATTCGGCC	TTCATGGCCT	ACACCTCAGC	CTCCAGAGCA	GCTGGGACTA	CAAACGTGTG	60
CCACCATGCC	GGGCTAATTT	TTGTATTTTC	AGCAGAGGTG	GGGTTTCACC	ATGCTGCTGG	120
CCAGGCTGGT	CTCGAACTCC	TGGCTTCAAG	TAATCTGCCC	ACCACAACCT	CCCAAAGTGC	180
TGGGATTACA	GGTGTGAGCC	ACTGCGCCCA	ACCAAGAGCT	CCTTTTTGTT	TTTCTTTTTT	240
TGTGAATTCG	GATTCTTTAT	ATTCAGGAGT	TTTACTTAAA	CTTTGAATCT	GAAAGAAACT	300
TTAGGAGGAG	CTCATAGATT	TGTGGGAAGA	AGCAAATCTA	CATTATTTTC	TCTCTTCTAA	360
AATCATATTC	CATGTATTTT	GATCTTTTAC	TGAATTTTAA	CACATTGTTT	CATCACTAAC	420
ATAAAGTGTT	TCAATAGTTT	TTGTAACTCA	CACACAAATA	CTGGATTTAA	AAGTTATATA	480
CCTGAGTATA	TTTTTATGGC	AGGTCTCGAG				510

- (2) INFORMATION FOR SEQ ID NO:641:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

GAATTCGGCC	TTCATGGCCT	AGTGTTCCCA	GCCAGTCTCT	ATTCTCTCAC	CTAACACTCT	60
CAAGGAGATA	GAAGCTTCAG	CTGAAGTCTC	ACCCACCACG	ATGACCTCCC	CCATCTCACC	120
CCACTTCACA	GTGACAGAAC	GCCAGACCTT	CCAGCCCTGG	CCTGAGAGGC	TCAGCAACAA	180
CGTGGAAGAG	CTCCTACAAT	CCTCCTTGTC	CCTGGGAGGC	CAGGAGCAAG	CGCCAGAGCA	240
CAAGCAGGAG	CAAGGAGTGG	AGCACAGGCA	GGAGCCGACA	CAAGAACACA	AGCAGGAAGA	300
GGCTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:642:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 305 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GAATTCGGCC	TTCATGGCCT	AGTTAGATGA	AAATCTAAAG	GATGAATACT	TTGAGGAAAT	60
CATGGAAGAA	TATGAAGATA	TTAGACAGGG	CCATTATGAG	TCTCTCAAGG	AGAGGAGATA	120
CTTACCCTTA	AGTCAAGCCA	GAAAAAGTGG	TTTCCAAATG	GATTGGCTGT	CTGAACCTCA	180
CCCAGTGAAG	CCCACGTTTA	TTGGGACCCA	GGTCTTTGAA	GACTATGACC	TGCAGAAGCT	240
GGTGGACTAC	ATTGACTGGA	AGCCTTTCTT	TGATGTCTGG	CAGCTCCGGG	GCAACCCCAC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:643:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 301 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

GCGATTGAAT	TCTAGACCTG	CACCCAGCCA	ACACTGAGAG	ATTTTAATGA	GTACTTTTAT	60
CCACCTGACC	ACCATCATTA	CCTATCACCT	GTCATTCTTC	ATCCACCCTA	CATCCATCCT	120
TCATCCCCCC	ATCATCCACC	CATCTATCCT	TCATCCATCC	ATTCATCATG	GAACCATTAT	180
CCATCCAACT	ATCATCCAGC	CAGCCAGAAA	TGACCCATTC	ATCTTCATCT	CTCATTTCCT	240
CTCTCTAAAC	CAGTTCTTAA	TCTGGGGCCA	AAGTCCTACC	CACACATCCC	TTAGTCTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:644:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 408 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GAATTCGGCC	TTCATGGCCT	AGATCCCCCG	TGGAGAAAGC	AGTGACACAT	TCACACAGCT	60
GTTCCCTCGC	ATGTTATTTC	ATGAACATGA	CCTGTTTTCG	TGCACTAGAC	ACACAGAGTG	120
GAACAGCCGT	ATGCTTAAAG	TACATGGGCC	AGTGGGACTG	GAAGTGACCT	GTACAAGTGA	180
TGCAAAGGAG	GGTTTCAAAG	AAAAAGGATT	TTGTTTAAAA	TACTTTAAAA	ATGTTATTTC	240
CTGCATCCCT	TGGCTGTGAT	GCCCCTCTCC	CGATTTCCCA	GGGGCTCTGG	GAGGGACCCT	300
TCTAAGAAGA	TTGGGCAGTT	GGGTTTCTGG	CTTGAGATGA	ATCCAAGCAG	CAGAATGAGC	360
CAGGAGTAGC	AGGAGATGGG	CAAAGAAAAC	TGGGGTGCAC	GCCTCGAG		408

- (2) INFORMATION FOR SEQ ID NO:645:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 364 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

GAATTCGGCC	TTCATGGCCT	AGTTATGTGA	TTAGGAGTAG	GGTTAGGATG	ANTGGGAAGA	60
AGAAAGAGAG	GAAGTAAAGT	TTAATTATGC	CTTTTTGGGT	TTATTATCCC	TGATGCATGT	120
GGCCCCCCAC	TGCTGTGTCC	TTCTCCTGTT	GGCTAGGGTT	AGACCACACA	GGCTAAACTA	180
ATTCCGATTG	GCTAATTTAA	AGAGAATGAC	GAGGTAAGTG	TTTTGGCGGG	AAAAATGGTT	240
ATGACAGAGC	AGGTAATAGG	AATGAGTTAG	GGTGGAGTAG	GTAATCGGAA	TGAGTCAGGG	300
TGGAGCAGGT	AATTGGAATG	AGTCAGGGTA	GAGCAGGTAA	TCGAAAAAGG	TTGCTTTGCT	360
CGAG						364

- (2) INFORMATION FOR SEQ ID NO:646:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

GCTGATGTGG GGCTTAGATT TATGTTTGTT GATATTATTG	TTCATGGCCT AGGAGTGCAT TTGGATCTAG TGTTTTCTAT CAATCT CACTACTGCA CCATTTACCA CAACATTAGA ATATGTCTGA GTAACT TTTTGCATTG AGTCCCACCC CATTTTCCAG AACTTTCATG GCTATT TTCCGTAAGA TCTTTAGGAT CAATTTGTCT AGTTCTAAAG AGGAAA ATTTAGTAAC TTTCCATGAA AAAAACCTAC CATCACAGGA AAGATC GTAGCTCGAG	CGGTT 120 CCTTA 180 ATTCT 240
(2) INFORMA	ATION FOR SEQ ID NO:647:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 267 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:647:	
TCACATGTTA CTTTAGCCAT TCACAGCCAT	TTCATGGCCT AGTCAGTGGC TAGATTGATT GATCCTCCAG AATTAG ACACCAGTCT CAGTTGGAGG GCTGATAGTA AACCTTATTG GTATCT GCCCATAGCC ATGCCCATGG AGCTTCTCAA GGAAGCTGTC ACTCAT TCACACCATA TGCATGGACA CAGTGACCAT GGGCATGGTC ACAGCC GGAGGCGAGG TCTCGAG	GTGC 120 CTGA 180
(2) INFORMA	ATION FOR SEQ ID NO:648:	
(i) :	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 321 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:648:	
TGATAATAAG GATGGCACAC ATGATTTTCT CTTGCACCAA	TCATGGCTAC TTTTGGTAAA GCATACCCAA CCTTCAGTTA GAATAT AAAGATCTCA TTGAAATTTA TTAATTCTTT TGTGTCTAGT AGATAA AGTGCTTTGA TTTTTACCTG CCCAGAATTT AACTCCTCAT CCTATC TTTTCCTCTC CCCCTTCCTC TTTTATTCCA TGTCACTGGG AATGGC GTAATGGCAG GTCTTGCACC AAGCAAGCCA GAAACCTGAG CTTTAG CACTTCTCGA G	CTTG 120 CTAC 180 AGGT 240
(2) INFORMA	ATION FOR SEQ ID NO:649:	
	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 559 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:649:	
TAAAGGGTGA	TTCATGGCCT AGAGGAAGTG AACGGATGGG GCCTCATCCT CCTGCC GGGTGGAAGG ATGGGGCTGT GCCCTCTTAG GGCAGGGAAA AACAGG	TTGG 120

AGTCTGGCCT	CCAGCCTCCC	TGGCCCCTTT	CTAGAGGCCT	CCATCCCACT	GGCGGCTTGC	240
TCCTGCCACC	GGGCCTCTGC	ACAGTCACCT	CCTGCAGCCT	GGGGTGTGTC	GCCTCTCCAC	300
GTCTTGATAT	TTTTGCTGGA	ATGCAGACGA	TACTATATTT	ACCGTATAAT	ATATTATCAG	360
CTCTCCTATA	TCTCAGTCAA	TTTACATAGT	TTAAAATAGA	ACATCTTATT	AAAAACATCT	420
AGATATACAC	AGATTAGGAA	ACGCTTACAA	CATACAAATA	CACAAACTAG	AAATAAATCT	480
TTAGCATACT	GGTATATACA	ACAGTGTGAT	ACAATAAATA	ATTTCATTCA	TGCTCTATCT	540
ACACATCATA	TTGCTCGAG					559

- (2) INFORMATION FOR SEQ ID NO:650:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 477 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GAATTCGGCC TTCATGG	CCT AGGGAGACTG	AGGCAGGCAG	ATCACCTGGG	GTCGGGAGTT	60
CGAGACCAGC CTGACCA	GCA GGGAGAAACC	CCGTCTCTAC	TAAGAATAGA	AAATTAGGTG	120
TGGCGGTGCA TGCCTGT	GGT CCCAGCTACT	CGGGAGGCTG	AGGTAGGAGA	ATCGCTTGAA	180
CCCGGGAGGC GGAGGTC	ATG GTGGGCCGGG	ATTGCACCAT	TGCACTCCAG	CCTGGGCAAC	240
AAGAGTGAAA CTCCATC	TCA AAAAAATAAA	AGCCTAGCCT	CCCAAAGTGC	CAGGATTACA	300
GGCATGAGCC ACCGCGC	CTG TCTGTCCGCC	CGTCTTCTTT	TTTAAGAGCA	AGAAAAGGTT	360
TCCCAGAAGT ACTCTGG	TAG ATTCTTATCA	CACACACATT	CCTAAACCAG	TTACTGGCAA	420
AGAAAATAGA ATTATCA	TGA TTAATTAGCA	TATTCTGAAG	NACATGCTTC	CCTCGAG	477

- (2) INFORMATION FOR SEQ ID NO:651:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 414 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GTGTGAACCT	ACGGGAAGGC	GGCCGCCTGC	ACCTCTGTGC	GGAGACCAAG	GATGATGCCC	60
TAGCATGGAA	GACAGCACTG	CTGGAGGCAA	ACTCCACCCC	GGTGCGCGTC	TACAGCCCGT	120
ACCAAGACTA	CTACGAGGTG	GTGCCCCCCA	ATGCACACGA	GGCCACGTAT	GTCCGCAGCT	180
ACTACGGACC	GCCCTACGCA	GGCCCTGGCG	TGACGCACGT	GATAGTGCGG	GAGGATCCCT	240
GCTACAGCGC	CGGCGCCCCT	CTGGCCATGG	GCATGCTTGC	GGGAGCCGCC	ACTGGGGCGG	300
CGCTGGGCTC	GCTCATGTGG	TCGCCCTGCT	GGTTCTGAGC	CCTGGGACTC	GGAGCACTGA	360
CCCCTGCGCT	TGGATTGCTA	GACTCCTCTT	CCTCCTGGAC	CCCATCCTCT	CGAG	414

- (2) INFORMATION FOR SEQ ID NO:652:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 325 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

GAAGGAAAAC	ATGGGCACAG	GGGATTTTAT	CTGCATTTCC	ATGACTGGAG	GGGCGCCCTG	60
GGGGTTCAGA	TTGCAAGGTG	GCAAGGAGCA	GAAGCAGCCC	TTACAAGTTG	CAAAGATTCG	120
AAATCAGAGC	AAAGCCTCTG	GGTCTGGGCT	CTGTGAGGGA	GATGAAGTGG	TTTCCATCAA	180
TGGCAACCCT	TGTGCAGATC	TCACCTACCC	TGAAGTCATC	AAGCTCATGG	AAAGCATAAC	240
AGACTCTCTC	CAAATGCTCA	TCAAAAGACC	ATCCAGTGGA	ATAAGTGAGG	CTTTGATATC	300
TGAAAATGAA	AACTCTAACC	TCGAG				325

- (2) INFORMATION FOR SEQ ID NO:653:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 443 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

	120
TCAGCTGCTT ATTGCAGGGA CACAGAGCCC GGCATGGTCC AGAAGGCGGG CTTATGGGGC	180
CTGCAGCACA CAGGGAAAGT GAGCCCACAC TGTGATAGGA GGGCAGACAC ACAGGATGTG	240
TTCTGTGTTA CAGGGTTGCC GTGAAGAATT TCATTCTTTT GCAAGGACTG GAGAGAAAAT	300
TTTATGTGGA AGGTAGCCCT TGGAAATGAC CTCAAAGAAT AGGTAGGATC TTAGCCTGCG	360
TTTGAAAGCC TGGAAAAAAA CAGGATGACA GGATGAAGAG GCCACAGCAC AGCTGCAGAC	420
AATGGGAGTG CGGAGATCTC GAG	443

- (2) INFORMATION FOR SEQ ID NO:654:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 311 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

GGGAGCGCCG	GTGGTTCATC	CTGACCGATA	ACTGCCTCTA	TTACTTTGAA	TACACAACAG	60
ATAAGGAGCC	CAGGGGAATC	ATCCCGTTGG	AAAACCTCAG	CATCAGGGAG	GTGGAGGACC	120
CCCGGAAACC	CAACTGTTTT	GAGCTCTACA	ATCCCAGCCA	CAAAGGGCAG	GTCATCAAGG	180
CCTGTAAGAC	GGAGGCCGAC	GGCNGCGTGG	TAGAGGGGAA	CCATGTGGTG	TACCGGATCT	240
CAGCCCCGAG	CCCGGAGGAG	AAGGAGGAGT	GGATGAAATC	CATCAAAGCC	AGTATCAGCA	300
GATCCCTCGA	G					311

- (2) INFORMATION FOR SEQ ID NO:655:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 346 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GGGGGATACG GATACCCAAA CTTCAATGTT CCTTGATAGT AGGAAGGAGG ACAGTTATAT AGACCATAAG GTGCCTTGCA CAGATTCACA AGTGCAGGTC AAGTTGGAGG ACCACAAAAT AGTAACTGCC TGCTTGCCTG TGGAACATGT TAATCAGCTG ACTACTGAGC CAGCTACAGG GCCCTTTTCT GAAACTCAGT CATCTTTAAG GGATTCTGAG GAGGAAGTAG ATGTGGTGGG AGATAGCAGT GCCTCAAAAG AGCAGTGTAA AGAAAACACC AATAACGAAC TGGACACAAG TCTTGAGAGT ATGCCAGCCT CCGGAGAACC TGAACCATCT CTCGAG	60 120 180 240 300 346
(2) INFORMATION FOR SEQ ID NO:656:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 116 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:	
GAATTCGGCC AAAGAGGCCT ACTAAACCGT CGATTGAATT CTCGAGGCAG GTCTAGAATT CAATCGACGG TTTAGGCTCC CTATAGTGAG TCGTATTAAT TTCAGAGGTG TATTTA	60 116
(2) INFORMATION FOR SEQ ID NO:657:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 482 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:	
GAATTCGGCC AAAGAGGCCT AGGGATGAGG GTGAAGAAGG GGAGAGGGTT GGTTAGAGAT ACAGTGTGGG TGGTGGGGGT GGTAGGAAAT GCAGGTTGAA GGGAATTCTC TGGGGCTTTG GGGAATTTAG TGCGTGGGTG AGCCAAGAAA ATACTAATTA ATAATAGTAA GTTGTTAGTG TTGGTTAAGT TGTTGCTNGG AAGTGAGAAG TTGCTTAGAA ACTTTCCAAA GTGCTTAGAA CTTTAAGTGC AAACAGACAA ACTAACAAAC AAAAATTGTT TTGCTTTGCT	60 120 180 240 300 360 420 480 482
(2) INFORMATION FOR SEQ ID NO:658:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 430 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:	
GAATTCGGCC AAAGAGGCCT AGTCGAGTCC CTTCTGTCCC AGTCGTTCGT GCCTCTTGTC CCACGCAACT CCAGCTTGTA CCATGCCGGT CAAAGGAGGT AGCAAGTGCA TCAAATACCT GCTCTTCGGA TTTAACTTCA TCTTCTGGCT CGCTGGCATT GCAGTGCTTG CTATTGGACT	60 120 180

TTTCTACACA GGAGTGTACA TTCTGATTGG AGCCGGGGCC CTCATGATGC TGGT. CCTGGGCTGC TGTGGAGCTG TACAAGAGTC CCAGTGCATG CTGGGATTGT TCTTC CCTCTTGGTG ATATTCGCCA TTGAGATAGC CGCCGCCGTC TGGGGCTATA CCCAC	TGGTTT 300 CGGGTT 360 CAAGAG 420
TCGAGTCGAG  (2) INFORMATION FOR SEQ ID NO:659:	430
(2) INFORMATION FOR SEQ ID NO: 655;	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 290 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:	
GAATTCGGCC TTCATGGCCT AAGAGTACAG AGATTTCACT TCATCTTGTG CTAATATTNAAAGTA TATTGACACT AGTAAAGACA CTTTATTTTA ATTTGAGGTA TAAATCCTAAAATAG ACTATTTCCA TTGAGTCATA CATTTTAAAT GTGGTATATA TTCTTCAGAAAATG ATAACTATCA TAGAAATCTA ATACTCATTA ATTTGATTAA TAATT	TGTCTA 120 TATATT 180
(2) INFORMATION FOR SEQ ID NO:660:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 406 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:	
GAATTCGGCC TTCATGGCCT AGTCAGAAGT CTTTGTGTCC CTGTTTTTGT GTCCA GGTACCTTGG CACTTTAAGG CTTGTCCTGC AAAATAAAAC ATTGCATCAT CACTT GGCAGAGCTT GGGAGTTTGC ACTGCTAAGA TGAGGATAGG AAAGAAATTT ATGCC GCCTTTGATG CTGCCCACTC ACCTGTCTGC ACAGCCAGGG CACGGCCAGC GGGAG AAGACGAGCG AGACCAAAAC CTTGCCGTGG GGAGGAGGGT GGCATAGCCA TTGAT GGGCCAGGCA TGATGCCTCA ACTCTAAAAA TATTTTTTAT CTGATTACAA AAGTA GGGCCAGGCA TGATGGCTCA TGCCTGTAAT CCCAACACTC CTCGAG	GTGAA 120 GCAGG 180 GTGGAG 240 GAAATC 300
(2) INFORMATION FOR SEQ ID NO:661:	•
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 461 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:	
GAATTCGGCC TTCATGGCCT AGTGGAACTG AAAACTCAGA GGAGGCATCA AACCC CGGGGGACAA AACTAAGTCT TGCCAGAGTC CTGAAGGATG AACAACAGTT AACCA GGGATACTGG AGGGCATGGA GGCTCTCTGG CCTGGAGTGC AGAGCATGGA GTGCT	AAGCAA 120

AGCTAGTTAG	CTCTGCAAAG	CTGAGTGTCA	GGAATGTAAA	GGGAGAGAAT	AGGAGTGAGA	240
GAAGAGTCTG	GCAAGGCAGA	CAGGGAAGGC	CTATATGCCT	TGATGGAGAA	CCACTGAAGG	300
ATTTAAAGAA	GGAGAGGGTT	AATTTTGTCC	AATAGAAAGA	TCACATTGTG	TGTAGTGTGG	360
AGGATGGGTT	GCAGAGAGAG	AAGCTAGAGA	CCAAAAGATG	AGACGGGAAC	AGCTGCAAAT	420
TTCGAGAGCT	CGTAAGATTA	TGTATGGCTG	GACCACTCGA	G	•	461

- (2) INFORMATION FOR SEQ ID NO:662:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 502 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GAATTCGGCC TTCATGGCCT	AGCCTGAGCT	CAGGAGTTCA	AGACCAGCCT	GGGCAACACA	60
GTGAAACTCC ATCTCTACTA	AAATACATAA	AAATTAGCTG	GGCCTGGAGG	CATGCACCTG	120
TGGTCCCAGT GCTACTGGGG	AGGCTGAGGC	AGGAGAATTG	CTTGGGCCCG	GGAGGCAGAG	180
GTTGCAGTGA GCCAAGATCG	CGCCACTGCA	CTCCAGCCTG	GGCAACAGAG	CGAGACTCCA	240
TCTCAAACAA ACAAACAAAC	AAACAAACAA	ACAAAACAAC	AGTTATTTTT	TTCTCACCAT	300
TCTAAAGAAT GTTACATTTG	ATTCTTTTTC	AAAATTTGGT	CAGTTTTGAT	AGTCTTATTT	360
CTCCATACTT TCATTCCCCC	TTTTTATTTC	TGTAAATAAT	TGAACTTTAT	ATTCCTTATA	420
TGATAATTTT AATATCCAAA	GTCATTGGTC	ATATTCTCCA	GTTCATGATT	TCTGCTGAGT	480
TTGTGGTGCT GATTTTCTCG	AG				502

- (2) INFORMATION FOR SEQ ID NO:663:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 485 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GAATTCGGCC	TTCATGGCCT	ACAACCACCA	ACATTTGTGT	TTTTGCAGAT	GAACAGGTTG	60
ACAGAAGTCC	CACTGGCTCA	GGAGTGACAG	CCCGAATTGC	CTTACAGTAT	CACAAAGGGC	120
TTCTGGAACT	GAACCAGATG	AGAGCCTTCA	AAAGCAGTGC	AACTGGCTCA	GTATTCACAG	180
GGAAAGCTGT	GAGGGTAAGT	GGCACCCTTA	GCTTCTTATT	TATAAATGTG	TCACTCATGA	240
GACTGGAGAG	GCCTGAGTTG	GGTGTTTGAT	AAATTTCTTC	ACTCAGCTCT	CAGAAGAGAA	300
TTTTAAAGCA	GGCCTGTAAA	AACTTCTTTT	CAACTAGGAC	ATTGGTTATC	CAGTGTGGTC	360
TTGGGGCCCC	AGCGGGCCCC	TAAGGTCCTT	TCCATGGGTT	CAGAGGGTCA	AAACTGTGTT	420
CATAATAATG	ACATTATTTG	CTTTTCACTC	TCATTCTCTC	AAGAGTGTAC	AGTGGGTTAC	480
TCGAG						485

- (2) INFORMATION FOR SEQ ID NO:664:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 348 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GAATTCGGCC	TTCATGGCCT	AAAAATTATA	AAGTGTAAAA	TATCTTTGTA	TCTCTAGTTT	60
TTCTCCTTTC	CCCAGATAAG	AATAAAAGCA	GGCTGCAGGC	TCCTGGGGTG	ATÄACCCACT	120
TGGGTCGAGT	TCCATCGCTG	TTGGCGATAA	ATCTTGTTGG	TGTTCACTTT	TTGGGTTCTC	180
ACTACCTTTA	TGAGCTATAA	CACTCACCCT	GAAGGTCTGC	AGCTTCACTC	CTGAAGCCAG	240
CGAGAGTACG	AACCCACAGG	CAGGAAGAAA	CTCTGAACAC	ATCCGAACAT	TGGAAAGAAC	300
AAACTCCAAA	CAAGCCGCTT	TTAAGAACTG	TAACACTCAC	AACTCGAG		348

- (2) INFORMATION FOR SEQ ID NO:665:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 571 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GAATTCGGCC TTCATGGCCT	AGTCGTTATC	AGAGGTGGAG	ACATTTAGAA	GTTGTTCTTA	60
ATCAGAGTGA AGCTTGTGCT	TCGGAAAGTC	AACCTCACTC	CTCAGCACTC	ACAGCACCTA	120
GCTCTCCAGG TTCCTCATGO	ATGAAGAAGG	ACCAGCCCAC	ATTTACCCTC	CGACAAGTTG	180
GCATAATATG TGAGCGCCTC	TTAAAAGACT	ATGAAGATAA	AATTCGGGAG	GAGTATGAGC	240
AAATCCTCAA TACCAAACTA	GCAGAACAAT	ATGAATCTTT	TGTGAAATTC	ACACATGATC	300
AGATTATGCG ACGGTATGGC	ACAAGGCCAA	CAAGCTATGT	GTCATGAAGC	TTTGTCACAT	360
ATCTGGGTAC CAGGTTTGAC	CTCAAGAGAT	GGCTGCTGTA	CACTTTTTGC	AACTGGTTTG	420
ATGTCACATT TCAGCTCCA	CTTTGCATCC	TGAGAACACT	TAAACGTTTC	TGCAGGTCCA	480
TTTTATACAA CTTGAAAGAC	CGTAAAACTT	TCTGGTTGCC	ACAAGCATAT	CTTTCTTTTC	540
TGCTCATCCA ATAAACAGCT	GAGCCCTCGA	G			571

- (2) INFORMATION FOR SEQ ID NO:666:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GGGATCATTA TTATTO	CAGCT ACTGAGAACT AG	AATATTAA GAGACTGO	TG GCAAGGCAAG	60
CAGTTAATTT TCAGT	TGAAA TTGCATTAAA TA	AAAAGTAT TTTCTTG	TT TGTGGAAGCA	120
CGTGAATTTT TGTAA	AAAGC TGCTTGTTTT CC	CCATTTAC AGGTTCTO	TA CAGAGTAATG	180
AGATGTGTGA CGGCTC	GCAAA CCAGGTGTTT TI	TTCTGAGG CTGTGTTC	SAC AGCTGCTAAT	240
GAGTGTGTTG GTGTT	TTGCT CGGCAGCTTG AA	TCCTAGCA TGACTATA	CA TTGTGACATG	300
GTCATTACAT ATGGAT	TTAGA CCAACTGGAG AA	TTGCCAGA CTTGTGG	AC CAATTATATC	360
ATCTCAGTCT TGAAT	TTACT CACGCTGGTA TO	TGAATTAT TCTTTTC	TT TTTAATGTGT	420
TGGTTTATTC AGGCC	CATCT CGAG			444

- (2) INFORMATION FOR SEQ ID NO:667:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 524 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GGGAACTGAC	AAGCAATTAA	CTGGAGAATA	AGTGAGGGGA	ATGGAGCAGT	AGTATTCTTT	60
AACTTAATTT	GCCATTTAAG	AGAGCACTTG	GAATCTGAAG	AAAGTCTATC	CCTACCAAGG	120
AAACGGAGTC	AAATTGCAAT	TAAGATTAAC	TTTGGTTATA	TGGAAGCAAG	AATCATGCTT	180
CTCATCATCA	ATTGCGTCTC	TTTGGTAGCC	AATAATTCCA	TCTGTAATCA	TGGCAGCAAC	240
TTAAGTATTG	CCAATGTTTT	CAAATGTGTT	ACAGCATTAA	GGCATCCACA	TCTAAAGAGG	300
CAGTTTTAAA	CAAGAGGAAA	ACGGAACTGA	AATGTGCCAA	GAAGTGAACA	CGGACATGGC	360
CTCTCCTGGA	ATACTGCCCA	CCATGCCAGC	AAGCTCTTCC	TCCAGTCAAG	AAGGCCTGTG	420
CCACGCTGCT	TGGTTCCCTG	CTGCCTGAAG	ATGCATTTGA	GCCCTATGAG	ATTAGTATGG	480
CTATTTCTGT	CTGCTGACCA	GGAGAGAAAT	GAGTAGTTCT	CGAG		524

- (2) INFORMATION FOR SEQ ID NO:668:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 554 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GAATTCGGCC	AAAGAGGCCT	ACACAGAGGG	ATAATTGGCA	TTGGTATCAA	CTGACATATT	60
CACAACTTTG	AATAAAACTT	TCCACATTTG	GAAAATCACC	ATGCCTGGCC	CCTAGGCTAT	120
ACTTTGAAAA	CCACTGCTTT	AGTGTTTTAG	AAATTGTTAC	CCTCATACTA	ATATTTACTA	180
CACCCCCCAC	CTTGACAATA	CATACAAAAG	AGGAGTAACA	GTTTCCCATA	ACCTTTCTAA	240
ATTTGAGTCT	TATTAAACCA	GACTCATAGC	CCTTGTTGAC	TTTTCTTCCT	GATCTGTGCC	300
TTATCCCTAG	GGCGGTGATC	ATGCGGGTAT	CTGCTAATTG	GCAGATGTGA	GTGGTTATAC	360
CTATTTACAA	GCAACTCATT	GCAAAAATAA	TTTTAGCTAA	AGAAAACATC	CATGGCCAGA	420
GAATAAGTTT	TGGAATTTGA	TATGTTAAAT	GAGCTTTATG	TTTACCTTTA	AAAGGTTAAA	480
ATATTTACCA	TTCATGGATT	ACCTTTTTTC	AGAAAGTAAG	AATATATAAA	TTACATTTAA	540
TCTTGAAGCT	CGAG		•			554

- (2) INFORMATION FOR SEQ ID NO:669:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 329 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GAATTCGGCC	TTCATGGCCT	AATCGTATTC	CATCTACTGC	ATACTTTTCA	TAGATGTCCT	60
CCATCAGAAG	CACCTATGGT	TGTTTGTTAA	ACGTGTTATT	TCCTGATCCC	ACCCCAGGAT	120
TTCTGAGTAT	TCTAAGAATT	TCTAAGTGTA	AGGCCTGGAA	ATATGCATTT	TACAACCCCC	180
TAGAACATTC	TTATGTGCAC	TAAAATTTGA	GAACCACTAA	TCTGGTGTAT	ATACTGTTGT	. 240
TACTTAATAT	TTTCTTAATG	ATAGATACTT	GGATGATTTT	TGACTTTATT	ATTATTATAA	300
GCAATGTTGT	AAACATCACA	CAGGCCAAG				329

(2) INFORMATION FOR SEQ ID NO:670:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

GGCGTATGAT	ACCTAAAGTG	GAGTGGTCGG	CGTTCCTGGA	GGCGGCCGAT	AACTTGCGTC	60
TGATCCAGGT	GCCGAAAGGG	CCGGTTGAGG	GATATGAGGA	GAATGAGGAG	TTTCTGAGGA	120
CCATGCACCA	CCTGCTGCTG	GAGGTGGAAG	TGATAGAGGG	CACCCTGCAG	TGCCCGGAAT	180
CTGGACGTAT	GTTCCCCATC	AGCCGCGGA	TCCCCAACAT	GCTGCTGAGT	GAAGAGGAAA	240
CTGAGAGTTG	ATTGCACCAG	ACTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:671:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 429 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GAATTCGGCC	TTCATGGCCT	ATTATCTCTC	AAAAACAAAG	CAATAAGTAC	CAAGAAATAG	60
CAACAAAAAT	TAGCTTGTAA	GGTTGGTTTC	TGAGGGTAGA	AATGGCTCTT	GATGCCATGT	120
GGAGCAATGG	GAAGGAGGCT	TTCTAGTTAC	ACAGACTCTT	GGTCCTGCCA	CTTATTCATT	180
TTATTTTATT	TTATATTTTA	CTTTAAATTT	TTTGAGATAG	GGTTTCACCC	TGTCGCCCAG	240
GCTGGTGGGC	AGTGGCTCAC	TGCAGCCTCG	AACTACCAGG	CTGAAGTGAT	GCTCTTACCT	300
CAGCCTTTCG	AGTAGTTGGG	ACAACAGGTG	CACACCACCA	TTCCTGGCTA	ATTAAAAAAA	360
TTTTTTTGTG	GGAACATGGC	AAGACCTTGT	CTCTATTAAC	AACAACAGCA	ACAGCAACAA	420
CAACTCGAG						429

- (2) INFORMATION FOR SEQ ID NO:672:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 357 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GTAAAATCGT	TCTTGAGAGG	AACGTCTCTG	TGCGAAGAGA	TAATGAGTTT	AGCTCTGAGA	60
AGTGAGCTTG	TAGTGGACAA	AACAAAGAGG	AAAAAAAGAA	GAGAACTGTC	TGAGGAACAG	120
AAACAAGAAA	TTAAAGATGC	TTTTGAACTA	TTTGATACAG	ACAAAGATGA	AGCAATAGAT	180
TATCATGAAT	TAAAGGTGGC	AATGAGAGCC	TTGGGGTTTG	ATGTAAAAAA	AGCTGATGTA	240
CTGAAGATTC	TTAAAGATTA	TGACAGAGAA	GCCACAGGGA	AAATCACCTT	TGAAGATTTT	300
AATGAAGTTG	TGACAGACTG	GATATTGGAA	AGAGATCCCC	ATGAAGAAAT	ACTCGAG	357

- (2) INFORMATION FOR SEQ ID NO:673:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GGTAGATACT	GGTTTTTCGT	ATCCTGCTTC	TCTTAAGGGC	AGCTCTTTTT	AGCATACTCC	60
CATGCAGCAA	CAGAAATTTG	TATCTTTTTT	TTCTTTTTTG	AGATGGAGTC	TCGCTCTATC	120
ACTAGGCTGG	AGTGCAGTGG	CACAATCTCG	GCTCACTGCA	ACCTCTGCCT	CCTGGTTCAA	180
GCGATTCTCC	TGCCCTAGCC	TCCTGAGTAC	CTGGGACTAC	AGGTGCGCGC	CACCACACCC	240
AGCTAATTTT	TATATTTTTA	GTAGAGACGG	GGTTTTACCA	TGTGGCCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:674:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 470 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GGATGGACAT	CAGCACTTTA	CGGCGCCAGC	TGAGACCCAC	AGGCCAGCTC	CGTGGAGGGC	60
TCAAGGGCTC	CAAGAGTGAG	GATTCGGAGC	TGCCCCGCA	GACGGCCTCC	GAGGCTCCCA	120
GTGAGGGGTC	TAGGAGAAGC	TCATCCGACC	TCATCACCCT	CCCAGCCACC	ACTCCCCCAT	180
GTCCCACCAA	GAAGGAATGG	GAAGGGCCAG	CCACCTCGTA	CATGACATGC	AGCGCCTACC	240
AGAAGGTCCA	GGACTCGGAG	ATCAGCTTCC	CCGCGGGCGT	GGAGGTGCAG	GTGCTGGAGA	300
AGCAGGAGAG	CGGGTGGTGG	TATGTGAGGT	TTGGGGAGCT	GGAGGGCTGG	GCCCCTTCCC	360
ACTATTTGGT	GCTGGATGAG	AACGAGCAAC	CTGACCCCTC	TGGCAAAGAG	CTGGACACAG	420
TGCCCGCCAA	GGGCAGGCAG	AACGAAGGCA	AGTCAGACAT	CCAACTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:675:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 637 base pairs
    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

AAAGAGGCCT	AGTCGCTCTT	GCTGAAACCT	TCAATGCAGT	GAGCGCCCAT	60
CCTACAGGCT	GAAGTTCTTC	CTCTGATGGA	CATGACCCCC	GTGTTGTCTC	120
ACTTTCACTC	TGTTCCAGCC	ACACGGGGTT	TCTGTCTTTC	TCGGGTCATG	, 180
GTGCCTCGGG	CCCTTTGCTC	ATGCTGTTCT	CTGCCTGGGA	TGCGCTTTAC	240
GATGGTCAGT	GATTCCATTT	CTCTCAGAGT	CTATTCACAG	GTCCCCTTCT	300
TTCTCTGGCT	CCACTGTCTA	AAATTTCAAC	AGCTGCCTCT	GCCCCCGAA	360
CCCTTATCTG	CCTTTTTTCC	TTCAGCTCTT	ACTTCCATCA	AATACAGTAT	420
AAGTCTTATC	TTGTTCACGG	TCATTTTCTT	CCACAGGTAA	TTTTGGTAAA	480
					540
					600
					637
	CCTACAGGCT ACTTTCACTC GTGCCTCGGG GATGGTCAGT TTCTCTGGCT CCCTTATCTG AAGTCTTATC TTGATGATGT GAATGAATGA	CCTACAGGCT GAAGTTCTTC ACTTTCACTC TGTTCCAGCC GTGCCTCGGG CCCTTTGCTC GATGGTCAGT GATTCCATTT TTCTCTGGCT CCACTGTCTA CCCTTATCTG CCTTTTTTCC AAGTCTTATC TTGTTCACGG TTGATGATGT TTAATACTGT GAATGAATGA CCAGTTTTA	CCTACAGGCT GAAGTTCTTC CTCTGATGGA ACTTTCACTC TGTTCCAGCC ACACGGGGTT GTGCCTCGGG CCCTTTGCTC ATGCTGTTCT GATGGTCAGT GATTCCATTT CTCTCAGAGT TTCTCTGGCT CCACTGTCTA AAATTTCAAC CCCTTATCTG CCTTTTTTCC TTCAGCTCTT AAGTCTTATC TTGTTCACGG TCATTTTCTT TTGATGATGT TTAATACTGT TTTGTTTAAT	CCTACAGGCT GAAGTTCTTC CTCTGATGGA CATGACCCCC ACTTTCACTC TGTTCCAGCC ACACGGGGTT TCTGTCTTTC GTGCCTCGGG CCCTTTGCTC ATGCTGTTCT CTGCCTGGGA GATGGTCAGT GATTCCATTT CTCTCAGAGT CTATTCACAG TTCTCTGGCT CCACTGTCTA AAATTTCAAC AGCTGCCTCT CCCTTATCTG CCTTTTTTCC TTCAGCTCTT ACTTCCATCA AAGTCTTATC TTGTTCACGG TCATTTTCTT CCACAGGTAA TTGATGATGT TTAATACTGT TTTGTTTAAT ACAGTACCCC GAATGAATGA CCAGTTTTTA TTCCCCTCTG AAGCGCTAAG	AAAGAGGCCT AGTCGCTCTT GCTGAAACCT TCAATGCAGT GAGCGCCCAT CCTACAGGCT GAAGTTCTTC CTCTGATGGA CATGACCCCC GTGTTGCTC ACTTTCACTC TGTTCCAGCC ACACGGGGTT TCTGTCTTTC TCGGGTCATG GATGGTCAGT GATTCCATTT CTCTCAGAGT CTATTCACAG GTCCCCTTCT TTCTCTGGCT CCACTGTCTA AAATTTCAAC AGCTGCCTCT GCCCCCGAA CCCTTATCT CTCTTTTCC TCAGCTCTT ACTTCCATCA AATACAGTAT TAGATGATGT TTAATACTGT TTTGTTTATA ACAGTACCC CAGTTTAGCA GAATGAATGA CCAGTTCTA TTCCCCTCTG AAGCGCTAAG AGCTGCCGCT CTGTAGCNGC TCCCGCTCCA ACTCGAG

## (2) INFORMATION FOR SEQ ID NO:676:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 513 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

GAACACGTCA '	TGAGGAAGGA	GCAGCGCAAG	GAGGAGAAGG	AGAAGCGGCG	CCTCGACCAG	60
CTGGAACGTA .	AGAAGGAGAC	GCAGCGCCTA	CTGGAGGAGG	AGGACTCCAA	GCTCAAGGGC	120
GGCAAGGCGC	CGCGGGTGGC	CACGTCCAGC	AAGGTCACCC	GGGCCCAGAT	CGAGGACACG	180
CTGCGCCGAG	ACCATCAGCT	CAGGGAGGCC	CCGGACACAG	CCGAGAAAGC	CAAGAGCCAT	240
CTGGAGGTGC	CGCTGGAGGA	GAACGTGAAC	CGCCGCGTGC	TGGAGGAGGG	CAGCGTGGAG	300
GCGCGCACCA '	TCGAGGACGC	CATTGCAGTG	CTCAGCGTGG	CGGAGGAGGC	GGCCGACCGG	360
CACCCAGAAA	GACGCATGCG	GGCAGCCTTC	ACAGCCTTTG	AGGAAGCCCA	GCTGCCGCGG	420
CTCAAACAAG	AGAACCCCAA	CATGCGGCTG	TCGCAGCTGA	AACAGCTGCT	CAAGAAGGAG	480
TGGCTCCGCT	CTCCTGACAA	CCCCAAACTC	GAG			513

- (2) INFORMATION FOR SEQ ID NO:677:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 376 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GTCCATCCTG	AGCTCCATGG	AGAAGCCACC	CAGCCTCGGT	GACCAGGAGA	CTCGGCGCAA	60
GGCCCGAGAA	CAGGCCGCCC	GCCTGAAGAA	ACTACAAGAG	CAAGAGAAAC	AACAGAAAGT	120
GGAGTTTCGT	AAAAGGATGG	AGAAGGAGGT	GTCAGATTTC	ATTCAAGACA	GTGGGCAGAT	180
CAAGAAAAAG	TTTCAGCCAA	TGAACAAGAT	CGAGAGGAGC	ATACTACATG	ATGTGGTGGA	240
AGTGGCTGGC	CTGACATCCT	TCTCCTTTGG	GGAAGATGAT	GACTGTCGCT	ATGTCATGAT	300
CTTCAAAAAG	GAGTTTGCAC	CCTCAGATGA	AGAGCTAGAC	TCTTACCGTC	GTGGAGAGGA	360
ATGGGCCCCC	CTCGAG					376

- (2) INFORMATION FOR SEQ ID NO:678:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

GAATTCGGCC	TTCATGCCTA	GCAGGAGGTT	TTATTGTAAA	GAGGCCGATT	GTACAGAGCA	60
AAGATTGTTC	TGACACGGGG	GGCTGGGTGG	TGGGACCCAG	AGGCCAGAGC	TGGGTGAAGG	120
ATGAGGGGTG	GCATCGCCCC	ATCCAGGCAG	TGGGCAGGGC	AGGGAGGACT	AAACGGCTGC	180
CTCCCAGTTC	CCTTCCCTGC	CCCTCATTAC	TGGGTAAGAG	GGAGCCAGGC	TATTTCCACG	240
GATCCAGGAG	AATATAGCAG	GAGACCCTCA	CCACCCCACA	CCATGCCCCA	AGGATACGGG	300

AGGTGCCCCA GTCTGGCTTT TGCAGTCGGC CAGCTCCCAG CCTCCTCGAG (2) INFORMATION FOR SEQ ID NO:679: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:679: GAATTCGGCC TTCATGGCCT AGTTCTCACC GGGGAAAAAC CCACTGTTAG GATGGCATGA 60 ACATTTCCTT AGATCGTGGT CAGCTCCGAG GAATGTGGCG TCCAGGCTCT TTGAGAGCCA TGGGCTGCAC CCGGCCGTAG GCTAGTGTAA CTCGCATCCC ATTGCAGTGC CGTTTCTTGA 180 CTGTGTTGCT GTCTCTTA~A TTAACCGTGC TGAGGCTCCA CATAGCTCCT GGACCTGTGT 240 CTAGTACATA CTGAAGCGAT GGTCAGAGTG TGTAGAGTGA AGTTGCTGTG CCCACATTGT TTGAACTCGC GTACCCCGTA GATACATTGT GCAACGTTCT TCTGTTATTC CCTCGAG (2) INFORMATION FOR SEQ ID NO:680: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 250 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:680: GGGGGTGGAA GGCGTAGTGC TTGAAATGCA GGGATCTGGC AGTCAGCAGA AGGATCTGAG ACCCAGTGTC GAGGTTAAAA AAAAAACAAA AAACCAAAAA CCAATGCAGG AATCCAGTGG 120 GTGGAGTGAG GGGATCTGGG ATCCAGTGAT GGGGGCCCCA GGATCCAGGC ATTGTGGTTG 180 TCAGGATCCA GTGGTGAGGT TTGTTGACAT CCAGAATCCA GCAGCTGAGC TTGGAGATCC 240 AGGGCTCGAG 250 (2) INFORMATION FOR SEQ ID NO:681: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 406 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:681: GGATTCCTAC AAAAATTGAG GCAGAAGATC AAAATCGGAG TGGTAGGCGG ATCGGACTTT 120 GAGAAAGTGC AGGAGCAACT GGGAAATGAT GAATATTCAA AGTCATCTGG GTGAGGCCCT AATCCAAGAT TTAATCAACT ACTGTCTGAG CTACATTGCG AAAATTAAAC TCCCGAAGAA 180 GAGGGGTACT TTCATTGAAT TCCGAAATGG GATGTTAAAC GTGTCCCCTA TTGGAAGAAG 240 CTGCAGCCAA GAAGAACGCA TTGAGTTCTA CGAACTCGAT AAAAAAGAAA ATATAAGACA 300

360

406

AAAGTTTGTA GCAGATCTAC GGAAAGAGTT TGCTGGAAAA GGCCTCACGT TTTCCATAGG

AGGCCAGATC AGCTTTGATG TCTTTCCTGA TGGATGGAAA CTCGAG

- (2) INFORMATION FOR SEQ ID NO:682:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

GAATTCGGCC	TTCATGGCCT	ACCCTTCTAG	GTGTCATCTC	CTTCCCTCCC	TTTCCCCCAA	60
GACTCCCTCT	GGGCCCAGCC	AGCAGGTGAA	GCCTGACTTA	GGGAAGGGGG	GATTTCCAGG	120
GGAGGGGCCC	TGGCCCCCAC	TGACCCAGCA	TTGCTATCCA	CAGGAGGAGC	AGCCCCCACA	180
ACATCGATCC	AAGAGGGGGG	GCTCAGTGGG	CGGCGTGTGC	TACCTGTCGA	TGGGCATGGT	240
CGTGCTGCTC	ATGGGCCTCG	TGTTCGCCTC	TGTCTACATC	TACAGATACT	TCTTCCTTGC	300
GCAGCTGTCC	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:683:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 394 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCGGCCTCCC	AAAGTGCTGG	60
GATTACAGGT	GTGAGCTAGC	ACTCCCAGCC	GACAGGTGCT	TCTTAAATGT	TTTCTTTGAG	120
CAGGAATTGG	TCCAGGAATT	GGTTCTCAAG	TTAGAAGGAA	AATTTGAGGG	GAAGAACTTG	180
TTTTTTCTCC	AATCAGTCTC	TGATTAAATA	GTTATTAGGA	AAAACTCCTT	GCTTATGTCT	240
TTGTATTGCA	CATTTTTATA	TATGTATATA	TGTGTAAATA	GAGATATTTA	TATATTCACA	300
GACAAACACG	TGTATGCACA	TTTCACAATG	GAGGAAGAAG	GGATATGGTG	TGCACTGAGG	360
TAAAGTGAGC	AGGGATACAG	AAGAGAAACT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:684:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 509 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GTCCTAACCT	TGGGTCCAAG	TTTCGTTATA	GTGGCAGGAC	ACAAGCGCAA	ACGAGAAGAG	60
CCAGTGCGTT	GATAGATCGC	CCAGCACCTT	ACTTTGAACG	CTCATCCAGC	AAACGTTATA	120
CCATGTCTCG	CAGCTTGGAT	GGAGCATCAG	TGAATGAAAA	CCATGAAATA	TACATGAAGG	180
ATTCTATGTC	TGCTGCAGAG	GTTGGTACTG	GCCAGTACGC	CACAACAAAA	GGCATCTCTC	240
AGACCAACTT	GATCACCACT	GTGACTCCGG	AGAAGAAGGC	TGAGGAGGAG	CGGGACGAGG	300
AAGAGGACAA	ACGGAGGAAG	GGGGAAGAAG	TCACGCCCAT	CTCGGCCATC	CGGCACGAGG	360
GAAAGACTGA	CAGTGAGCGC	ACGGACACCG	CAGCCGACGG	GGAGACCACC	GCCACTGAGT	420
CGGACCAGGA	GGAAGATGCA	GAGCTCAAGG	CACAGGAGCT	AGAAAAAACT	CAAGATGACC	480

509

TGATGAAACA TCAAACCAAC ATTCTCGAG

(2) INFORMATION FOR SEQ ID NO:685:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 441 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:	
GAATTCGGCC TTCATGGCCT ACCAAAGTGC TAGGATTACA GGCGTGAGCC ACTGCGCCTG GCCTCTTTCT TCTTCTTGA ATTCTCTCT TTTTATGTTC CTGGGAAAAT CCTACTCATT TTATATGATT TGGCTGATGT AAAGCCACCA TTGTCTTCCT AAGCAGAGAG GGTCTTGCTT TTGGGTGCTG CACAACTTTG TGCAATTTTT CTGTTACATC ATTTATCTTT TGGGGATTGT TTATTTTCAT ACTTATCTCT CTTCCAGGAC CATGTTAGGG AGAGGTGTTT TTAATTTTTA CCTTTTCTGC AGCACTTAGC ACAGTGCCTA ATCATAGTAA ATATCACGTA AAAGTTGAAT GAAGGAATGG ATGTTTGATA TAGAGTTAGG ACACCTGTGT CCAGGTCTGG CTTTGCTTTT CCTTTNACCC CCCACCTCGA G	60 120 180 240 300 360 420 441
(2) INFORMATION FOR SEQ ID NO:686:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 273 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:	
GAATTCGGCC TTCATGGCCT AGTTGGTTTA TGTTATGTAA AGTTATGTAG TTATGTAAAG GTGCTGAAAT GTCACTCTTG TGATTATGTT TTATTATATA AGGCTCTATC TTAGCAAACC AGGAGAGAAA TTCTCCTGAT GGCCTTGAAG AAGCAAACAG CCACCTGGTT AAGCCCCTGT GGATAGTGCC AAGTGGCAGG AAAGTGGGAG CCACCTCTAG GACCTGAGGA TTAAAGTCAG TAAGAGCTGG GACCTCACTC ATGCAGACTC GAG	60 120 180 240 273
(2) INFORMATION FOR SEQ ID NO:687:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 124 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	60 120 124

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 426 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:	
GAATTCGGCC AAAGAGGCCT ATGCCATCTT AGTCCCTCTT CCCAACCCCA TTTTTTAGTT ACTTTCCTTT CATTAAAATA TCCTTATGCA CTTACAAATA AAACTAAGTC CCAAGAGGGC AACAAAATAT AAGATTCTTA ATGATACAAA AACAAATCTT TCTGATACTA GATCTTTTAT ACTAGAAAAA TAAATTCTTG TGCTTGAACA TCATTTTTAA GCACTTAGTG AATTGAGAAT CTGAACTGCC ACTTGAAATA TTCCCGGGAA AGAAACATTA TGAACCAAAT GAAGGAACAT AGCTATTCAA AGGGACATAT TTTTGTACTT GTTTTGCTCC AATTTCTGCT ACATAGACTG CTCCAGTCTT TCTGTCGACT CTAGGAGATG CCTAAACCGT CGATTGAATT CTAGACCTGC CTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:689:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 205 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:	
GAATTCGGCC AAAGAGGCCT ATAGTTTTTT CATGTTACAT CTTTTAGATT ATTTTCTTTT TAATCTATCT GTGACTATAT TTAAAGTCAA TTCTTGTTTT TTCCTTTTCC TTTTTGTGGG TAACGGGGTC TCGCTGTGTT GCCCAGGCAG ATCTCAAACT CCTGGGCTCA AGCTGTCCTC CCACCTCTGC CACCCTAGGC TCGAG	60 120 180 205
(2) INFORMATION FOR SEQ ID NO:690:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 100 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:	
GAATTCGGCC AAAGAGGCCT ACGTTGATTG AGCACTGAGC CCTTACTACG TGCTAGGCAT GGTACATGCA TGGCCTTATT TAATCCTATC AACCCTCGAG	60 100
(2) INFORMATION FOR SEQ ID NO:691:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 302 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

GAATTCGGCC	AAAGAGGCCT	ACATCATACA	AGTCGTCGTA	AAGCAAATCT	GAGCTGTTGT	60
CATTGGAAGG	CACTTTAGTT	TTGATGCAGT	ATTCCGCCAG	GGTTGTGGGG	ACCTTCACTC	120
CATCCTTTTC	TGCTTCGGCC	TTAGTGGCTG	AAACTTGTTT	CCTAATAATT	TCAGCATATT	180
CTTTGTCTTT	TCCTTTACTG	TCTCTCCATT	TCCTGAACAT	AACTGAAGCA	TCGACATTGG	240
CTGGGGAGAA	GGTGTTGGGC	TCATTAAGCA	GTGAGATTAC	ACTTAATAGG	ATAGTCCTCG	300
AG						302

- (2) INFORMATION FOR SEQ ID NO:692:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 662 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GAATTCGGCC	AAAGAGGCCT	ACCAAATACC	AGGCTACCAT	GGTCTACAAG	ACTCTCTTCG	60
CTCTTTGCAT	CTTAACTGCA	GGATGGAGGG	TACAGAGTCT	GCCTACATCA	GCTCCTTTGT	120
CTGTTTCTCT	TCCGACAAAC	ATTGTACCAC	CGACCACCAT	CTGGACTAGC	TCTCCACAAA	180
ACACTGATGC	AGACACTGCC	TCCCCATCCA	ACGGCACTCA	CAACAACTCG	GTGCTCCCAG	240
TTACAGCATC	AGCCCCAACA	TCTCTGCTTC	CTAAGAACAT	TTCCATAGAG	TCCAGAGAAG	300
AGGAGATCAC	CAGCCCAGGT	TCGAATTGGG	AAGGCACAAA	CACAGACCCC	TCACCTTCTG	360
GGTTCTCGTC	AACAAGCGGT	GGAGTCCACT	TAACAACCAC	GTTGGAGGAA	CACAGCTCGG	420
GCACTCCTGA	AGCAGGCGTG	GCAGCTACAC	TGTCGCAGTC	CGCTGCTGAG	CCTCCCACAC	480
TCATCTCCCC	TCAAGCTCCA	GCCTCATCAC	CCTCATCCCT	ATCAACCTCA	CCACCTGAGG	540
TCTTTTCTGC	CTCCGTTACT	ACCAACCATA	GCTCCACTGT	GACCAGCACC	CAACCCACTG	600
GAGCTCCAAC	TGCACCAGAG	TCCCCGACAG	AGGAGTCCAG	CTCTGACCAC	ACGACCCTCG	660
AG						662

- (2) INFORMATION FOR SEQ ID NO:693:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 321 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GAATTCGGCC	AAAGAGGCCT	AAGCCCCCAA	AACACGCTCT	TTTGTGCCTC	CCCTCAAATC	60
CTTCACAGTG	TTCTTCCATA	TCCACTCCTT	CCAGGAAGCA	TGTTCTCACT	ACCCCAGTTC	120
ATGTGGGTTT	CTTCCCTCTC	AGAATTTCTA	TCATGCCCCT	ATAAGTTTAG	CAAATTGTCC	180
TTCTCTAATT	GTTTCACATC	TGTCCATCCG	ATATCCCAGG	AGGACTGTCA	GCTCTATGAA	240
GGCAGGGGTT	GTCTTTCCTT	TACCATGCCT	ACCATGCCTT	ATAGTGTTAA	TAAATTAACC	300
TACCCAGAAA	TGTTTCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:694:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 357 base pairs

WO 98/45437 PCT/US98/06956\_

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GCGATTGAAT TCTAGACCT	CCTCAATCCC	CTCCCTACTT	GCTTTTTCTT	AGCATATAAA	60
AGTCCACAAG TTTTACTCA	CTTTTTAAAA	AACGAAAACA	TCCTTAGACC	GTGTCCTCCA	120
TTAGTTGCTA TCCTGCCTT	TTCTCTCAGC	TGAGCTGTCT	GAAACATGCT	AACATGCTTA	180
TACAATACTT GCTGTCCTG	CTTCTGCTCT	CAGCTGAGCT	CTCTGAAACA	TGCTAACATG	240
CTTATACAAT ACTTGCTGT	CTGCCTTCTC	CTCTCAGCTG	AGCTCTCTGG	AACATGCTTT	300
TTATACAATA CTTGCTGTC	TGCCTTCTTC	TCTCAGCTGA	GCTCTCTGGA	ACTCGAG	357

- (2) INFORMATION FOR SEQ ID NO:695:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 225 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GAATTCGGCC	AAAGAGGCCT	ATGGGTTTTT	AAAAATTTTG	TTTTTATTTT	TTCCTTTGAT	60
GTGCAGAGGC	TGTTTACTTT	GATGCAGTCT	CACTTGTTTA	TATTTTATTT	TGTTGCTGGC	120
CTAGGCCTCT	TTGGCCGAAT	TCGGCCAAAG	AGGCCTAGTC	GGGTGTGGCA	GTGCCATTCT	180
GCAGTCCCAG	CCACCGGGAA	GACCGAAGCG	GGAGGATCAC	TCGAG		225

- (2) INFORMATION FOR SEQ ID NO:696:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 3:14 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

GAATTCGGCC	AAAGAGGCCT	ATCCGCTTCT	GTTGCAGCTG	GCGGTGCTCG	GCGCGGCGCT	60
GGCGGCCGCA	GCCCTCGTAC	TGATTTCCAT	CGTTGCATTT	ACAACTGCTA	CAAAAATGCC	120
AGCACTCCAT	CGACATGAAG	AAGAGAAATT	CTTCTTAAAT	GCCAAAGGCC	AGAAAGAAAC	180
TTTACCCAGC	ATGGGACTCA	CCTACCAAAC	AACTTTCTGT	CGTTGTGCCT	TCAAACAATG	240
AAGAAAAACG	GTTGCCTGTG	ATGATGGATG	AAGCTCTGAG	CTATGTAGAG	AAGAGACAGA	300
AACGAGACCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:697:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 353 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

PCT/US98/06956 WO 98/45437

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GAATTCGGCC	TTCATGGCCT	ACAGAGTGTG	GACGGCCCAC	TGGGTTGGTG	GTGGTGGGTG	60
CCCGTCACAG	GGCTGGAGGT	GTGGCCGGCC	CACTGGGTTG	TGCTTTCTGC	CGTACGTCCC	120
TTCCCATGAG	GATGAGATGA	CCCATCTGTT	GCATCCCGGC	TGCTGATAAA	ACAAGACCCT	180
CGGAGCCAAG	AAACAACACT	GAGTTCCAGA	TTTCGGAAGG	TTCACGAGTG	TTGCCGACAC	240
GCCCTCCCAA	CTGCAGACAT	CCTCCCTGGA	GGACCTGCTG	TGCTCACATG	CCCCCTGTC	300
CAGCGAGGAC	GACACCTCCC	CGGGCTGTGC	AGCCCCCTCC	CAGGCCCCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:698:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 449 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GAATTCGGCC TTCATGGCCT	AGATTGACAG	AGGTCAGTTG	TCACTTCTTG	CCTCTCTCCC	60
CTTCCAGCAA CATGTATAAT	CCTGTGAGTG	TTTCTTCAGC	ACCCTTCTCT	GTTGTTTACA	120
CTACTGCAAG AGCCTCCCTA	AGTGGTCTGC	CTGTTTCCAC	CCTGTTGTCT	TGGAATTTAG	180
TTTTCTCGCA AAAGCCAGAG	AATGTTTTCA	GAAGGTAGCT	CTTGAGCAAC	TTCCCACTTT	240
CTTGGAGGGG AGATCCAGCT	TCCCCAACAA	GACCAGCAGG	CCCCTGTGCG	GCCTGGCTCC	300
TGTTCACCCT ACCAGTCTTG	GCTCAGGCTC	ACGGCTGGAA	TATGCCGAGC	TCTTTCTTGT	360
CCTGGGGCCT TTGCACTTGG	CTTCCCTCTG	TCCAAAATCA	TCTTCCTGTA	GCTTTGTGCT	420
TGCCTAGCTC ATCATCATAG	CAGCTCGAG				449

- (2) INFORMATION FOR SEQ ID NO:699:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 340 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GAATTCGGCC	TTCATGGCCT	ACAGAGAACT	GAGGAAAACC	AACTACGTGG	AGAATCTCAA	60
AGAAAAAAGC	GAGGGAGAAG	CTTCACTGTA	TGAAGATAGA	ATAATAACAA	GAGAGAAGGA	120
CATGAGGAGA	GTGAGAGATG	AGCCCGAGAA	GGTGGTGAAG	CAGTGGGACC	ATAGTGAGGA	180
TGAGAAAGAG	ACAGATGAGG	ACGATGAGGC	TTTTGGGGAA	GCTCTGCAGA	GCCCAGCAAG	240
CGGAAAGCAG	AGTGTGGAAG	CAGGAAAAGC	CAGAAGCGAT	TTGGGAGCAG	TTGCCAAGGG	300
CCTGTCAGGA	GAATTAGGCA	CAAGATCAAG	AGGGCTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:700:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 380 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GAATTCGGCC TTCATGGCC	r aagccaagca	AGGCTGTACC	TTTAATTACT	GCTGCCCTCA	60
TTTGCATCTG GCTGCCCTC	A TTATAGTGCT	ATTAGCAGAG	TGCAGGGGTC	CTCCTGCTGG	120
CCCATCGGGA GTGGTGCGT	G CACAGTTGTG	GGGCCTTGCT	TTGGTGGTCT	TTGCTGCCTT	180
CTGGGCAAAA TGAAGGATT	r ggagtagaca	GCAAGCAGGC	ATACATCCTG	GGCCAGAAGC	240
AGCCTGCGGA GCTCATCGT	G GCTTGCCTTA	AATTGTTTCT	CAACAATAAA	GTTGTTGAAA	300
AACAATTTGT GTTTTCTTT	C TCCTTATTAA	AAACCCAAAA	TTATATTCAT	TATAGAAAAT	360
TAAAGAAGAT AGCTCTCGA	3				380

- (2) INFORMATION FOR SEQ ID NO:701:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 319 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCAGCCTCCC	AAAGTGCTGG	60
GATTATAGGC	GTGAGCCACC	GCGCCCAGCC	GAAAATCTAA	AGATATTGAA	AAGATACAAA	120
GGAGCACATT	ATGAACATTT	TTTTCGTATC	ACTGAGTATT	TTATAACTGC	ATCATTGATT	180
TTAAAAGAAT	TCATGACTTT	GAAAACTAAT	ATTCTACAAA	GTAGCTTTTG	ATTTAACATG	240
AGATTTTATA	TATGTGCTTA	TCTTGGTTCT	CTATGAAACC	CCATTGAAAT	AAGAAAATGT	300
AAACACCAGC	CAACTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:702:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 549 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GAATTCGGCC	AAAGAGGCCT	AATAGTCAAG	ACCTTTGCAG	TTTTGATCAC	AGAAATATGA	60
AAGATTACAC	AGCTACAGCT	ATATGAATGA	TAAAAGTGAC	AGCTATGGAT	TTTTAAAGTT	120
ATAAGTTGCT	ATACTACATA	TATGTAATGT	GTGTGTGTAT	AGTGTGTAGG	TATATATATT	180
TATATTTATA	CACACACTAT	ACATGTATTT	TAAAATATTG	AAAATCCAGA	ATTATTTAT	240
GGTAAAAATT	ACTAAAATTG	ACTTCACATG	CTGAATGAAG	AGAGCCTGAG	TAGACCAACA	300
AACAAATGAA	AAATTAAGAC	GGTTAGAAGA	TACGCTTTCT	AAAAGAATAC	ATTTAGAATC	360
TAACTTTAAA	TAAAAAAAA	CCTACTCTCC	TGAGCCAGAG	TGGTCTCAGA	GAGACTCCGA	420
GAACCTAATT	TTTTACAAGT	AAAATCTTTG	AAGAATTGGT	AATTGCTAAA	TTTTTCCAAC	480
ATACTATTCT	ACAAGACTAA	CCTAAAACTG	ATTATAAGAA	CTAGGTGAGG	AGGGCCGGCA	540
AAACTCGAG						549

- (2) INFORMATION FOR SEQ ID NO:703:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 758 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAATTCGGCC	AAAGAGGCCT	ATCGAGCCAC	TGCACCTGGC	CGATGTGTTC	TGTTTGAAAT	60
CTTACTCAAA	AGTATTTGAA	GAGTTGTGTA	TAGTTGTATG	GATATGTCTG	TAGTAAACAG	120
AAACAAATTG	CTTCAGTTTC	TCTTTACTTA	TTTTCTAGGT	TACAGTACCT	TTACCAGCAT	180
CCCAGCTTTC	CTTGCCTAAT	TTTGGATCTA	CAGGGCAACC	TCTAATTGCT	TTGCCTCAGA	240
CTCTTCAGCC	CCCATTACAG	CATACCACTC	CCCAAGCACA	GGCTCAGAGT	CTGAGTCGTC	300
CTGCACAAGT	AAGCCAGCCT	TTCAGAGGAT	TAATTCCTGC	TGGAACACAG	CATAGCATGA	360
TTGCAACCAC	CGGAAAAGTA	AGTAAAGAGA	CATTTGCACA	GGTTATTTGĄ	GAATTTAAGG	420
TAGTGTGTTC	AGATATATGC	ATCTGTGTTA	TCTAAAAAAC	TAAAATGCGT	CAGTTTTTAC	480
CACCCTGCAA	AAATCTCAAA	CCCCAGTATA	TTTACATTTT	ATCTATTTAC	TTTTAATGTG	540
TTTGGCCCCA	TCTAGTTTTT	ACCTAATAAC	AAAGAATTCA	CAAATTTATT	GGAAGAATTG	600
GATTTATAGT	GTCTCTTCGG	CTTATTTAAT	TATAAGTCTG	TTTGGTCAGG	TAATTCCATA	660
ATACTTGAAG	CCTAACTATA	GGAGTTTTGT	ACTAAGGTTC	TTTGCCCTTT	CCTAGATTAC	720
GTCTTCACGT	ATAGGACATG	TAAACACAGC	AACTCGAG	•		758

- (2) INFORMATION FOR SEQ ID NO:704:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 663 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GAATTCGGCC	AAAGAGGCCT	AAGATGGCCT	TCCCATGTTA	TGGCTACATG	GCTGTGATAA	60
CAAGTAGAGT	TATGTGTCTG	CGCTCTAAAC	TCACTGAGTC	TTGCAGGATG	TAAACATCCT	120
AGCTCAGCCT	ATCCTTGACC	AAAGCACANT	CATGCTCCTT	ACAAACTCCA	ACCAGCCTGC	180
ACACTGGGAG	GAGCGCGTGC	TGGGCTAGAG	CCACAGAATT	TTGTACCGTT	GGCAGCAGGG	240
AGGAGCCTGG	CCCCTCCTTT	CCTAGGTAGA	ATCTGGAATT	CAATCTGTGA	GGTGGGAAGC	300
ATATACTAGG	AGGACTTTCA	CTCTGCTGAG	TCCCTGTTCC	CCCTCCCTTT	TTTTTCCTTT	360
TTGCCCAATA	AACCCCTTTA	TTCTCACACT	TCAAATTGTC	TGTGAGACTA	ATCTTTTGTG	420
GCCATGTGAC	ATGGACCCTG	TCTGTAGCTG	AAACTAAGAA	AAAGCCCCTC	CCGCACAGTC	480
TGATGTTTCC	TCAGTCAGAC	ACTGCAAGCT	GTGATGTTGG	GGTGAGTACA	GGATATTTGG	540
CAATATTTGC	AGACAGTTTT	GGCTGTCAGA	GAGGAAGATG	CTGTATGCAG	ACACACTTGA	600
CAGCAATAAC	TTAAGCCCAC	CCTGAGACTG	ACTCTGCATG	GTGATGCACC	TGAAGGCCTC	660
GAG						663

- (2) INFORMATION FOR SEQ ID NO:705:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 334 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GAATTCGGCC TTCATGGCCT AGAGCGATGT CAAGTGATCT GCCCGCCTCA GCTCCCCAAA

GTGGTGGAAT TACAGGCGTA AGCCACTGCG CCTGGCCCCA AGTGTCCATT TTTTAATTTA	120
GTAATTCTAA CCTAGGTATT TTTCCTGCAG TACAAAATGA GGATAAAGCT TTACATGAAA	180
ACATGTTGTT CCTATTATGT TTATTGCAGC AAAAACACAA CCTAAAAACC CAATCTGAGC	240
AGGTTTTAAC TAAATACTAA TAATTCTGAC ACTAGAACGT TATGTAGCTA ACAAAAATAT	300
GTCGTAAAAA TAATCATGTA GAAACTGGCT CGAG	334
(2) INFORMATION FOR SEQ ID NO:706:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 369 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:	
GAATTCGGCC TTCATGGCCT ACCGAGCTTC AGAGCATCAG CAGTGTTCCT CCTTCACTGT	60
GACGCTTGTC CTCACTTCCC AGGTGAGGAG TCTAAGAAAA CAGCCTTTCC ATCAGCCCCT	120
GTCGTGACAG ACCCTCCAGT GGGATGGTAG TGGCTGCCTC ACCCATTTAC AGGGCAACCC	180
AGTTTTGCTC CTTCTGCCTT GAAATTTGTT CCTCCCAGAA ACTGTCCCTC ACAAGGCATG	240
AACAATCAAT AGAAGATATA CGTGGTCTTC CCAGCACTAC AG&TGCAGAA TGAGCTGTGG	300
AGTGCCCCGT CCGGAGTCCT GAACAGCTTC AAACTTTTCC CCTTTAGAAA TGCCTAACAC GCCCTCGAG	360 369
GCCCTCGAG	205
(2) INFORMATION FOR SEQ ID NO:707:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 365 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:	
GAATTCGGCC TTCATGGCCT AGGCATCCTT GGTGCGGCAT CCTTGGTGCA TTATATCAGG AGGCAAATGA TGTGGGTTTG TCCCATTGTT TGTAATGGTA ACATTGGTTG CTTGGTTAAG GTGAAGGGTG CCAAGCTTCT CCACTGTAAA GTTCCTATTT TTTTCTCTGT AATTAATAAG TAATTTGTAT GATACTTTGA GATAACAAAG TAGACTGTTC ATCAAAACTTT CATCAATGAA TTAACCATCC AAAGACGCCT CAAGAATGAT CATCAAAAGC AGCCTACTAA TGACTGTCAT TACCATTTA ATACATTCA AACAGTGCAC GTGCTCTGTG ACATATTCTG GGAAGGAATC TCGAG	60 120 180 240 300 360 365
(2) INFORMATION FOR SEQ ID NO:708:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 436 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:	

60

GAGCAAAGAG	CATGAGAAGC	TGATGGAGGG	AGAACTTGAA	GCTTTGCGGC	AGGAATTTAA	120
AAAGAAAGAC	AAGACGTTGA	AAGAGAATTC	CAGAAAGTTG	GAGGAAGAAA	ATGAGAATCT	180
CCGAGCAGAG	CTACAGTGTT	GTTCTACACA	ACTGGAATCC	TCTCTCAACA	AATACAACAC	240
CAGCCAGCAA	GTCATCCAAG	ACTTGAATAA	AGAGATAGCC	CTTCAGAAGG	AGTCCTTAAT	300
GAGCCTGCAG	GCCCAGCTGG	ACAAAGCTCT	GCAGAAGGAG	AAGCACTATC	TCCAGACTAC	360
CATCACCAAA	GAAGCCTATG	ATGCATTATC	CCGGAAGTCA	GCCGCCTGCC	AGGATGACCT	420
GACACAAGCC	CTCGAG					436

- (2) INFORMATION FOR SEQ ID NO:709:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 383 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GCTGCTCTAT ATCTTAGAGA	AAATAAAAGA	ACCACATGTT	GCTTCCCTGC	CTGCAAGCTC	60
TTCTGAATTC ATCACCATTC	ATGTTCCTTC	CTTCAGGGGA	AATGAAGGCA	GATTGTTCTG	120
TTGGTGCTCA CAGATCTCTT	TCTGTTCTGA	TACCCTCCTC	TTCCTCTCCT	GCTTCTTTCC	180
CTTCATCATG TGCTCCTATA	CAAGTCTCTC	CCAACTTTAA	AACAAAAACA	AACCCTTCCC	240
TAAATCTTGT GTTTGTTCCA	GCCATTAGAC	TGTATCGTCC	TTGCCATCCA	CGTTATTGGA	300
AGAAGGCCAG CTCACCTCTA	CTCCCTTTCT	GCCCTTTCCC	TCTTAATCTG	CTGTCCTCTG	360
ATTTCTGCCC CCACAAACTC	GAG				383

- (2) INFORMATION FOR SEQ ID NO:710:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 496 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

GAATTCGGCC TTCATGGCCT	AGGGGCCTGA	AGATCTTCGG	GTATTTGGCT	CCCAGAATCT	60
GACCACAGTG AAGCTAAAAG	GGGTGGGTGA	CAGCTTCAAG	AAGTATCCTG	ACTACGAGTC	120
CAAGGGCATC AAGGCTCACT	TCAACCTGGA	TGAGAGTGGC	GTGCTCAGTC	TAGACAGGGT	180
GGAGTCTGTA TTTGAGACAC	TGGTAGAGGA	CAGCGCAGAA	GAGGAATCTA	CTCTCACCAA	240
ACTTGGCAAC ACCATTTCCA	GCCTGTTTGG	AGGCGGTACC	ACACCAGATG	CCAAGGAGAA	300
TGGTACTGAT ACTGTCCAGG	AGGAAGAGGA	GAGCCCTGCA	GAGGGGAGCA	AGGACGAGCC	360
TGGGGAGCAG GTGGAGCTCA	AGGAGGAAGC	TGAGGCCCCA	GTGGAGGATG	GCTCTCAGCC	420
CCCACCCCT GAACCTAAGG	GAGATGCAAC	CCCTGAGGGA	GAAAAGGCCA	CAGAAAAAGA	480
AAATGGGGAA CTCGAG					496

- (2) INFORMATION FOR SEQ ID NO:711:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 475 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

GAATTCGGCC	TTCATGGCCT	AGTATGGAAG	GTGGAACTAA	AACTGAAATG	ATCAGTTCAC	60
ATATTTGTAA	ACTGCGTATT	TTATATCAGT	CGCTGGATTA	GGCCCCTAGA	GACAGTGGTG	120
GCTAAGTGAT	AAAGTCTTTG	CGCTTGTGGC	ATTTTATAGT	GTAGTGGGAA	GACAGAAAGC	180
AAACAAGTAG	AGAATCATAT	ATGTAATGTG	ACCTCAGGTC	CAGCTAAGCG	CCAGACAGAA	240
GAAAAAAGTA	AGGTGAAGGT	AGAGGGGTTG	GAGCAGGAGG	AAGGTGTTAT	TTTAGGTAAA	300
GTGGCCAGGG	AAGGCCTTTT	GAAGAATTGA	TATCGATTCC	AAAATGATGA	GAAGGTGCAA	360
TTGTGCCACC	ATGGAGGAGA	AGAGCTTTCT	AGGCAGAGGG	CAGGTGCAAA	GATGGTAGGA	420
ACAAACACGG	CTTGTTGAAA	GAACAGCAAT	GTTTGAGGAA	TGAGCCAGAC	TCGAG	475

- (2) INFORMATION FOR SEQ ID NO:712:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 608 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

GAATTCGGCC	TTCATGGCCT	AATTTTGCAT	AAAACCTCAT	CAATCTCTGC	CAATCACTGA	60
GCCCAAAACC	ATTTTCACTT	TGTTTTAGGT	ATTTATAATA	ACAGCACTCC	CACTTCTCAT	120
GATCAATTTC	CATCTTCAGC	GGTTCAGGCT	GCTTTAATAA	AGTTCCATAA	CCTGAGTGGC	180
TTTTAAATAA	CGGAATGCAC	ATCTCACAGT	TCTGGAGGCT	GGAAGTCCAA	CAGCAGAGTG	240
CCAGCATAAT	TGGGTTCTGG	TGAGAGAGCT	CTCTTGGGTT	TCAGACTGCT	GCCTTCTCAA	300
TGCAGCTTCA	CATGGTGGAC	AGAAAGAGCT	CTCAAGAGTC	ATTTTTAAGG	GCACCAATCT	360
AATTTATGAA	GCCTCCACCA	TAATAAGCTA	ATTACTTCCC	AAAGTGCTGA	GATTACAGCT	420
GTCAGCCACC	GTACCTGCCT	GGGAATTTTT	TTAAAGCTCA	AATTGGATAA	GAGGGTTATA	480
GGAATATATT	CATCTATCAT	ATAGAAAAGA	ATATGTGCTC	AGTCCCAGGA	AATAGAAAAT	540
ATATTACCTT	ATTTATACTG	TTTTAATTAA	TGCTTTTTAA	AATCTGATTA	ACTCTGGGAG	600
AGCTCGAG						608

- (2) INFORMATION FOR SEQ ID NO:713:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 531 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

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GAATTCGGCC TTCTTGGCCT AGTGCACTCC TGTAATCCCA GCTACTCGGG AGGCTGAGGC
                                                                       60
AGGAGAATCA CTTGAACCCA GGAGGTGGAG GTTGCAGTGA CCCAAGATCA TGCCACTGCA
                                                                      120
CTCCAGCCTG GGTGACAGAG CGAGAACGTC TTTAAAAAAAA TTAAAAAAAA AAAAAAAAAGA
                                                                      180
TTGCACAAAT CAGACAGTGA CCCAGAGCTC AGCCTTGAGG AAAGTCAGTG TTGGGGAGGG
                                                                      240
GAGGGCAAAG AAGCAAGTAA AGGTTTAGCA GACATGGCAC CTCAGTCTGG ACTTGAAGGA
                                                                      300
GGGCTAGGCA CAAAGGAAGG GGAACATGTC AGATGAGAAA CACGTGAAGG TTCAGCCAGA
                                                                      360
TGAGCAAGGA AGGTTGGTTA GAAAGAGGAG CTGCTGGTGT GGCTCCTGTG AACACAGGTA
                                                                      420
GATAGGGCAC GATAGAGTCA GGCAGTTAGA AGCCAAGCTG AGGAATCGAC ACTTGATTCC
                                                                      480
ATAGGTAAGT AGGGGAACTT GAGGATGTTT AATCAGAAAT GAGATCTCGA G
                                                                      531
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(2) INFORMATION FOR SEQ ID NO:714:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 499 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GAATTCGGCC	TTCATGGCCT	AATTTATCCC	ATCCTTATCC	CATCCTTATA	AGGAATAATG	60
TATTGAATAA	AGATTGTATC	AGTATTTGTA	ATTCAATAAA	CCAGAACTTG	TGGAAATAAA	120
TATGTAGGAG	ACATAAATAT	GGTGTCCTCA	AATTGAATTA	TGTGGGAAAA	AAGTGGGGTG	180
GAGTTAAAGT	CCAAGCCAAT	AAAGTTGTAA	CATTAAAGAA	AGACAGGTAT	GGGATGCAAG	240
GTGCAAAGAA	AAGGTCATCA	TATCTCATAC	TGGGGTGAGA	TAGAAGACTT	CCTGAAGTAG	300
GCGATGCCTA	TATTGAATCT	ATAAGGACAA	ACTGGCATCA	ATATGTCAGG	GAAGACAGGT	360
TGAAGGTGGT	CCTGCCAGAG	AAAGGAGCAA	GGATAAAGGC	AAGGAAGCAT	GTAACGTAAT	420
TGTTTGTGGA	GAAACCTCAA	ATCGGCTGAG	GAAAAACGAC	TCAGGTATGT	AGTAGGGCAC	480
AGTATAAGTA	GGTCTCGAG					499

- (2) INFORMATION FOR SEQ ID NO:715:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 430 base pairs
    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GAATTCGGCT	TCATGGCCTA	GAGATTTAAT	GTTCCCTTAC	CTTGCTGGAG	GAACATCAAT	60
GTTGGAGGAA	ACAACTTTTC	TTTTTTGCTC	AAGGAGACAG	ATGGAGCGAG	TGTTTTCTTT	120
TTCATGGTCA	AGGATCCGGC	${\tt TGGCTTTTTT}$	GGTGTCTGCT	GTTTTCACAT	CTTCCTCCAT	180
GGCCAAGGAA	AACACGTGTT	GATGAGACAT	TTTTTTACCA	CAGTCACGTT	TTAAGTCCTC	240
TGACTGAAAT	GTGAAGGTCA	TTTCCCGCTT	AATGCTCCCC	ACCTGTGAAA	TGAAACACAG	300
AAATTCTTAC	TCACATAAAA	CATCACCTTT	GTACGACTAC	TGCAGATGGC	GGTGAGGAGA	360
GATTACAGAC	ACTGTCCTTC	CTGTTCATCT	GAAAGATTGT	ATAATTTTAA	TAAGAAAAAT	420
GCAACTCGAG						430

- (2) INFORMATION FOR SEQ ID NO:716:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 471 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

GAATTCGGCC	TTCATGGCCT	AGACCTTCTG	GGTGAACGAG	GGCAAGCACG	CCAAGTTCCG	60
CTGCTACGTG	ATGGGCAAGC	CCGAGCCCGA	GATCGAATGG	CACTGGGAGG	GCCGCCCGCT	120
GCTCCCGGAC	CGCCGCCGCC	TCATGTACCG	CGACCGCGAC	GGCGGCTTCG	TGCTCAAGGT	180
GCTCTACTGC	CAGGCCAAGG	ATCGTGGGCT	CTACGTCTGC	GCCGCGCGCA	ACTCGGCGGG	240
CCAGACGCTC	AGTGCCGTGC	AGCTGCACGT	GAAAGAGCCC	CGCCTCCGGT	TCACACGGCC	300
CCTGCAGGAC	GTGGAGGGCC	GTGAGCACGG	GATTGCCGTG	CTGGAATGTA	AAGTACCCAA	360

PCT/US98/06956 WO 98/45437

(2) INFORMATION FOR SEQ ID NO:717:

CTCCCGCATC CCCACGGCCT GGTTCCGTGA GGACCAGCGG CTGCTGCCCT GCCGCAAGTA CGAGCAGATC GAAGAGGGCA CTGTCCGGCG CCTCATCATC ACAGGCTCGA G

420

<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 397 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:	
GAATTCGGCC TTCATGGCCT AGCCACTCTT AGCAACACAG ATTTTCTTCC AAATTATGCC TTGAAGCTGC TCCCGGAGCC ACCCGCTCAT CAGCACCCTG CTCCTGTGGT CCTTCTCGTG AAAGGCAGGA GGGAGATGCC TGTTGCCCGC AGCTCTCTCT GCAGCTGCCG TGGGAACAGG CACCATGCCA CTGCAGAACA TTTGTTTGTT TTTAGATCCC ACGTCTGACG GTTTAGAACA CATGGTTAAA CATGTTTACA AAGCAAGGGA GACATCTCTT ACCTTGACAA CACGAGGCCT CCACAGACCG CCTTCCCCCA GCTCGAG	60 120 180 240 300 360 397
(2) INFORMATION FOR SEQ ID NO:718:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 539 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:	
GAATTCGGCC TTCATGGCCT AGAAGGAAAG AAATTTTATG TGAGAGAGCA TCTTGTATGG CAAATTCTTG TCCTAAAGTA GAATGACTAG GAAAGACAA AATATAGGAC AAGTCAGAAA GTCATAAGAT GGGAAAGAAA AACTTACAAC TGCTAGATCT TCTCCTGTCT AGAAGTGTTG TGTGTGTGT GCTTATATGA AGGTACTCTA ATTAATTGGA TTAAGAGAAA ATGAAACCCC ATCTCTACTA AAATACAGA ATTAGCCGGG TGTAGTGACA CATGCCTGTA GTCGCAGCTA CTCAGCAGGC TGAGACAGGA AGATAACTTT AACCCAGGAG TTGGAGGGCTG CAGTGAGCCA AGATCGCGCC ACTGCACTCT AGCCTGGGAG AGACAGAGCG AGACTCCGTC TCAAAAATGA AAAAGTAGAG CCTGGTAGAG TGAAGCCACT TGCAGGAGTC GTTTAGTTAG GGCTGTGTTG CCTTACAGTG CTGGTGCCT CACAGATGAT AATAGTAATA AAAAACACCA CAACTCGAG  (2) INFORMATION FOR SEQ ID NO:719:	60 120 180 240 300 360 420 480 539
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 387 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:	
GAATTCGGCC TTCATGGCCT AGGCAGTGGA TAATTGTCCT CTGGAGGAAC CATCTGTGAC ACATTCTACA TGGTTCCTTA GAGGGTCCCC AAGTGGGATT GAGTCCCTCT TGTTCCTAGC	60 120
330	

AGTAAGCAGT TCTGTTATAC ACTCTTTATA TGCTTTTCCT CCTTTCCTCT CTCAGTCTCT CTGATCCTTC CACCTGTGCT CTGGGTTCAC CTCTCAAGTA AACCACCTGC ACACAAGTCC CTGTCTCAGG CTCCATTTGG GGAAACCAAA CTAAGACACC ACCTCAAAAC ACAGAATTTC ACGAGGCTCC AAATGCCTCA GAAAAGTAAT GTAAATATAA AATGACCAAT TTTTTGAAGT ATATTAATCC TAGTTATTTA ACTCGAG	180 240 300 360 387
(2) INFORMATION FOR SEQ ID NO:720:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 239 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:	
CCCGTGTATA GTTTGCAAAT ATTTTCTCCT CTTCTGTAGG CTGTTTACTC TTGTTGATAG TTTCTTTTGC CATGCACAAG CTTTTTGGTT TAATTAGATC CCATTTGTCA ATTTTTGCTT TTGTTGCAAT TGTTTTTGGC GTCTTCATCA CGATATCTTT GCCAGTTCCT ATGTTCAAAA TGGTATTACC TAGGTTGCCT TCCAGAGTTT TTATAGTTTT GGGTTTTTAT TTACTCGAG	60 120 180 239
(2) INFORMATION FOR SEQ ID NO:721:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 323 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:	
CTCGAGCACT ACCCTAGACG GTCTCATCAC TATACTGGCT CCTCCTTACC CCCGTAAATC TCCCAGGTAC ACTTCCTGAT CACCCTCCGG ATACCTCATC CCTATCTATT CCTTTATAA ATAATTCCCT GCTCCTCCTT CTCACCCACA ATCCACTCGC AGTTCAAGGC CTCACTGCCA TCGACTCCAC TGTCTGTGAG TGCTTCCCAA TATGCCCCAG GACCCCTCCT GGTGTCACGC TCTGTATCCT GACACCCCTT GTAGACGAGT CCCGAAATTC CCGCCCCGTC CCTGGAGCTC CCTAGGCCAT GAAGGCCGAA TTC	60 120 180 240 300 323
(2) INFORMATION FOR SEQ ID NO:722:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 275 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:	
GAATTCGGCC TTCATGGCCT AGGCCTGTGG AGCCCCAGCT CTGGGTCCCT AGCCCGGGTC CAGGCAGCCA GGCTCCCTCC TGAGCTGAGA AACGGAACCT CGCGAACCAC TGGTGGCACA TCCTTCTCCT CCCCCGCCCC TGATCACCCG CCCCCGGATC AGAAATATAT CTATATTCTC GACTAAAGTC TCATCAGGAA ATATTTCCTG TCTTTTATTT TAAGCATCAA ATTGTTTTAG	60 120 180 240

TTGATTTAAA AAGGAAAAAA TACAGACGAC TCGAG

275

## (2) INFORMATION FOR SEQ ID NO:723:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 317 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GAATTCGGCC	TTCATGGCCT	AAGAAGCAAC	AATCATATTA	GCTGGGGGAG	GAGGATAGTT	60
TGGTATTTTT	GTAGTTTGCA	CAGTGACCTT	TTTAAAAATC	TGGTTAGGCA	AAAATAGTGT	120
GATCTTGTTT	GTTGTCTCAC	TTCATTATGA	TCACAGAATG	ACCTGGTATG	ATGTTAGTGT	180
TTTATGAGAG	TGTTATGTTT	TAACAGGGGA	ACACCGCAGT	CAATTCCTAA	CAACACTAAA	240
GTGTCAGTTC	TGTTCGTGAC	ACCAAGGGCT	GTTTTTCTTT	TTCTCATATA	ATGTTGAGGC	300
AACCAGGAAG	ACTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:724:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 267 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GGCCTCAGCA	GGTGTGAAGC	GTGTGCTTTA	GTTTCGTGGG	AGGCCTGGCA	TCCCCGAGAG	60
GGAGGGGAAA	GGTAACCACT	CCTTTGTGGA	GGTCGCCAGG	GTCATTGTCG	TGGATTTGCA	120
CAGTCGGCTG	GGCGGTGCAA	TGGCGGAAAG	AAAAGGAACA	GCCAAAGTGG	ACTTTTTGAA	180
GAAGATTGAG	AAAGAAATCC	AACAGAAATG	GGATACTGAG	AGAGTGTTTG	AGGTCAATGC	240
ATCTAATTTA	GAGAAAGCAG	ACTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:725:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 354 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

GAATTCGGCC	TTCATGGCCT	AAGTCAGTGG	TAAGCCGCAG	CAGTTTCCTG	CCACTCGTAA	60
TATGGCAATT	AAAAATTTTA	AATTTGTGGC	TGCTTGGGGT	CTGGGAGGTG	ACCTGCTCCT	120
CAGCAAATTT	TGACTGATAA	ATTAATGCCT	GGGTCTTCAG	CCTGGTTCTT	TGCTGGCCAG	180
TGTGACAACA	GTCTGTCACG	TCTCTGGGGG	CACATTATAA	TTAACAGATG	TAATCTTTCT	240
CCGGTTCAGG	GTCATCTGTG	AATCAGGGGT	ACTGCCCCAG	TAGAACTAGG	AACATCCAGC	300
AAAAGACTGT	TTTCAAAATA	TACAATTAAG	TGAAAAAAGC	ATGAAGAACT	CGAG	354

- (2) INFORMATION FOR SEQ ID NO:726:
  - (i) SEQUENCE CHARACTERISTICS:

PCT/US98/06956 WO 98/45437

(A) LENGTH: 154 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:	
GAATTCGGCC AAAGAGGCCT AGAGGTTGAC CTGAAAAACA ATGAAACACA TGAACACACT TCCGATTTTC TCCTCGCTGA TTAGCTTCCT GCCTGCTGTC AGTGCTGGAC GAAGTGCTAT AACTACTTTA TGTAACATTA CAGAACAGCT CGAG	60 120 154
(2) INFORMATION FOR SEQ ID NO:727:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 338 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:	
GAATTCGGCC TTCATGGCCT AGTGGGAAGA TGTGGATGAT GAGAAGGGAG ATAGCAATGA TGACTATGAC TCTGCAGGCC TATTGTCAGA TGAAGACTGT ATGTCTGTGC CCGGAAAAAC TCACAGAGCT ATAGCAGATC ACTTGTTCTG GAGTGAGGAA ACAAAGAGTC GCTTCACGGA GTATTCGATG ACTTCCTCAG TCATGAGGAG AAATGAACAG CTGACCCTAC ATGATGAGAG GTTTGAGAAG TCTATTCAAG TAGACAGCAC GACTCGAG ATTGGAAGGT TCTATTCAAG TAGACAGCAC GACTCGAG	60 120 180 240 300 338
(2) INFORMATION FOR SEQ ID NO:728:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 433 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:	
GAATTCGGCC TTCATGGCCT AATTGAATTC TAGAACTCTC CCAGAGAAAC CAGGCAGATA CTGCTCCACA CCGGTGAGCT GCTTCTCACC TGGGTAGTCT AGGGTGGTTT GCTCCAGAAT TGTATTTCTG CTTTTTCTTT TTTTAACTTG GCAGTGGTTA ACCATTCCCT GGAGCAGCAC CAGGTAGGTC AGCTTGTATC AGAGTCATCT GCTTTACCTG ACATGAGCAC ACGTTGTCAT ATATTTGCAC ATGCAGATAT CATATGTTAA ACAATATCAC ATTGTTGAAG TGGAAAGCGT AAAATATAGT TTGGATGCCA TATTGAGTGT AACTTAATCC ACCCGATTCA GAACTTTTGT AGAGTGCCTC GGAGTTCCTA TTTGGAAATA TCAGTTAGCA GTTTTAGTCA GTAGAGACTC GAG	60 120 180 240 300 360 420 433

- (2) INFORMATION FOR SEQ ID NO:729:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 315 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double

(D)	TOPOLOGY:	linear
(D)	TOPOLOGI.	1111041

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

GAATTCGGCC	TTCATGGCCT	AACAAGAAAC	ACCAAGTACC	TCGACCTCAA	GAATTCACAA	60
GAGATGCTCC	GCTACAAAGA	GGTCTGCTAC	TACATGCTCT	TTGCCCTGGC	TGCCTACGGG	120
TGGCCCATGT	ACCTGATGCG	GAAGCCCGCC	TGCGGCCTCT	GCCAACTGGC	TCGGTCCTGC	180
TCGTGTTGCC	TGTGTCCTGC	GAGGCCGCGG	TTCGCCCCTG	GAGTCACCAT	CGAGGAAGAC	240
AACTGCTGTG	GCTGTAATGC	CATTGCCATC	CGGCGCCACT	TCCTGGACGA	GAACATGACT	300
GCGGTGGGAC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:730:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 156 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GAGTTGTCTC	TCTGAATTAA	CTTTCTCACC	AATAGCTCCT	CTTTAAGATC	AATAACTCTT	60
ATGTTTGCAC	TTTTTAGGCT	ATTTTCTAGA	TCTTGTATGT	GTGTCTTATT	ATTTTTTATT	120
СТТТТТСТСТ	CCTCTGTGAA	TTTTCAAATA	GTCGAG			156

- (2) INFORMATION FOR SEQ ID NO:731:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 223 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

GAATTCGGCC TTCATGGCCT	ACTTGAACCT	AGATCTCACC	CCCAGGATGT	TGCGGAGGCT	60
GCTGGAGCGG CCTTGCACGC	TGGCCCTGCT	TGTGGGCTCC	CAGCTGGCTG	TCATGATGTA	120
CCTGTCACTG GGGGGCTTCC	GAAGTCTCAG	TGCCCTATTT	GGCCGAGATC	AGGGACCGAC	180
ATTTGACTAT TCTCACCCTC	GTGATGTCTA	CAGTAACCTC	GAG .		223

- (2) INFORMATION FOR SEQ ID NO:732:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 309 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

GAATTCGGCC	TTCATGGCCT AAATTATTGC AAAGT	STATA TTGGTTAAAA	AAAAAAAGGA	60
GGAAGAGGCA	GTTTTCATG ACGGTTAAAA GTGCA	GGATT TGGAGTCCCA	TGGTCCTGGG	120
TGTGAATCCT	GGCTGTGGCA CTAACTATCT GTGTG	ACTGG CTGTGAACCT	CTCGTGCCTC	180 240
ACTTTCTTCA	TCTGCAAAAT GGGTAGTTGT ATAGC TTGGAAGCAC TCAGTAAATG TTAAT	AAATG CACATAGAGA TGTTA TTATTGTTGC	TCTAAAGAGA	300
ATCCTCGAG	11GGAAGCAC ICAGIAAAIG IIAAI	IGITA TTATTOTTOE		309
ATCCTCOAC				
(2) INFORMA	TION FOR SEQ ID NO:733:			
(i)	SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 275 base pair	S		
	<pre>(B) TYPE: nucleic acid (C) STRANDEDNESS: double</pre>			
	(D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:733:		
GAATTCGGCC	TTCATGGCCT AGATTAATTC TAGAC	CTGCC TCAGCTCCAC	TCCTTATGGT	60
TTGCCACCAT	AACCTACAAC ATTTGTCCGT CCACC	CCACG TGTCTTCTTC	CTTTGTGGCA	120
GGAACTCTTA	TCTCTGCCTA CCAACCAATT GGTCA	GGAGC ATGCACCCTA	GTGTCTCAAT	180
	TAACATCCTG CCAAACAACC AGACC		GTGACCCCTA	240 275
TCTCATCCTC	TTCCACATGC AGTAGGCAGG TCTAG	•		2,3
(2) INFORM	ATION FOR SEQ ID NO:734:			
(i)	SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 250 base pai: (B) TYPE: nucleic acid	cs ·		
	(C) STRANDEDNESS: double			
	(D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			·
1	SEQUENCE DESCRIPTION: SEQ	ID NO.734.		
(X1)	SEQUENCE DESCRIPTION: SEQ	1D NO. /54.		
	GGCACGTTTC CCACAACTGC GAAGA	ACCCCC TCACCCAATT	CTGCAAGAAG	60
ATTTTGGGGT	TTTGGAAAAG AAGCTATGGA AAACC	GAGGG GCAGGCACTO	TGCAGATAAG	120
GCAAGTCCTG	CTTTTCTTTG TTTTGCTGGG AATG	CTCAG GCGGGCTCTG	AAACTGGGAA	180
CTTTTTGGTG	ATGGAGGAAT TGCAGAGCGG GAGC	rttgta ggaaatttgo	CAAAGACCCT	240
GGGACTCGAG				250
(2) INFORM	ATION FOR SEQ ID NO:735:			
(i)	SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 324 base pai	rs		
	(B) TYPE: nucleic acid			
	<pre>(C) STRANDEDNESS: double (D) TOPOLOGY: linear</pre>			
	(b) Topologi: Timear			
(ii	) MOLECULE TYPE: cDNA			
(xi	) SEQUENCE DESCRIPTION: SEQ	ID NO:735:		
ርል <mark>አ</mark> ሞሞርርርርርር	TTCATGGCCT ACACAGACTG GGCA	ATTTAT AATGAACAG	A AGTTTATTTG	60
GCTCTTGGGT	CCAGAGGCTA GGAAGTCCAA GAGC	ATGGTG TCAAGCATC	A GGTGAGGATC	120
ATCACCCCGT	GGTAGAAGAT GGAAGGCAGA AGTG	AGCGTG TGAGACAGA	G AGGGAGAATT	180
CCACTCAACT	CATCCTTTTA ATCAGGAACC CACT	CTGTCA GTAACGAAC	C CATCCCCACA	240

TGGAGTTTTG CTCTTGAGCT CGAG

ATAATGGCAT TAATCCATTC ATGAGGCCCC TACCTCTTTT TCTCCCCCCG CCCCCGAGA

300

324

(2) INFORMATION FOR SEQ ID NO:736:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 259 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:	
GAATTCGGCC TTCATGGCCT AAACACATAC CAGATTCTTA GATTCATTTG GTGAAGGAAG CCTCTGAATT AAAACTTTTA AATATTTCTG ATTTGCAACC AGACGAAAAA GAAGAAAATT GACAACTTTT TTGATGCAAC TTTGTGAAAT CATGGTGTTC CTGGTTTTTC TGGTCTGGTT TTTGTTGTTG TTTTGCCACA GTTTAGTTCC TCACCTGATC TTTCCTTGTA TCCACTTCAG AGTCTCGAG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:737:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 409 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:	
CTCGAGGCGG TGCCAGACAC GGGTCTCCTC CGACTGGGCG GTGCGTGGGA TGCCGCCAGC GTCCAGGTAC TGCGTGATGC GGATGTAGGC GATGCAGGCT GACTCGTCGC CCATCAGGTG GATGTGGGGA TTCAGGATGG TGGTGTGCAC GGGCTTGCTG TTCCGGGACC ACAGGTTTTC AAAATAGAAT CGATGCAGGT CCAGGCCCTC AACCAGGTTC CCCAGGGCCT CAGGTTCGAA GGCTGTCATG CCAGGGTCGC ACATCTTCGT GTAGGACTCA AAATCTCCAT TGCTTATGGC TTCAATCAGC TGCTCGTCA CTTTTATAAT TTCCTGTTTC CGCACTTTGG TGTCTTCATC CTCGATGGGC GTGTTGGTGC TCTCTGAGTA GGCCATGAAG GCCGAATTC	60 120 180 240 300 360 409
(2) INFORMATION FOR SEQ ID NO:738:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 466 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:	
GAATTCGGCC TTCATGGCCT ACTTTCCCCT CCTTCCTTCC TTCCTTCCTC CCTCCCTCCT	60 120 180 240 300 360
336	

ATTCAGTTGC ATTTTTGCTG AGATAGTGCT GTTACCAAAA GCAGGGGTGC TGCTTGAAGA AGTAAACCTA ACTCTGAAAA ATAGAGACTC TCCAGAAACA CTCGAG

420 466

(2) INFORMATION FOR SEQ ID NO:739:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 367 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739;	
GAATTCGGCC TTCATGGCCT ACATTCTGCA AACTATTTG TTATTAGCTT TTTCACTTAA AAATAGCCCT GCTTGCAAGC AGGCTCTGTG GTGCAATGGA TAGCGCATTG GACTTCTAGC CTAAATCAAG AGATTCAAAA ATAGCCCTGC TAAATATTTG CAATCTTTCC TACGCTCCTT TTTCCCCCAA AGTGACTTTG GATATCCAGA GTTACCAAAT CTAGTATTTG AAGTCCTTAG GTTTGAGGGT TGAAAGTGAA AGGCAAGCTG TTTTAATGAA AATTCCTAAC TGAAGAGAGC GGAGACTTAA GATGCTTAAA TTTTGGTCAC ACCTGAGCGG TATTTGTTTG CATGGCAGGA GCTCGAG	300
(2) INFORMATION FOR SEQ ID NO:740:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:  GTGATGGACA AAGACAGGGA AGGCCTCATC AGCAGGGATG AGATCACAGC CTACTTCATG AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG	180
GTGATGGACA AAGACAGGGA AGGCCTCATC AGCAGGGATG AGATCACAGC CTACTTCATG AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT	120 180 240
GTGATGGACA AAGACAGGGA AGGCCTCATC AGCAGGGATG AGATCACAGC CTACTTCATG AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG	120 180 240
GTGATGGACA AAGACAGGGA AGGCCTCATC AGCAGGGATG AGATCACAGC CTACTTCATG AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG  (2) INFORMATION FOR SEQ ID NO:741:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 318 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	120 180 240
GTGATGGACA AAGACAGGGA AGGCCTCATC AGCAGGGATG AGATCACAGC CTACTTCATG AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG  (2) INFORMATION FOR SEQ ID NO:741:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 318 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	120 180 240
GTGATGGACA AAGACAGGGA AGGCCTCATC AGCAGGGATG AGATCACAGC CTACTTCATG AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG  (2) INFORMATION FOR SEQ ID NO:741:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 318 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	120 180 240

- (2) INFORMATION FOR SEQ ID NO:742:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 256 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GAATTCGGCC	TTCATGGCCT	AAGAAATGAA	AAAGATTATT	GAAACTATGC	CAATGACTGA	60
GAAAGTTGAA	GAATTGCTGC	GTGTCATAGG	TCCATTTTAT	GAAATTGTCG	AGGACAAAAA	120
GAGTGGCAGG	AGTTCTGATA	TAACCTCAGT	CCGACTGGAG	AAAATCTCTA	AATGTTTAGA	180
AGCTGAAAGC	AGTGACAGTG	GAGCCGAGTC	TGAGGAAGAA	GAGGCCCAAG	AAGAAGTGAA	240
AGGAGCAGCC	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:743:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 580 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GAATTCGGCC	TTCATGGCCT	ATGTTTTTAT	AGCACCGATG	GTACTGTTTT	ATTTATTGCC	60
AATAGACCAC	AACATTCACA	TCTGTTTTTC	CTCAAGGGAA	CCGTATTTGC	TTTTGGTTGA	120
AGGATTTATO	TATTTGATAC	TATCCAGAAT	ATTGTGAAGC	TATAATTTCC	TGGGTTATAT	180
TTTAGATGGG	TTGTCTGCAT	GGTGGTAAAA	TAAGCTTTTT	CCTCTCGCCT	ACGTCCTTTG	240
GAAGATCTCC	TGATCATACA	TAACTAGGTA	GGGCTTATTC	TTGCTGCCGG	AGCTTGGCAC	300
CCAGCTCTAG	ACTGTTTCTT	TGAGCATTAC	TGCAGATTGG	AGACGTGTGT	GAGAGGAGCA	360
GCGCTCAGAA	ATAGGGCTTG	AGGCTCAAGC	AGAAACTGAA	GCTCTCATTC	AAATGAAGAT	420
GCTCTCTCTA	CCGCACGATC	GGCAGTGAGA	AAAGGAGGAT	GAAAATCCTT	CTCATCACAA	480
AGAGCTTGAA	GGAACCCACG	TCCCCAGATT	AGCAACCCTA	GAGTTCATCT	GCTCAGGCCG	540
GGAAATGTGT	AAGCTTCCTT	GATCAACTCC	AGGCCTCGAG			580

- (2) INFORMATION FOR SEQ ID NO:744:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 374 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GAATTCGGCC 3	TCATGGCCT	ACCCAGAGAC	TCGCGGACGC	TCACGATAAC	CAAGGACGAC	60
CGCGAACCAA C	GGCAAAATA	ACATGGCAGC	CAGACGAATT	ACACAGGAGA	CTTTTGATGC	120
TGTATTACAA (	GAAAAAGCCA	AACGATATCA	CATGGATGCC	AGTGGTGAGG	CTGTAAGCGA	180
AACTCTTCAG	TTAAAGCTC	AAGATCTCTT	AAGGGCAGTC	CCAAGATCCA	GAGCAGAGAT	240
GTATGATGAC (	GTCCACAGCG	ATGGCAGATA	CTCCCTCAGT	GGATCTGTAG	CTCACTCTAG	300
AGATGCCGGA A	AGAGAAGGCC	TGAGAAGTGA	CGTATTTCCA	GGGCCTTCCT	TCAGATCAAG	360

CAACCCCTCT CGAG (2) INFORMATION FOR SEQ ID NO:745: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:745: GAATTCGGCC AAAGAGGCCT ATTGGTTTCC CTGCTTCCAT TCTTACTCCC CTACACTCTG 60 TTCTCCAAAA AATAACCATT GTGATCCTTT AAAATCCTGA CTCTCCTG CTCAGAGTCA 120 TCCAGTGGCT TCCCATATCA CGTAAAATGA AACCCCAATC GCTCCTTACT CTGGCCTGCA 180 GGGGCCTGTG TGATGGGCCT TCTCCAGCTT CGTTCTTCCT TTCCTTCTGT TCTCCCCTCT 240 GCTTACCTAC TCCATCTCCA GGGCTTCTTT CCAGCTCAAG CCCTTTCCTG TTGAGAGCAT 300 TTGCTTTCCC CAGGGCACTC GAG 323 (2) INFORMATION FOR SEO ID NO: 746: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:746: GAGAACAGTG TTACCAAAGA AAAGGACATG TTCAATTTCA AACGAGCCCA GGAGGACATC TCTAGACTTC GCAGGAAGCT GGAGACCACA AAGAAACCAG ACAATGTACC CAAGTGTGAT 120 GAGATTCTGA TGGAAGAGAT TAAGGATTAC AAGGCACGCT TGACCTGTCC ATGCTGTAAC 180 ATGCGTAAAA AGGATGCTGT TCTTACTAAG TGTTTTCATG TCTTCTGCTT TGAGTGTGTG 240 -AAGACACGCT ATGACACCCC CCCCGCGCTC GAG 273 (2) INFORMATION FOR SEQ ID NO:747: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 666 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:747: GAAGATCTTC GCTGTCCTCT CTGCCTCTAT CACACCAAAT ACAAGCGCAA CATGATTGAC 120 CACATCGTGC TGCACCGAGA AGAGCGTGTT GTCCCCATTG AAGTTTGCCG GTCCAAACTG TCCAAATACT TGCAGGGAGT AGTTTTCCGC TGTGATAAGT GTACCTTCAC CTGCTCCAGT GATGAGAGCC TCCAGCAACA TATAGAAAAG CACAATGAAC TGAAACCTTA CAAATGCCAG 240

300

360

420

CTCTGCTACT ATGAGACCAA GCACACGGAG GAACTGGACA GCCACCTTCG GGATGAGCAT

AAGGTAAGCC GTAACTTTGA GCTGGTTGGA CGGGTTAACT TGGATCAGCT GGAACAGATG

AAGGAGAAAA TGGAGAGCTC CAGCAGCGAT GATGAGGACA AGGAAGAAGA AATGAACAGC

AAGGCTGAAG ACAGAGAGCT GATGAGATTT TCTGACCACG GGGCTGCTCT TAACACTGAG

AAGCGTTTTC CATGTGAATT TTGTGGACGG GCGTTTTCAC AGGGCTCTGA GTGGGAAAGA

540

	GACACGGCAT GGCATTGAAT GACACCAAGC AGGTGAGCAG AGAAGAAATC AGATCATGGA GAACAGTGTT AAAATGCCCT CCATAGAGGA AAAGGAAAGT	600 660 666
(2) INFORMA	TION FOR SEQ ID NO:748:	
(i) :	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 379 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:748:	
AAGCTACTGT GAAATTAGAC GGGTTTGGTT TGAGATTCAG	AAAGAGGCCT AACAACCGAA TATAGTACAC GACCTTCCTG CAGCAGTTCT CAAGTATGGA AAATCCCGGC AATTCTGTAC TTGTGTTATA CTGATGTGAT CTAATCACAG TGGAAGCTTT TAAGCCTATA CTTTCTACCA GAAGCTTGAA AAGAATATTC CCCAAAAGCAC TGAGATACTA AAGAAATTGA TGACAACNAA AGTAACATTT ATACATGATC TTAAACATTG TTTTTGTAGTG TATATTACTT TTAAGGGGAG CAGCCTGCAC TCTTTTGTAG ATTACTTTTG GGGGATATAT ATGAAACGG	60 120 180 240 300 360 379
(2) INFORMA	TION FOR SEQ ID NO:749:	
(i) !	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 335 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:749:	
TCACACCCCA GTTGGGGAAG CCCTCGTCTC ATGCCACGTG	TTCATGGCCT AGGCGCAAGG CCGAGCGTTC CCAGCAGGGG GAGAAACCCT GGCCCTTCAG GAACTGGGGC CTTGCCTTGC AGCCACTGG CCCCATCCCA CCAGGTGAGC TCTGACCCTT GGGCCTGGGC CTCTGCCCCT CCCAACCCAG CCTCGACAGC GCCCTGCTG TCTTCCCCAC CGCAGTCACC ACCACCCGAA GTCACTGTGC ACTGCCCTGT TCATGTGCCT CTGCGGGGCA GGGCCTTCCT ACTGCTGTAC CCAGATAGCC TCGAG	60 120 180 240 300 335
(2) INFORMA	TION FOR SEQ ID NO:750:	
( <b>i</b> ) ,	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 648 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:750:	
CAGCAGCAGC	AAGAACTGAA TATGCTCCGG GAACAGACCA CTGGGCTGGC AGCTGAGTTG AGGCTGAGTA CGAGGACCTT ATGGGACAGA AAGATGACCT CAACTCCCAG CATTACGGGC CAATAGTCGA CTGCTGGAAC AACTTCAAGA AATAGGGCAG	60 120 180

GAGAAGGAGC AGTTGACCCA GGAATTACAG GAGGCTCGGA AGAGTGCGGA GAAGCGGAAG GCCATGCTGG ATGAGCTAGC AATGGAAACG CTGCAAGAGA AGTCCCAGCA CAAGGAAGAG	240 300
CTGGGAGCAG TTCGTCTACG GCATGAGAAG GAGGTGCTGG GGGTGCGTGC CCGCTATGAG	360
CGTGAGCTCC GAGAGCTGCA TGAAGACAAG AAGCGTCAGG AGGAGGAGCT CCGTGGGCAG	420
ATCCGGGAGG AGAAGGCCCG GACACGGGAG CTGGAGACTC TCCAGCAGAC AGTGGAAGAA CTTCAAGCTC AGGTACATTC CATGGATGGA GCCAAGGGCT GGTTTGAACG GCGCTTGAAG	480 540
GAAGCCGAGG AATCCCTGCA GCAGCAGCAG CAGGAACAAG AGGAAGCCCT CAAGCAGTGT	600
CGGGAGCAGC ACGCTGCCGA GCTGAAGGGC AAGAAGGAGG CGCTCGAG	648
(2) INFORMATION FOR SEQ ID NO:751:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 266 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:	
GGAAAGAATC TAAAAGAAGA GAAGCGACCG GTGCTTTTAA GGGTGTCTAA TTTTCAAAAG	60
AGACGTCTGG GAGTATTTTG CTCTGGGCGT TTGGGTGAGC AGGACCGGGG CGTTGGAGGG	120
TGCGGCGGGC TTGGGAGCAG GGAAGGTTCC GAGTCCTAGG GAGGCGGCAG CGCTCGGCTA	180
TGCCCTCTGG AGACTGGCGG GGCTGCGGGG CCGAGGGGAC CCGCGAGGGA GCCGCGCTGC GGACGCGCTG AGCGCGGGAG CTCGAG	240 266
(2) INFORMATION FOR SEQ ID NO:752:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 288 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:	
GAATTCGGCC TTCATGGCCT AGGATGTTTT AAGGCTAGGC CTGAGCGAGG AGGAGGCAGG	60
GGAGACCTGG CAGGTATTGA AGTACCTGGG AAGAAAGGCA ATGGGGATGG TGGTCCTGCT	120
CCAAGATGAT AAGTGGAGGC TGAGCGTCAC TGGTACTGGG GGCCATGATC CCCAGGGCCA CCCTGGCACC AGGGTGCAGG GGATGCGGGG CCTGAGCAGG AAGAACAGAG ATCTGCGGGC	180 240
TGCACCGACC CATCCCTGCC CCTAGGCTGA AGAACGGCAT CACTCGAG	288
(2) INFORMATION FOR SEQ ID NO:753:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 487 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:	
GAATTCGGCC TTCATGGCCT ACTGAATTTG CTTTTCTTGC CTCTCTTTAG TCACCTGTCA	60
CAGGAGGTTC CTGCTCAGTA ATGATATTG GAGTTAGGAT AATAACTTTT TTTTTTTTGT	120

GCTTCAGATT	TAGAAGAAAA	GATCCTGTTT	CCATTTGAAA	GGAACTGTAA	GCTTTTATCT	180
			GCCTAGGGAT			240
			TACTGTTAAA			300
			AAAGGAAGGG			360
			CCATGGAGAA			420
						480
	AACACCCTGT	GGCAGTTCAG	AGACACGCTT	TICCIACACI	GCATGCAGCC	487
GCTCGAG						48/

- (2) INFORMATION FOR SEQ ID NO:754:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 443 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

GCTGGGTTTA	GGCGATCCTC	TTGCTTCAGC	CTCCCAAGAA	GCTGGAGCCA	CAGGCATGCA	60
CCACCACGCC	CAGTTAATTT	TTGTATTTTT	TGTGGGGACG	${\tt GGGTCTCACT}$	TTGTTGCCCA	120
GGCTTATCTG	GAACTCCTGG	TTTCAGGCAG	TTCTCCTTCC	TTAACCTCCC	AAAGTGCTGA	180
GATTATAGGT	GTGTGTGAGC	TATCACACCT	GGCCTAGAAA	ATTATAAGAA	AATATTAATC	240
ACATAATCTC	ACTACCCATT	GATGATTTAA	CATCTAGTAT	ATACATATGT	TTAATATAT	300
TTAAAAGTAG	GGTTATATTA	TATAATTACT	TCATTATTCT	TGTTTTCCAC	TTAATATACT	360
TAAGATATCT	TTCAAAATCA	CTAAATACAG	GAACATAGTA	TATCATCTTT	CAGTAGCCTC	420
ATTGTATAGC	TAACCCCCTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:755:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 584 base pairs
      (B) TYPE: nucleic acid

    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GAATTCGGCC	TTCATGGCCT	ATTGATTTCC	TGGGCTCAGG	AGAGGATGGG	GAAGGGGCTC	60
CAGACCCTCG	GCGGTGCACT	GTGGATGGGA	GCCCCCATGA	GCTGGAAAGC	CGTCGGGTCA	120
AACTCCAAGG	CATTCTGGCT	GACCTGCGGG	ATGTGGATGG	GCTGCCCCCA	AAAGTGACTG	180
GCCCGCCTCC	TGGCACACCC	CAGCCCCGGC	CACATGAAGG	TTCCTTTGGC	TTCTCCTCAG	240
ACGTCTTCAT	CATGGACACT	ATCGGGGGCG	GGGAGGTGAG	CCTGGGGGAC	TTGGCAGATC	300
TCACCGTCAC	CAACGACAAC	GACCTCAGCT	GCGATCTGTC	TGACAGCAAA	GATGCTTTTA	360
AGAAGACGTĠ	GAACCCCAAG	TTCACCCTGC	GCTCGCACTA	CGACGCCATT	CGTTCCCTGG	420
CCTTCCACCA	CAGCCAGTCG	GCTCTGCTCA	CCGCCTCCGA	GGACGGCACG	CTCAAGCTCT	480
GGAACCTGCA	GAAGGCGGTC	ACGGCCAAGA	AGAATGCGGC	GCTAGATGTG	GAACCTATAC	540
ATGCTTTCCG	GGCTCACAGG	GGCCCAGTGT	TGGCTGGACT	CGAG	•	584

- (2) INFORMATION FOR SEQ ID NO:756:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 285 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

GAAATTAAAA AAATAAAATC	AAGTTCTTGG	GTGGTGGGAA	ATTGGCCTGT	ATTTTTTCTT	60
CTCAGTGGAA TTTGCTGAGT	TATTAAAAAA	AGGCTCAAAA	ACTGAGAACT	TTGAAGATAT	120
TGCACCATAT TCTTTTTGTA	TTGAGTGTTG	CTGATGAGAA	GTCTGAGGTC	AGTCTGTTGC	180
TTGCTCTTTC TAGGTAAACT	GTGCTTTTTA	TATTTTTTCC	CCTCTAGAGG	TTTTGAGAAT	240
TTACTCCTTA TCCATGTTAT	TCTTAAATTT	CACCACATTC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:757:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

GAATTCGGCC TTCATGGCC	T AGAATGCTTT	GAATCCATAT	CTTTTTCAGA	AACATACATG	60
GAAATACAGA ACTACACCI	G TAATTACAGA	GGGCATATGA	ACCCTAGTTT	GATAAGCCTT	120
GCTTTAAAGG ATGCAGTGT	G TTCTATTAAA	TGTATTTAAT	ACAATTGCAG	AAATGGAAAA	180
TGTGGACCTC CATTAAACA	A ATTTTTTAGT	TCCTAATGAG	ATAAACTTGG	GACCAAACCG	240
ATTCCTCTTG TTTTAGTGC	T CAAAAATAGT	TTCATTTTTA	GGTATTTATG	CTTTAGTGGC	300
CTTTCTCGAG			•		310

- (2) INFORMATION FOR SEQ ID NO:758:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 196 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

GAATTCGGCC AAAGA	AGGCCT AAGAAAAGAA	AGCAAGAACA	GAAAACGAAG	CCACAGGAAG	60
GGAAGTAGAC ATTG	TATGCT TATGGTTTCT	CATTATGAAG	GTGCAGCTTG	TAGGAGGTTT	120
GTACGGATGT GCTTT	TGAAGT TATGTATATT	ACATATAACA	GGAAAAAATA	TTAAAATAAA	180
CAGTGCTGGT CTCG	AG				.196

- (2) INFORMATION FOR SEQ ID NO:759:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 360 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

AAGTCAGATA	TTCATGGCCT ACAGCAAATC TGCCTTCACA TGGTCTGCAT TCTAGTGGAG GAGGTAAGTA CGAAGACCAC AAAGCAGGTT AAAAAGTAAG GTGGGAAAGG TAGACAAGGT GGTCAGGGCA AGCCTCTCAG AAGAGGGGAT AAGTGCTCAG	60 120 180
	GAAGTGAGAG TGAGCTATTG ACACGGAGAA GGGCATTTCA GACTCTGAAG	240
	GGCAGGCTTT GGAGGGAGAG CTTGTTTATG TAGACAAGGA GGGGCAAAGA	300
GTCTTGTGGA	TAAAGCAGAA TGAACAAGAG TAAATGGGAT TGTAAATGAA ATGACTCGAG	360
	ATION FOR SEQ ID NO:760:	
(1)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 192 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:760:	
	AGTCAAAAGT AGGTGCCCAT ATATATAATG AAATACCAAA AGGACAATTT	60
	ATGGAAACAT TATGGCATGC TTTAGACGTT CTGTTTTGGT TTTCTTATTC ATCTTTTAGG TCTATCCATT GGTAAAGATA TATTAGGACT CACATCAACT	120
CAAGGTCTTG		180 192
(2) INFORM	ATION FOR SEQ ID NO:761:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 326 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:761:	
	TTCATGGCCT AGTTTATTGC TCCCAACTAT ACATCTTCAG ACTTCACTTA	60
	GGTGGTTAGG TTCCAGGATT ATTGAGATCT ATTTCTACTC ACAATTGCTT ATCTATCGTC ACCTTAATTG CCTGTGCCTA AAAATATAGC ATGCTTGTCT	120
	ATTCAGCCTG GTATGTGAGT GACTGAAATG CAACTCCGTG GAAACACCCC	240
	ATTCATCCCC TTGGTAACTC AGCACAGTCA CAGAAACTGA AGAAGTAAAA	300
TGATCCTCTT	TATTTGGCTT CTCGAG	326
(2) INFORM	ATION FOR SEQ ID NO:762:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 205 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:762:	
GAATTCGGCC	TTCATGGCCT ACTGGCCCAA GTGAAACTTT TAACAGGCTT TTTGGAGATC	6
	GATCCAAAAA TTCATCAGGT ATATTTTCTG TTTTCCAAGT TCATGCAGGC	12
	CTAATATATA ATACTAGTTG CCTTGTTCAA GCTGCCATAT CAGTTTCATC	18
ACTCCTTTCC	CAGTGCCCAC TCGAG	20

(2) INFORMATION FOR SEQ ID NO:763:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 285 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:	
GAATTCGGCC TTCATGGCCT AAAAATGAAT ATATTCCTAT CCTATATTAA GACACTTTCC CTAACCTAAA AGTTTATTCT GTTTTTAAAA TAAATGAAAG TATTTGTATG GGCCCTGGGC CTGACGGAGA TATGCCCTGC CCCCTCTCTA GAGTGCTGGG AATTCTCAGG TGACCCAGTC CCACAGGCAG CCAAGTGCCC ACACATTTCC AGGCTGCCCT CCACCAGGGC AGCGACCTCG GGTCACCAGG GACACGCACA CCTAGAAAGC CGTGGGCTCC TCGAG	60 120 180 240 285
(2) INFORMATION FOR SEQ ID NO:764:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 345 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:	
AATTCTTTAT CATTTCAGAT ATTAAGGATT TCAGATTTTA AGAGTTATCA GTGAAACTGT GTTACAAGAA TATTTTGTTC CTGAGACATC TCAGTATTAT AGGTGGCTTC AGACTAACAG GCACAGAATA GGATAGTGT AAGTATCTCA TTAGCTTTAC TGTACTTGGT ACCTTTAGGA CCTTCAGCCA GAGGTGATTG GAGGGATTTG CACGTCTACC ACTCGTGTG GTACTCTGTA ACCATATCTC CTTTAGTGCC TGCTTTTGAA CTTTATATAA ACAGAATGAT GCTGCCTGTT TATCTCTATA ATTTTCTTCT TTCCCTTAGC ACGTGCTCAC TCGAG	60 120 180 240 300 345
(2) INFORMATION FOR SEQ ID NO:765:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 100 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:	
GAATTCGGCC TTCATGGCCT AGAGAATGTT TTCATGTTAC TTATACTAAC ATTAGTTCTT CTATAGGGTG ATAGATTGGT CCAATTGGGT GTATCTCGAG	60 100
(2) INFORMATION FOR SEQ ID NO:766:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 333 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

GGATTGAATT	CTAGACCCTG	CCTCGTCATT	GTGGAACCCA	TGGAGCAGTT	TGATGATGAA	60
GATGGCTTGC	CAGAGAAGCT	GATGCAGAAA	ACTCAACAAT	ATCATAAGGA	AAGAGAACAA	120
CCACCACGTT	TTGCTCAACC	TGGGACATTT	GAATTTGAGT	ATGCATCTCG	ATGGAAGGCT	180
CTTGATGAAA	TGGAAAAGCA	GCAGCGTGAG	CAGGTTGATA	GAAACATCAG	AGAAGCCAAA	240
GAGAAACTGG	AGGCAGAAAT	GGAAGCAGCT	AGGCATGAAC	ACCAATTAAT	GCTAATGAGG	300
CAAGATCTAA	TGAGGCGTCA	AGAAGAACTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:767:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 238 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

GAATTCGGCC	TTCATGGCCT	AGATAATATT	TTATGTTCAT	TGTGTGTTAG	ACTGTGTTGA	60
AGTGGAAACT	TTGGAACATT	GTTGGAACCA	GTAAGAATCC	CATTCCTCAG	GTATCAGGTC	120
GTTAAAGTAG	TTTAAAATAA	CGTATTCCTT	AATTTTCCTC	AGCAGGTTCC	CCCTCCCTTT	180
AACTTGTGTG	TATAAATATA	TGTGTGTGAT	GTTTTCTCTT	ACAAAGATAG	TACTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:768:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 234 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

GAATTCGGCC	TTCATGGCCT	AGGGATCCCA	CCTTTTACAT	CCTAGGTGTG	AACAGATTCA	60
AATCCACTAT	TCCTCCAGAT	TTTATAGATG	AGGAAACCAA	GGTGCACAAG	AGGGATTTTT	120
TTGTTTTGTT	TTTTGTTTTT	GTTTGTTTTT	GAGACAGGAT	TTTGCTTTGT	TGCCCAGGCT	180
GGAATGCAGT	GGCACAAACA	TGGCTCGCTG	CAGTCTCGAA	CTCCTACGCT	CGAG	234

- (2) INFORMATION FOR SEQ ID NO:769:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 291 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

GATGTCTCTC GGACACAGAC TGCAATATCG GTAGTTGAAG AGGATCTAAA GCTTTTACAG CTTAAGCTAA GAGCCTCCGT GTCCACTAAA TGTAACCTGG AAGACCAGGT AAAGAAATTG GAAGATGACC GCAACTCACT ACAAGCTGCC AAAGCTGGAC TGGAAGATGA ATGCAAAACC TTGAGGCAGA AAGTGGAGAT TCTGAATGAG CTCTATCAGC AGAATCTCGA G	120 180 240 291
(2) INFORMATION FOR SEQ ID NO:770:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 432 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:	
CGCTGCGTGC TTGTGAGACT GCCTGTTCTG GGACCAGCCC CTGGGCTCTT CCACCAAGAT TTGGTGAGGG TCCCCCTCTG CCTCTCACAG AAGCCCCTGG CCCTGGACTG TCCTGGGGGC AGGGACACCT GTGGCTGGG AAGGGATGGC CAACAGCGGG AAGCAGTTTG CGCCTGGTGC CTGATGATGG TGAACCACGA GACAGATGGA GACGGGAGTC AGGGGACCCT GGGGACCCTT CCAGGTCCAG TGACCTTTTC CCAGACAGGC ACTCTCCAGG CCTAGGACAG ACAGGGCCCC AACTCCTCAT CACCCCATGA CTTGGCCTGG AGGAACCTGG GGTGGGAAAC AAGTAGTCCC CCAACCTCAG AGGCCAGAAC CACAGGTGGG GGACAGGGAC CTCGACAGAG CTGTGCCTGC TCAACGCTCG AG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:771:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 399 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:	
GGTGTGGCTT TGCCCCGTAC GAGCGGCGCG CCATGGAGTT ACTGAAGGTC TCCAAGGACA AACGGCCCT CAAATTTATC AAGAAAAGGG TGGGGACGCA CATCCGCGCC AAGAGGAAGC GGGAGGAGCT GACATCTACC TGGCCCGCCA TGAGGAAAGC TGCTGCCAAG AAAGACTGAG CCCCTCCCCT GCCCTTCCCC TGAAATAAAG AACAGCTTGA CAGAAGCCCT GGCTCTCCTG CTGTCCGTGG GTGGGTGTGG GTGTGTCGGG GGCCCGCAGT CCCCTGTCTG GTGCCCGCTC TGAGCCACAC CCTCTCCGGG TGCTGCCTGG TCGTGAATCA AAAGCCGTGG CCCGCCCACC CTTCCCGGGG CAGCAGGTGA GGAAGCCGCT GTACTCGAG	60 120 180 240 300 360 399
(2) INFORMATION FOR SEQ ID NO:772:	
(i) SEQUENCE CHARACTERISTICS:	

- - (A) LENGTH: 520 base pairs (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

AGTTGAATCT AAACCGGATA AACCATCGGG AAAGTCAGGC ATGGATGCTG CTTTGGATGA CTTAATAGAT ACTTTAGGAG GACCTGAAGA AACTGAAGAA GAAAATACAA CGTATACTGG	120 180
ACCAGAAGTT TCAGATCCAA TGAGTTCCAC CTACATAGAG GAATTGGGTA AAAGAGAAGT	240
CACAATTCCT CCAAAATATA GGGAACTATT GGCTAAAAAG GAAGGGATCA CAGGGCCTCC	300
TGCAGACTCT TCGAAACCCA TAGGGCCAGA TGATGCTATA GACGCCTTGT CATCTGACTT	360
CACCTGTGGG TCGCCTACAG CTGCTGGAAA GAAAACTGAA AAAGAGGAAT CTACAGAAGT	420
TTTAAAAGCT CAGTCAGCAG GGACAGTCAG AAGTGGTGCT CCACCCCAAG AGAAGAAAAG	480
AAAGGTGGAG AAGGATACAA TGAGTGATCA AGCACTCGAG	520
(2) INFORMATION FOR SEQ ID NO:773:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 129 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:	
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GAATTCGGCC AAAGAGGCCT AGTTTATTGT TTGCATATAT TTTATAGTGT AGAGATTAGG	60
CATTTTAATA AAATTTTAAA ATTTCCAGGA TCTTACAGAA TGCTTTTATG TTACAGCTTA	120
CTCCTCGAG	129
(2) INFORMATION FOR SEQ ID NO:774:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 337 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:	
GAATTCGGCC TTCATGGCCT ACACAACGGA AAGCTGTTTT TCTGATCGAG GCTCTCTGAA	60
GAGCATAATG CAGTCCAACA CATTAACCAA AGATGAGGAT GTGCAGCGGG ACCTGGAGCA	120
CAGCCTGCAG ATGGAAGCTT ACGAGAGGAG GATTCGGAGG CTGGAACAGG AGAAGCTGGA	180
GCTGAGCAGG AAGCTGCAAG AGTCCACCCA GACCGTGCAG TCCCTCCACG GCTCATCTCG	240
GGCCCTCAGC AATTCAAACC GAGATAAAGA AATCAAAAAG CTAAATGAAG AAATCGAACG	300
CTTGAAGAAT AAAATAGCAG ATTCAAACAG GCTCGAG	337
CITCHAGEST PROFITAGES STATES CO.	
(2) INFORMATION FOR SEQ ID NO:775:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 276 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(wi) CRAHENCE DECEDEDATON, ORG. ID NO. 225	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:	
GAATTCGGCC AAAGAGGCCT AGTGAGCGCG ACCATCATGT CCATGCTCGT GGTCTTTCTC	60
TTGCTGTGGG GTGTCACCTG GGGCCCAGTG ACAGAAGCAG CCATATTTTA TGAGACGCAG	120
CCCAGCCTGT GGGCAGAGTC CGAATCACTG CTGAAACCCT TGGCCAATGT GACGCTGACG	180

	GCCTGGAGAC TCCAGACTTC CAGCTGTTCA AGAATGGGGT GGCCCAGGAG TTGACTCACC TGCCATCAAG CACCAG	240 276
(2) INFORM	ATION FOR SEQ ID NO:776:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 586 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:776:	
CAGTTCAGAG CACTGAGTCA AAAGGCTTTA GAAAAAAGAA CACTGAACCT TAAAGAAGAA TCCAAAGGAA CTTGAATTTA ACAAGAAACA	AAAGAGGCCT ATGAAATAGA AGAAGGTAAA AATAAGGAAC AAGCAATAAA AACATAATGA ACATCAATGA GGAACCAGGA ACAACTGAAG GTGAAGAAAT AGTAGCACTG AAGAAATGGA GGTCAGAAGT GTGGTGGCTG ATACTGACCA GGAAGTGAAG TTCTAAAAGT ACTACCAGA TAGATAAAGA ATTCCAGTGT CAATTAAAAAA AGAGCCTGAA GTTACTGTAG TTTCACAGCC CAGCCTGTTC TAATACCCAG TATTAATATC AACTCTGACA GTGGAGAAAA ATAGATAATG ATTCAGAGAC TGGTTCCACT GCTGATACTA GCAGTATTGA AATGATAATG ATTCAGGCAC TGGTTCCACT GCTGATACTA GCAGTATTGA TCCATCTCTA GCTTTCTAAG TAAAACTAAA GACAGTGGAT CGATATCTT AGAAGACAAA AGAAAACATT GAAGAAAACA CTCGAG	60 120 180 240 300 360 420 480 540 586
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 463 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:777:	
CTGAGATTTC AGCTTCAAAC AGTATTCTAC GGGCCACAAG ACTCTCAATC CCACAACTGT	TTCATGGCCT AGTTTATATA GAGTAGGTTT ACATAGAAAA GGAAAGTTCA TAGGTACAAG ATCTANCAAC ATGCACAAAC CAATATTGTT TATGTATAAC AATTAGAAAT TGTAATAACC ATTATTAAAG TGATGAAAAT TGTATTGCTT CAAAATTATT AAGTAATTTT TTTTTTTTT TTTNANACGG AGTCCCGCCT NGCNAAAATT TGTTTCNAAA AAAAAAAAGA AAAGAAAGAA AAAAAATTGA CCTAGATGTA AAATCAACCT CGTGTTCTTG ATTTCACCAG TAATTCATAA TGTGTCTTGA ACACTTACTA TGCTTGGCAT ACTTATAATT TTTATTTCAC AATTTAAGAT GAAGTTTCTC CTACTAACTC GAG	60 120 180 240 300 360 420 463
(2) INFORM	ATION FOR SEQ ID NO:778:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 466 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

PCT/US98/06956 WO 98/45437

1	GAATTCGGCC	TTCATGGCCT	AGCTGGGAGT	TACCTGNTAT	CCTGATGGTG	CCATGTGCTA	60
	GCTGGGTGAC	AATAACCCAG	CCACCTAACA	TCTCAAAGAT	TGTTCCTTTT	TGTGTGAAAT	120
	AGGGATAGAG	TTGTCTACTT	CCCAGAGCCA	GATAGAGAAC	TTAAGAGATG	AATCTGAAAA	180
	TACAATAGCC	TAAATAAATT	CAAGGAAACA	CTATTATCTT	ACTGGATCTT	TCCAGCAACC	240
	ATGTTACTTT	TGGCTGGATT	TTGTATTTTC	CAATTTGTGA	ATGACACAAC	AAAGAGCTAG	300
	GTAGGTTAAG	TAAATGGTTT	CAGATAATAA	GCCCAGTTAG	CCCAGACGTT	TATTTTCCAT	360
•	TTGCATAGAA	AATGAATGTT	TTATGCATAC	ATTTGTTTGC	CCAGGGCTAG	GATATTACTT	420
(	GCATATGATG	TTCTTATATA	AAAAAATTA	AGAATACAAC	CTCGAG		466

- (2) INFORMATION FOR SEQ ID NO:779:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GAATTCGGCC	TTCATGGCCT	AATTCCACAG	GGAAATGGGC	AGACTGAACC	AGTCCAGGTG	60
GTGAATTTTC	CAAGAACATA	GTTTAAGTTG	ATTAAAAATG	CTTTTAGAAT	GCAGGAGCCT	120
ACTTCTAGCT	GTATTTTTTG	TATGCTTAAA	TAAAAATAAA	AATTCATAAC	CAAAGAGAAT	180
CCCACATTAG	CTTGTTAGTA	ATGCTCTGAC	CAAGCCGAGA	TGCCCATTCT	CTTAGTGATG	240
GCGGCGTTAG	GGTTTGAGAG	AAGGGAATTT	GGCTCAACTT	CAGTTGAGAG	GGTGCAGTCC	300
AGACAGCTTG	ACTGCTTTTA	AATGACCAAA	GATGACCTGT	GGTAAGCAAC	CTGGGCATCT	360
TAGGAAGCAG	TCCCTGGAGA	AGGCATGTTC	CCAGAAAGGT	CTCTGGAGGG	ACAAACTCAC	420
TCAGTAAAAC	ATAATGTATC	ATGAAGAAAA	CTGATTCTCT	ATGACATGAA	ATGAAAATTT	480
TAATGCATTG	TTATAATTAC	TAATGTACGC	AGACTCGAG			519

- (2) INFORMATION FOR SEQ ID NO:780:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 321 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

GAATTCGGCC TTCATGGCCT	ACTAGACCCC	CGCCACAGCA	GCCTCTGAAG	TTGGACAGCA	60
AAACCATTGC TTCACTACCC	ATCGGTGTCC	ATTTATAGAA	TAATGTGGGA	AGAAACAAAC	120
CCGTTTTATG ATTTACTCAT	TATCGCCTTT	TGACAGCTGT	GCTGTAACAC	AAGTAGATGC	180
CTGAACTTGA ATTAATCCAC	ACATCAGTAA	TGTATTCTAT	CTCTCTTTAC	ATTTTGGTCT	240
CTATACTACA TTATTAATGO	GTTTTGTGTA	CTGTAAAGAA	TTTAGCTGTA	TCAAACTAGT	300
GCATGAATAG ATTCTCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:781:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 560 base pairs

    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

GAATTCGGCC	TTCATGGCCT	AAATGGGAAT	CATCATTGCA	TAACAAACCT	AAAGAGAAAA	60
TGAGAACATT	TACGAAGAAG	AAACAGAGTT	ACTGTACCAA	GGGCAAAAAG	AAAAGAAGGG	120
GGAAAAAAA	TAAGTCCATA	AAAGAAAAAC	AAAAGGAATC	CATGAGCCTG	GACGACAAGC	180
CGTGGGGGAT	GTAAGAAGGT	TTGGAACCCA	AAAGGCAAGT	CTAATCAGCT	GGGGTAACAT	240
GGCGAGGCAG	TTCCACATGC	TGAGACTTGT	GGCTACCACA	TTAAAAAAGA	CTGTGCATAT	300
TCTAAATGAC	AGCAGTCCTG	CAGTGACGTG	GATATTCACT	CTAGAAGCTA	TGCAGGCAGG	360
CGTGGGAAAA	GCGAAGAGAT	GTTGCACCAT	GCAGCTGCAA	TCTTTATGTC	TCTACTGGCA	420
CAACCGAAAA	GAGTAATGTG	GAAATTATCC	AGAGAATTTA	GGTGAGAAAA	ACAGAAGÇCA	480
TCAGATTTTC	TCCTTTAAAT	CTTCAGAGGG	GTATACACTC	CCCTGGAAAA	CCAAGTTGCC	540
TCTCTGCTCA	CATCCTCGAG					560

- (2) INFORMATION FOR SEQ ID NO:782:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 633 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

GAATTCGGCC TTCATGGCCT	AGGGGAGTCC	TCATTCTGAC	CTCAAAGAAA	GGACTGTATT	60
GTCTGGCTCC ATAATGCAGG	GGACACCAAG	AGCAACAACT	GAAAGCTTTG	AAGATGGCCT	120
TAAATATCCC AAACAAATTA	AAAGGGAAAG	TCCTCCCATA	CGAGCATTTG	AAGGTGCCAT	180
TACCAAAGGA AAACCATATG	ATGGCATCAC	CACCATCAAA	GAAATGGGGC	GTTCCATTCA	240
TGAGATTCCA AGGCAAGATA	TTTTAACTCA	GGAAAGTCGG	AAAACTCCAG	AAGTGGTCCA	300
GAGCACACGG CCGATAATTG	AGGGTTCCAT	TTCCCAGGGC	ACACCAATAA	AGTTTGACAA	360
CAACTCAGGT CAATCTGCCA	TCAAACACAA	TGTCAAATCC	TTAATCACGG	GGCCTAGCAA	420
ACTATCCCGT GGAATGCCTC	CGCTGGAAAT	TGTGCCAGAG	AACATAAAAG	TGGTAGAACG	480
GGGAAAATAT GAGGATGTGA	AAGCAGGCGA	GACCGTGCGT	TCCCGGCACA	CGTCAGTGGT	540
AAGCTCTGGC CCCTCCGTTC	TTAGGTCCAC	ACTGCATGAA	GCTCCCAAAG	CACAACTGAG	600
CCCTGGGATT TATGATGACA	CCAGTGTCTC	GAG			633

- (2) INFORMATION FOR SEQ ID NO:783:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

AAATGACACT	GAATGACACG	TTAGCCAAAA	CTAACAGAGA	ATTATTAGAT	GTGAAGAAAA	60
AATTTGAAGA	TATAAATCAG	GAATTTGTAA	AAATAAAAGA	TAAGAATGAA	ATATTAAAAA	120
GAAACCTGGA	AAACACTCAG	AACCAAATAA	AAGCTGAGTA	CATCAGCCTG	GCAGAGCACG	180
AGGCAAAGAT	GAGCTCGCTA	AGTCAGAGCA	TGAGAAAGGT	GCAGGATAGT	AATGCTGAAA	240
TCTTGGCCAA	CTACAGAAAA	GGCCAAGAAG	AGATTGTGAC	ACTGCATGCC	GAAATTAAAG	300
CCCAGAAGAA	GGAGCTCGAC	ACAATACAAG	AATGCATTAA	GGTAAAATAT	GCCCCAATTG	360
TCAGCTTTGA	GGAGTGCGAG	AGAAAATTTA	AAGCAACAGA	GCTCGAG		407

(2) INFORMATION FOR SEQ ID NO:784:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 342 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GCAGAAAAGT	CAGAACAATT	TGAGGAGCTT	CAAAGCATCC	TTAAGAAAGG	GAAACTAACT	60
TTTGAGAATA	TTATGGAAAA	ACTGCGAATC	AAGTATTCCG	AAATGTACAC	CATAGTCCCT	120
GCAGAGATTG	AATCCCAGGT	GGAAGAATGC	AGAAAAGCTT	TAGAAGACAT	AGATGAGAAG	180
ATTAGCAATG	AAGTCTTAAA	AAGCTCACCA	TCATATGCAA	TGAGGAGAAA	AATAGAAGAA	240
ATTAACAATG	GGCTTCATAA	TGTTGAAAAG	ATGTTGCAGC	AGAAAAGCAA	AAATATTGAG	300
AAAGCTCAAG	AAATTCAAAA	GAAAATGTGG	GACTCACTCG	AG		342

- (2) INFORMATION FOR SEQ ID NO:785:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 456 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

GAGATAATGG ATGAAAGGAT	TCAGAGGAAA	GTAGAGAAAC	TAGAGCAACA	ATGTCAGAAA	60
GAAGCCAAGG AATTTGCCAA	GAAGGTACAA	GAGCTGCAGA	AAAGCAATCA	GGTTGCCTTC	120
CAACATTTCC AAGAACTAGA	TGAGCACATT	AGCTATGTAG	CAACTAAAGT	CTGTCACCTT	180
GGAGACCAGT TAGAGGGGGT	AAACACACCC	AGACAACGGG	CAGTGGAGGC	TCAGAAATTG	240
ATGAAATACT TTAATGAGTT	TCTAGATGGA	GAATTGAAAT	CTGATGTTTT	AACAAATTCT	300
GAAAAGATAA AGGAAGCAGC	AGACATCATT	CAGAAGTTGC	ACCTAATTGC	CCAAGAGTTA	360
CCTTTTGATA GATTTTCAGA	AGTTAAATCC	AAAATTGCAA	GTAAATACCA	TGATTTAGAA	420
TGCCAGCNGA TTCAGGAGTA	TACCAGTGCT	CTCGAG			456

- (2) INFORMATION FOR SEQ ID NO:786:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 488 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GAATTCGGCC	TTCATGGCCT	AGGGGTGAGA	GTGTAGACGG	CTTTCCCAGT	TGTATCCAAG	60
GCAGTCAGAC	AGGGGGATTT	GGGCTGTGTT	GTGCCCCAGC	GCTGCAAGGT	GGCCAACAGC	120
GACGGCGGTC	GGGGGACACC	TGCAGTGAGA	GGCTCCCCTC	TCAGCACACT	CGTCTCGCTT	180
CCCTCAGGCT	TTGGCTGATT	TGGATCTGGT	TGCTGAACTT	CCAACAATTC	CTCAAAATCA	240
TCCACAAAGA	ACTCCTTCAG	TGGAGGGCGC	TTTGGCCTCT	TCAGGGTGTT	CAGAAGCTGC	300
TGGATTTTGG	AGGACACTCT	GCTGTTCACA	GGGACACCAT	CTGCTGTTTC	CAGCATGCTC	360
CCGCTGCACC	CCCGAGGAAC	ACTTCTCACA	GAAGCCACCT	GTGGACGCTC	AAAGTACGAA	420
TGCTCCACGA	GGCCCGTGGT	GACATCAGGA	GGGGCAGAAT	GCAGATCTAT	GTGGGTGTGG	480
GCCTCGAG						488

- (2) INFORMATION FOR SEQ ID NO:787:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 452 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double .
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

GAATTCGCCT	TCATGGCCTA	AGTGTCCGGA	ACATATGTCA	TGATTCTATG	TCCAAACAAC	60
AGGCCAACCC	TCAGGACAGA	CCCCGCCACC	CCCCTTCTCT	GCAGCTCCTG	GCAGGGACGG	120
TGCACAGTGG	TGCCGTGTGC	AGGGGGCCAG	CGCAGCCACT	GGGCATCTGG	GGCAGCGCTG	180
GTCGCCTGGC	CACCTCCTTG	CTGGGGCCGC	TGGGCCTCCG	GCCTAGAAGG	ACAGGAAGCC	240
ATCCACCTCA	AGGCGCAGGA	AGGGGTCCAG	CAGGGCCCGG	AGCTTCCAGA	TGGTGGCACG	300
GCTCAGCAGG	GGCGGCACCA	GCCCCTCGAA	GGGCCTGGGG	TTCACCATGT	ACACGTAGGC	360
GACCAGCAGG	GTGCCCAGCA	GCAGCCTCAG	GATCAGCAGC	CTGAGAATCT	CCAGCTGGAT	420
GTCCTCCATC	TGGTCCCTAG	ACCTGCCTCG	AG	•		452

- (2) INFORMATION FOR SEQ ID NO:788:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

GAATTCGGCC	TICATGGCCT	ACAGGACAGA	GGCAAATAGT	AGACAAAGGT	GAAGCCAAAG	60
GCATAATTAA	GGAAGGAAGA	ACGATATTAC	CAAAAGATGA	AACTGAAAAG	AAAGTCTTAA	120
CTGTGTCAAA	TTCTCAAATT	GAAACTGAAA	TTGAAGTTCC	ATCGTCCGCA	GTTCCAGAAC	180
ACAGAATGTA	TGAAAATCAA	AGTCAGGTGG	TTCTTGTAGA	AAACCTTCAT	GTTAACAAAA	240
CAAATGAAAC	AATCAGACAT	GAAAATAAAC	CGTATGTTCC	TAGTTCAGCA	CAAATGACAA	300
GAAGGAAATT	CCAAAAGGCT	AAGCCAAATT	TGGGAAGAGC	ACACAGTAAG	AAAGAGGAAC	360
CAGTTTTAGA	AAAAGTCACA	AACTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:789:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 457 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

GCCTGAAGAC ATO	CAAAAAGG AGGCAG	CCCG GGCTTCT	GG AAGATCTGCT	TTGTGTGCAA	60
GAAAAAGGGA GCT	IGCTATCA ACTGCC	AGAA GGATCAG	GC CTCAGAAACT	TCCATCTGCC	120
TTGTGGCCAA GAZ	AAGGGGTT GCCTTT	CACA ATTTTTT	GA GAGTACAAAT	CATTTTGTGA	180
CAAACATCGC CCA	AACACAGA ACATCC	AACA TGGGCAT	TG GGGGAGGAAA	GCTGCATCTT	240
ATGTTGTGAA GAG	CTTATCCC AACAGA	GTGT TGAGAAC	TC CAGAGCCCGT	GTTGTAGTCA	300
AGCCATCTAC CAC	CCGCAAGT GCATAC	AGAA ATATGCC	AC ACATCAGCAA	AGCATTTCTT	360

CAAATGTCCA CAGTGTAACA ATCGAAAAGA GTTTCCTCAA GAAATGCTGA GAATGGGAAT TCATATTCCA GACAGAGATG CTGCCTGGGA ACTCGAG	420 457						
(2) INFORMATION FOR SEQ ID NO:790:							
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 582 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear							
(ii) MOLECULE TYPE: cDNA							
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:							
GAATTCGGCC TTCATGGCCT AGCGGCAGCG GCTCTTCAAA GCGGAGCCGG GAGTTTTTGC TACAGTTTTC GCCACCATGA GTCGCAGCTA TAATGATGAG CTGCAGTTCT TGGAGAGAT CAATAAAAAC TGCTGGAGGA TCAAGAAGGG CTTCGTGCCC AACATGCAGG TTGAAGGTGT TTTCTATGTG AATGATGCTC TGGAGAAATT GATGTTTGAG GAATTAAGGA ATGCCTGTCG AGGTGGTGGT GTTGGTGGCT TCCTGCCAGC CATGAAACAG ATTGGCAATG TGGCAGCCCT GCCTGGAATT GTTCATCGAT CTATTGGGCT TCCTGATGTC CATTCAGGAT ATGGCTTTGC TATTGGGAAC ATGGCAGCCT TTGATATGAA TGACCCTGAA GCAGTAGTAT CCCCAGGTGG TGTCGGGTTT GACATCAACT GTGGTGTCCG CTTGCTAAGA ACCAATTTAG ATGAAAGTGA TGTCCAGCCT GTGAAGGAGC AACTTGCCCA AGCTATGTTT GACCACATTC CTGTTGGGGT GGGGTCAAAA GGTGTCATCC CAATGAATGA CAAAGACTCG AG  (2) INFORMATION FOR SEQ ID NO:791:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 468 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	60 120 180 240 300 360 420 480 540 582						
(ii) MOLECULE TYPE: cDNA							
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:							
GAATTCGGCC TTCATGGCCT ACATTTTCTG AGAAAGGTTT GGATGACTGA AATATTTCCT CTACAGTCAA GGACTTTGGC ATGTGGTGGC TGAAACTGAG CTTTTTTTGT TGGGCTCCAG TTCTCACTGT TCTGCAATGC TCATGGCAAG TTGAATGGTG AGCTAGCTTA TAAATTAAAG AGCTCTGAAC TGTATTCAGA CCGACTGGGT ATCTAGCTTA CTGTTTTTAAC ATCATTGTTG AAACCAGACC CTGTAGTCCA GTGGTGCTGC CCTGTTGTGC AAACTGCTCC TTTTTCTCGT GTTTTTGTAA AGAGCTTCCA TCTGGGCTGG ACCCAGTTCT TGCACATACA AGACACCGCT GCAGTCAGCT AGGACCTTCC CGCCATGTAT TCTATTCTGT AGTAAAGCAT TTCCATCAAC AATGCCTAAT TGTATCTGTT ATTTTTGGTT TAACACACAC TGCTCGAG	60 120 180 240 300 360 420 468						
(2) INFORMATION FOR SEQ ID NO:792:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 519 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double							

(ii) MOLECULE TYPE: cDNA

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

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GAATTCGGCC TTCATGGCCT ACGTGGCTAT AACTGGAAAA CTGGATCCGA AATCGACCAG
                                                                       60
TAAACTGGGT AGCTCGGTCT ACGCCCCGCC CACCACCCTT GCTAGCCAAT AGCCTTCACA
                                                                      120
ACTCTTCTGC CACTCCCGCC CATTCCAGTG CTGTGCCGCT GCTTTTTCTT CCACTCGGAT
                                                                      180
CTCTTGAGCG CCCTTAGCCC GCTGTATACG CGCCCCTCCT CGGCTTCAGT AGGCAAGAGG
                                                                      240
GCCATCTGCC CTTCCTTCCT GAAGGTAGAG GGGACAACAC CAGCTACGAC GGGGACTCCA
                                                                      300
GAAGTCCATC TCCCGAACAG CAGCGGGGCG AAAAGAAAGA AAAAGGGTTT CCGAAGACTC
                                                                      360
CTACTCACAC CCACGCTTTC CCTTAACCCG GAAGTGATTT CCGCCCCTCC TCTCCCTCTT
                                                                      420
CGGTTGATAC TGGAGGAGAA GGACGGCCAG GTCTGGCCCG GCATGCCCTG GGCTTCCGGT
                                                                      480
GACCTCTGGC CCTTTTCTGT CGTCCACTCT CCGCTCGAG
                                                                      519
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- (2) INFORMATION FOR SEQ ID NO:793:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 338 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GAATTCGGCC	AAAGAGGCCT	ACAGAAACAT	CCAATTCTCA	AACTGAAGCT	CGCACTCTCG	60
CCTCCAGCAT	GAAAGTCTCT	GCCGCCCTTC	TGTGCCTGCT	GCTCATAGCA	GCCACCTTCA	120
TTCCCCAAGG	GCTCGCTCAG	CCAGATGCAA	TCAATGCCCC	AGTCACCTGC	TGCTATAACT	180
TCACCAATAG	GAAGATCTCA	GTGCAGAGGC	TCGCGAGCTA	TAGAAGAATC	ACCAGCAGCA	240
AGTGTCCCAA	AGAAGCTGTG	ATCTTCAAGA	CCATTGTGGC	CAAGGAGATC	TGTGCTGACC	300
CCAAGCAGAA	GTGGGTTCAG	GATTCCATGA	ACCTCGAG			338

- (2) INFORMATION FOR SEQ ID NO:794:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 756 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GAATTCGGCC	AAAGAGGCCT	ACCAGGATGG	TCTCAATCTC	CTGACCTCAT	GATCTGCCTG	60
CCTCGGCCTC	CCAAAGTGCT	GGGATTACAG	GCGTGAGCCA	CCGCACCCGG	CCCTAAACCC	120
TAGGTTTTGA	CTTCTGTAAG	AAGGAAAGAT	TTAAACAAAC	AAACAAACAT	TAAATTACAA	180
CCATAATAAA	·CAAAAAAACA	CTAAACTAAA	TTACAACCAT	AATAAAATCT	CCCAAAGTCC	240
GTAGGCACTG	ACATATTACA	GCCTTGCCAA	ATCAGAATAG	ATTTCTCATG	TGTTGTCAAT	300
TTACCAGACA	CAAAGAGTAG	CTCAGATCTC	ATAGACTCTT	CAGATCTTGT	AGACTAATTT	360
CAAGTCTTTT	TAAAGTTTTG	AAAAACATGT	GCTATTTGGA	ATTACGTCAT	CCTCGAATAT	420
TAAACCTGAG	CTCAAAAACC	TATTGTTTGA	TATTGGAAAT	AGTTAACTCC	AGTTTTCTTC	480
TATTAAGATA	AAATTCTTTC	ATCATGTCTG	TGCCCTCTAA	AATAATACTC	CTATTGCTTT	540
GTCTTCCCCT	TCTCCCCTCC	TAGTCCTTCT	TTAGTCATTC	TATTTAGAAT	CAAGTCGCTC	600
ATGAGTTTAA	GAATTAGAGC	AGCAAGAAAT	TGGGCTAGAG	ATGTACAAAA	GCTTTGGACA	660
ATAGTAGTTT	TGCTTGTCCT	CATTCTTATT	AGAAGTGCTG	TTAATTTACT	GATAAATTCT	720
AGGACGGAAG	ACAAATCTTT	GCAACTGGTA	CTCGAG			756

- (2) INFORMATION FOR SEQ ID NO:795:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 648 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (11) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GAATTCGGCC	AAAGAGGCCT	ACCAGGAAGC	TCTCCTGCTT	GTCATGAAGT	GAGAACAATG	60
AAAAGTCATA	GCAGATACTC	AGTTTAACTC	TGTGTAGAAC	CTATTAGTGT	TTGAGCTGTT	120
ATTCAGATTT	GAATTCAGAC	TGTGTGTTGT	TTGCTTATGG	ACACTGCCTG	TCGTTCTGTC	180
ACTGTTAAAT	TAATGAGTCT	ATAAGGTTTT	TCTTCCAGAG	GCCATAGGTG	ACATCACTAA	240
AATTGCAAGA	TAAATTGTAA	TCTTTGNTGN	TGCTGCACTC	CCCAACCTCT	CCCCCACCCC	300
CCGTGGTGTG	CTGCTTTCTA	GATGAGCGTG	TTTTGGAGCA	GGCCCATCTG	GGACACTCTA	360
TGCTTTCACC	AAGGAAGTGC	GATCTGAGCA	GCCACAATCC	AGCCAAAAGA	GGATCGTAGA	420
TATTTGCTCT	GATCAACTAG	ATGAAAATAT	AGCAGAATGG	ATTTAGCCCA	CTGCTCTGTT	480
TTATCCAACT	GAGTCTCTGA	CCAGCAATTG	GTGCATAATT	ATTACAGCAA	AAGTTAAGAA	540
ATGAAACTGT	AGCAATTATG	TAAATGAATG	TGTTGGCCTC	TTAATACCTG	TTACTAGTGG	600
ACTTCCTGTG	AGGAAGTTAG	TTTTTTTTTT	TGATGAAATG	CTCTCGAG		648

- (2) INFORMATION FOR SEQ ID NO:796:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 610 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GAATTCGGCC	AAAGAGGCCT	AAGAGGCTGG	CCCCAGTCCC	AAGGAACAAG	AGATGGTCAA	60
GTCGCTAGAG	ACATATCAGG	GGACATTAGG	ATTGGGGAAG	ACACTTGACT	GCTAGAATCA	120
GAGGTTGGAC	ACTATACATA	AGAACAGGCT	CACATGGGAG	GCTGGAGGTG	GGTACCCAGC	180
TGCTGTGGAA	CGGGTATGGA	CAGGTCATAA	ACCTAGAGTC	AGTGTCCTGT	TGGTCCTAGC	240
CCATTTCAGC	ACCCTGCCAC	TTGGAGTGGA	CCCCTCCTAC	TCTTCTTAGC	GCCTACCCTC	300
ATACCTATCT	CCCTCCTCCC	ATCTCCTAGG	GGACTGGCGC	CAAATGGTCT	CTCCCTGCCA	360
ATTTTGGTAT	CTTCTCTGGC	CTCTCCAGTC	CTGCTTACTC	CTCTATTTTT	AAAGTGCCAA	420
ACAAATCCCC	TTCCTCTTTC	TCAAAGCACA	GTAATGTGGC	ACTGAGCCCT	ACCCAGCACC	480
TCAGTGAAGG	GGGCCTGCTT	GCTCTTTATT	TTGGTCCCGG	ATCCTGGGGT	GGGGCAGAAA	540
TATTTTCTGG	GCTGGGGTAG	GAGGAAGGTT	GTTGCAGCCA	TCTACTGCTG	CTGTACCCTA	600
GAAGCTCGAG						610

- (2) INFORMATION FOR SEQ ID NO:797:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

GAATTCGGCC	AAAGAGGCCT	AGCCACTATC	CTGGTTACTT	GTGGATTCAC	CAAGCAGTCC	60
AGCAAGTCAT	CCGTAGAAAT	GAATGTTTGA	GGAGTCGTAG	TAGTATTTGA	GGCAATCTGT	120
TCCTCAATTG	CATTTTCACT	GTTGCTCATT	ATTTGTTGTC	TCTTGGCACA	ATGCAATTTT	180
CCAAAGTGTT	CTCCATCCTT	GTCCACAAAG	TCTTTCCCAT	CACTTCCAAA	TATGCCTCCT	240

286

CTTTCTGAAG GCGGTTCTTC GGACCTCTGT GCTACAGGGA CTCGAG

(2) INFORMATION FOR SEQ ID NO:798:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 163 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:	
GAATTCGGCC AAAGAGGCCT AGTTTTTTAT TGGTTTGGAG ACTAGAGCCA ATAGTATAAT GTTCTCAAAG GAAACAGACT TGAGTTGTTG GATTAGAGGA ACTAACCCAA CTTATATGAT TTTTTTTTTG TTTTTGTCGT GTAGTTATGG CACTAGTCTC GAG	60 120 163
(2) INFORMATION FOR SEQ ID NO:799:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 443 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:	
GAATTCGGCC TTCATGGCCT AGAGGGAATG CGGAGAGGGG TGGAGAAATT CCATCTTTGT TAGGGCAGCA GTCAAGGATG AGTGAGTTAG CCTCTTTAAGG AAGAGGCTAA GCTGTTAGAA TAAAGAGGTT TACAACATCA GCGGCTTAAA TCAAATAGAA GTGTGTTTCT CTTTCACATG ACAGAGTAGA TGTGGCCTGG CATCTAGAAA GCATATTTGT CTCTGGTCCA CTGTGTCTTC CAGGGACCCA TTCTTCTCTT GTCTTCATGC TCCATCACTT CCTAGGGTGT TGTCTACACC TGCATAGCCA TAGCTAATTT TCCATTCTCA GCACCAACCA GGGGAAGAGG AGGAAAGGTA GCCTCCTTTT CATGATAGGT GTGAAGTTAT GCAGGACACT CTCAGGGTGA ATGGACCACA GTGTGGCTCC TCCTGGGCTC GAG	60 120 180 240 300 360 420 443
(2) INFORMATION FOR SEQ ID NO:BOO:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 305 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:	
GCATGTGCAG CGGCAAAGAG AACCCGGACA GTGATGCTGA CTTGGATGTG GATGGGGATG ACACTCTGGA GTATGGGAAG CACACAATACA CAGAGGCTGA TGTCATCCCC TGCACAGGCCG AGGAGCCTGG TGAAGCCAAG GAGAGGAGG CACTTCGGGG CGCAGTCCTA AATGGCGGCC CTCCCAGCAC GCGCATCACA CCTGAGTTCT CTAAATGGGC CAGTGATGAG ATGCCATCCA CCAGCAATGG TGAAAGCAGC AAGCAGGAGG CCATGCAGAA GACCTGCAAG AACGGTCGAC TCGAG	60 120 180 240 300 305
(2) INFORMATION FOR SEQ ID NO:801:	

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 464 base pairs(B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

GAATTCGGCC	AAAGAGGCCT	AAACACTCAA	ATTTTACATT	TTGAGCAGTA	TTTACGCCTG	60
AATTAATTCA	CAAGTTTCAA	GGTCACTAAC	TTTGGTTATA	TTATATTATT	ATTTTCCAAT	120
TTAGCCACCT	CTTTATTTGT	ATAATAGAGC	ATACAGCAGC	ACATAAAACG	CAAAACTCTA	180
GGACATAAAA	AGTGGCATTC	GGACGATGTT	GCTCTGAAAT	TTATGCATTA	ATTAAACCGG	240
TATATATGTA	TGCATTAATT	AAACCAATAT	TTATGAAGTT	CCTACTGTGT	TACAGACGTG	300
GATCCAGGCA	CTGAGGATGC	AGCAGGCCAT	CCAAATATAA	AGTTACTTCC	TTAGGAAGCT	360
TCCATTCTAA	TGGGAGAGTG	TTGTTAAAGA	GATATATAAT	AATATGTAAA	ATGAATCCAT	420
AATGGTGAGT	ATTATGAAGA	ATAAAATTGC	CAGGTTTTCT	CGAG		464

- (2) INFORMATION FOR SEQ ID NO:802:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 650 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

GAATTCGGCC	AAAGAGGCCT	AATCTTCTGC	CTGTTCTGAA	AAAGCTTTGC	TTCTTGTGAT	60
TTGTATCACG	AGGGGGAAAG	GTCCTTACTG	TTTTTCCAGA	CCTACAGTTG	TGATAGAGGC	120
TCCTCCCAGC	CCCGCCCACA	GACCCCAACA	GTGCCCTCTC	TCACAAATGG	ATTCTGGGGC	180
TTGGTCTTTA	TTTTTGTTTT	TGTTGGGGGC	AGCATATGGA	ACCCAAAAAT	AGTATCATAG	240
CCTAAATTTG	GAGCTTTGTG	CCAGCCTTGT	CTGTAGGATG	ACCCGTGTGG	GTCTCACCTG	300
GTGACTGGGA	GTCCACAGGG	GTCAGTTAGT	AGCAGGGAGC	TGCAGGGCGC	CTGTCAGCAG	360
AGACCGTCTC	ATTCCCCAAA	CCCAGGAGCC	AGAGGAACTG	ACGCCCGGAT	AAATGCCCAA	420
GCCGCCCCGG	GTGGGATTAG	TCGTCTACCT	TCCCAGAAAT	ACACCCTCCC	ATCCTGTGAC	480
TTGGATACAG	TTTACTGATG	AAATTAGGGA	ACCTCCTGCG	CCTTACCAAG	AAGCTGTGGC	540
TGGAACTTAG	TCAATGAAAA	ATGATTTGTA	AACTCTTTGG	AGCTGGCTTT	GAAAGAATGT	600
TTAAAATGAT	AGCTGATACT	GCCAGACAAC	AGAACAGGCC	GGCCCTCGAG		650

- (2) INFORMATION FOR SEQ ID NO:803:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 101 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

GAATTCGGCC AAAGAGGCCT AAGAGAACAG GAGCATTACA GTAAAATTCC TAAGTAGCCA
ACTGATTTGC AGTGCCAGAA ATGAATACCG ATCCACTCGA G 101

(2) INFORMATION FOR SEQ ID NO:804:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 723 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:804: GAATTCGGCC AAAGAGGCCT AGCTCTCTGT ACCCAAGGAA AGTGCAGCTG AGACTCAGAC AAGATTACAA TGAACCAACT CAGCTTCCTG CTGTTTCTCA TAGCGACCAC CAGAGGATGG 120 AGTACAGATG AGGCTAATAC TTACTTCAAG GAATGGACCT GTTCTTCGTC TCCATCTCTG 180 CCCAGAAGCT GCAAGGAAAT CAAAGACGAA TGTCCTAGTG CATTTGATGG CCTGTATTTT 240 CTCCGCACTG AGAATGGTGT TATCTACCAG ACCTTCTGTG ACATGACCTC TGGGGGTGGC 300 GGCTGGACCC TGGTGGCCAG CGTGCATGAG AATGACATGC GTGGGAAGTG CACGGTGGGC 360 GATCGCTGGT CCAGTCAGCA GGGCAGCAAA GCAGACTACC CAGAGGGGGA CGGCAACTGG 420 GCCAACTACA ACACCTTTGG ATCTGCAGAG GCGGCCACGA GCGATGACTA CAAGAACCCT 480 GGCTACTACG ACATCCAGGC CAAGGACCTG GGCATCTGGC ACGTGCCCAA TAAGTCCCCC 540 ATGCAGCACT GGAGAAACAG CTCCCTGCTG AGGTACCGCA CGGACACTGG CTTCCTCCAG 600 ACACTGGGAC ATAATCTGTT TGGCATCTAC CAGAAATATC CAGTGAAATA TGGAGAAGGA 660 AAGTGTTGGA CTGACAACGG CCCGGTGATC CCTGTGGTCT ATGATTTTGG CGACATCCTC 720 723 (2) INFORMATION FOR SEQ ID NO:805: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 406 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:805: GAATTCGGCC TTCATGGCCT ACGGCCAAAG AGGAGGAGAT GGCGCCAGTC AGGGAGCGGC 60 -CGTGGCCCAG ACAGTGAGGA AGCGCGAAGG CGGAGCAACC GAGGAATCCT CCGGAGAAGA 120 ATCAGAGCCG TCGCTACCGC CACTACCGCC ACCACCATGG AAGGAGCAAA GCCGACATTG 180 CAGCTCGTGT ACCAGGCAGT GCAGGCGCTT ACCACGACCC AGATCCCAGC GGAAAGGAGC 240 GCGCCTCTTT TTGGCTTGGG GAGCTGCAGC GTTCGGTTCA TGCATGGGAG ATCTCAGACC 300 AGTTGTTACA GATCCGGCAG GATGTGGAGT CATGCTATTT TGCTGCACAG ACCATGAAAA 360 TGAAGATTCA GACCTCATTT TATGAGCTCC CCACAGTACT CTCGAG 406 (2) INFORMATION FOR SEQ ID NO:806: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

GAATTCGGCC TTCATGGCCT ACGCCCGGGT TGGAAGTGTG CAGTCAATGA GCTCCCGCTC 60
CTCCTGGATC CGTCTGTAGG TCTCCCCGGT GTGCATGAGC AGCTCACTCA CTGGCTTCTT 120
TAGGTGTTCG CTGAGGGCTT CCTGCTGCTT CTTCCGCAGG GCTGTGTTAC GCTGCCAGTT 180

TTTCAGAAAG TTGTGCTGAG GAGGTGGGGC CCAGGGAGGT CTCTTCTCTT	240 300 329
(2) INFORMATION FOR SEQ ID NO:807:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 225 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:	
GAATTCGGCC TTCATGGCCT AAGGTACTTT AATCAGTCTA AATACTTGAA CATTTTTATT TCAGTGGTAA AAAATAGACT GAGGCAGAGT GAAGTTATAA ATTAGAATCT AAAAATTTAC CCTTCAACAT TAATATTTTT TAGTGCTCTA ATATAAAACA CAGAAAACCT ATCTCAAATA TAAAAGATGA ATATAAAATT ATTAATTAAA CAACTGGCGC TCGAG	60 120 180 225
(2) INFORMATION FOR SEQ ID NO:808:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 275 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:	
GAATTCGGCC TTCATGGCCT AACTTGCTCT TCTGTTTCTA GTTTTATAAA GTGAAAGCTG CAATCATTGA TTAGAGACAG TTCTACGCTA AAGTCATAAT GACATTTTAT GTAATTTCTT TTTTCTTTTT TTTGAGACAG AGTCTCGCTC TGTTGCTCAG GCTGGAGTGC AGTGGAGTGA TCTCAGCTCA CTGCAACCTC TGCCTCCCAG GTTCAAGCGA TTCTCCTGCC TCAGCCTCCC GAGTAGCTGG GATTACAGGC CCCCACCAAC TCGAG	60 120 180 240 275
(2) INFORMATION FOR SEQ ID NO:809:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 253 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:	
GCGATTGAAT TCTAGTTGCC TACCTACCAA ACTACCTACT GAACTTTTTA ATTTGAAGAT ATTCTTCCTG GACTACTTGT TTATAGTTTA TTAAATGAAC TGCTCTATTT CTAAAAACTT TATTTTTAAA GTCCTTTCCC GTTTAGAATG CGGCATACTC TTGCTTGTGG GGTATATATC TCTGATCGTG ATAACTACCT ACCGAAAACC TTTCATGGCT CCTTGCCAAC TACAAAATTG CGATATCCTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEO ID NO:810:	

(A) LENGTH: 283 base pairs

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:
GAATTCGGCC TTCATGGCCT AGATTGAATT CTAGACCTGC CGACGCGGGG AGAGACAAAA 60
AAGAGAAAGT CTTTGAAAAG CACAAGGAGA AGAAGGATAA AGAGTCCACA GAAAAGTACA 120
AGGACAGGAA GGACAGAGCC TCAGTGGACT CCACGCAAGA TAAGAAAAAT AAACAGAAGC 180
TCCCCGAGAA GGCTGAAAAG AAGCACGCTG CCGAAGACAA GGCTAAAAGC AAACACAAAAG 240
AGAAGTCGGA CAAAGAACAT TCCAAGGAGA GGAAGTCCTC GAG 283
(2) INFORMATION FOR SEQ ID NO:811:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
/ IN CHANGE PROCESSING ON AN INC. OA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:
GAATTCGGCC AAAGAGGCCT AGGCTTCCAC CCAGGAAATG ATCCAGAGCC TCTTTTATGT 60
TATGTTTTTT GTTTGTTCCT TTCAAGACAA TCGATCAAGC CAGAGGCATT CCCCACCCTT 120
CAGCAAGACA CTTCCCAGTA AGCCCAGCTG GCCTTCAGAG AAAGCAAGGC TCACCTCCAC 180
CCTGCCGGCC CTGACTGCTT TGCAGAAACC TCAAGTCCCA CCCAAACCCA AAGGCCTCCT 240
TGAGGATGAG GCTGATTATG TGGTCCCCGT GGAAGATAAT GATGAAAACT ATATTCATCC 300
CACAGAAAAG CTCGAG 316
(2) INFORMATION FOR SEQ ID NO:812:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:
GGGATGCATA GATTTAGTTC TGCCTCACAG GCAGGTAGCC TGAGCTCCTA GGGGGAACTG 6
TTTTTGCTAA GTAGGGAATG AAAAGCATGT TTATTTAAGC ACAAAATTAA ATCTCTCCTA 12
TTTTTATATG ATTTCCCGTT GTTTTCTTCC CTGTAGGGAA ATCTGCTGTG ATAGAGAACT 18
GCGTAACAGG CCTTTTCTGT GAGCGCTCAC TCATACATTA TGCACGACGT GGCTAAGATC 24
TTTGATGGCA CTCGAG 25
(2) INFORMATION FOR SEQ ID NO:813:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GCAAGCGGCG CATGCAGGAG	GAGAAGCAGA	AGTCTGTCAA	CGTCAAGAAG	ACCATCCTGG	60
AGATGCGCTA CGGGGCTGAT	GTGGATGCCG	GCTCCATTGT	GCACGCCGCC	CAGAAGCTGG	120
GCGAGCCTCC CGTGCTGCCC	GTATCTCGCA	TGGCCTCCAT	CCCCTCCATG	ATCGGGGAGA	180
AGCTGCCCAC CGCCAAGGGG	TTGGAGGCCG	GGCTGGACAC	ACCCAAGGTA	GCCACCAAAG	240
GCAACTATAT CGAGGTGCGC	ACAGGCGCCG	GCGGGGACGG	TCTGGCTCGG	CCCGAGGATG	300
ACCTCCCGGA CCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:814:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GAATTCGGCC	TTCATGGCCT	ACGAACTCCT	GACCTCAAGT	GATCGGCCTG	CCTCAGCCTC	60
CTAAAGTGCT	GGGATAGCCA	CTGTGCCCAG	CCTAGCCCTT	CTTCAAATGT	TTGGTAAAAT	120
TCAGCATTGA	AGCCATCAGG	TCTTGGGCTT	TTTGCTGGGA	GATTTTTTAT	TATGGCATCA	180
ATCTCATTAC	TTGTTACTGG	CCTGTTTAGG	TTTTCAGTTT	TTTCATGGTT	CAATCTTGGT	240
AGGTTGTTTG	TGTCTAGGAA	TGTATCTGTT	TCTTCTAGGT	TTTCCAGTTT	CTTGGCGTAT	300
AGTTACTCAT	AGTAGCCACT	AATTATCCTT	TGGATTTCTG	CGGTATTGGT	TGTAGTGTCC	360
CCATCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:815:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 382 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCAAGCCTAT	CTTTTAGTCT	60
TCCTAGAAGC	ACCGTGTTCT	GTGGAACTCA	GCATCAGCAG	CTTTGCTGAG	GACTCCCCCA	120
TCTTCCTTTC	CTTCCCCGGA	AAGCACAGAC	CTAAGTGAGT	CTTCACTGGA	TCCCAGCTAA	180
CAGCTTCTGC	CCATTCCTAT	CTTTCCACAG	AGCCAGTGGC	AGCCCCAGCT	GCAGCAGCTA	240
CGTGACATGG	GCATCCAGGA	CGATGAGCTG	AGCCTGCGGG	CCCTGCAGGC	CACCGGTGGG	300
GACATCCAAG	CAGCCCTGGA	GCTCATCTTT	GCTGGAGGAG	CCCCATGAAC	TCCCTGCTTC	360
CCCTGAACCC	CCAGCACTCG	AG				382

- (2) INFORMATION FOR SEQ ID NO:816:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 274 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GCCACGGTGC TCATTCAGAC	TACCCGTGTG	CCCAAGCAGG	TGGCAGTACC	CGCGACAGAC	60
ACCACTGACA AGATGCAGAC	CAGCCTGGAT	GAAGTCATGA	AGACCACCAA	GATCATCATT	120
GGCTGCTTTG TGGCAGTGAC	TCTGCTAGCT	GCCGCCATGT	TGATTGTCTT	CTATAAACTT	180
CGTAAGCGGC ACCAGCAGCG	GAGTACAGTC	ACAGCCGCCC	GGACTGTTGA	GATAATCCAG	240
GTGGACGAAG ACATCCCAGC	TGCAACATCT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:817:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 356 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

GAATTCGGCC	TTCATGGCCT	ACAAAAATAC	ACCTGTGGTC	CCAGCTGCTC	GGGAGGCTGA	60
NTTACGAGAG	TCCCTTGAAC	CTGGGAGGCG	GAGGTTGCAG	TGAGCTGAAA	TCATGCCACT	120
GCACTCCAGC	CTGGGCAACA	GAGCGAGACT	CTGTTNAAAA	TAAAAAAAA	AGCGAGAGAT	180
CGAGAGAGAG	TGCACGTGAG	AAGACTAGTA	GTTGCTATGG	ACTGGGGGAG	AAGGAACGGG	240
TTACAGGGTT	TCTTTTGGGG	ATAACGAAAA	TGTTCTAAAA	CTGGACTGTG	GTGATAACTG	300
CACAACTCTG	TGAATGTACT	AAAAACTACT	GAACTGGCCG	GGCGCGGCAG	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:818:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 184 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GAATTCGGCC	TTCATGGCCT	AGGCAGGGTG	TCAACTTATT	TAATTCTAAA	AATAGTATAT	60
TCATAGAGAT	ACTATCATCC	TCATTTCATA	TATTCAAAAA	ATTCAAAGAA	GTTAAGTAAA	120
TTGCCAAAAG	TCACCCAGAT	AATAAGTAGA	AAAGATGGTA	ATGAAATCCA	GGTTGGCCTT	180
CGAG						184

- (2) INFORMATION FOR SEQ ID NO:819:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 349 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GAATTCGGCC	TTCATGGCCT	ACAACAACAA	CAACAAAAA	ACATCATCCG	GGGAAGCTTT	60
TCAATATCCT	GACGTTGGGT	CTCTCCAGTG	TAGATGGAAA	TATGGAATTG	GGAATAGACA	120
TCGATATTTT	TGGAGGTCCC	CAGGGGTTAC	CAATGTGCAG	ACAGGTTTGG	GAACCACTGC	180
ATTAGGCATT	TTACATTTAT	TTAGGGCTTT	CACTGGATTT	GTCACCCCAT	ACTTTCATAA	240
TCCATTTTTT	${\tt CTGATTTTT}$	TTCTGGTTTT	TGGTGAGGGT	ATAGTTGGGA	TGGGGTTTTT	300
TTTTTTGTCC	TCCCACCGCT	CGCCCCCATC	CAGTGTGGAC	GTACTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:820:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 167 base pairs
    - (B) TYPE: nucleic acid
    - . (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

GAATTCGGCC	TTCATGGCCT	ACTCTTTCCT	TGAAGAATTT	GTTGAAGACT	TCAGAAGTGA	60
TGCTGGCTGC	TTTCTTCATT	AGGTTGAGCT	CCCCATCCTC	CTTTACAGCG	ATGGTATATG	120
CCACAACTGC	ACTGATATCT	ATTTTGTCAA	AGCCTTCAGG	TCTCGAG		167

- (2) INFORMATION FOR SEQ ID NO:821:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 733 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

GAATTCGGCC	AAAGAGGCCT	AGCGAAATAA	AACAAGGGAG	TCAGCAAAAC	CAGAAATTTC	60
AGCAATGTCA	GCTCATGACA	AGGCTGCATT	ATCAGAAGAG	GAACTGGAGA	GGAAGTCGAA	120
ATCTATCATT	GATGAATTTC	TACACATTAA	TGATTTTAAG	GAAGCCATGC	AGTGTGTGGA	180
AGAGCTGAAT	GCCCAGGGCC	TACTACATGT	TTTTGTGAGA	GTGGGAGTGG	AGTCCACCCT	240
GGAAAGGAGC	CAGATCACCA	GGGATCACAT	GGGCCAACTA	CTCTATCAGC	TGGTACAGTC	300
AGAAAAACTC	AGCAAACAGG	ACTTTTTCAA	AGGTTTTTCA	GAAACTTTGG	AATTGGCAGA	360
TGACATGGCC	ATTGATATTC	CCCATATTTG	GTTGTACCTT	GCTGAACTGG	TGACCCCCAT	420
GTTAAAAGAA	GGTGGAATCT	CCATGAGAGA	ACTTACCATA	GAATTTAGCA	AACCTTTACT	480
TCCTGTTGGA	AGAGCTGGGG	TCTTGCTATC	TGAAATATTG	CACCTACTAT	GCAAACAAAT	540
GAGCCATAAG	AAAGTGGGAG	CCTTATGGAG	GGAGGCTGAC	CTCAGCTGGA	AGGACTTTTT	600
ACCAGAAGGA	GAAGATGTAC	ATAATTTTCT	TTTGGAGCAG	AAGTTGGACT	TCATAGAGTC	660
TGACAGTCCC	TGTTCCTCTG	AAGCACTTTC	AAAGAAAGAA	CTGTCTGCCG	AAGAGCTGTA	720
TAAGCGACTC	GAG					733

- (2) INFORMATION FOR SEQ ID NO:822:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 512 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

TGCCAGATAG	TTCTGCAGAA	GAAATCACTG	TTTGTCCTGA	GACACAGGTA	AGTTCCTCTG	60
AAACTTTTGA	CCTTGAAAGA	GAAGTCTCTC	CAGGTAGCAG	AGATATCTTG	GATGGAGTCA	120
GAATAATAAT	GGCAGATAAG	GAGGTTGGTA	ACAAGGAAGA	TGCTGAGAAG	GAAGTAGCTA	180
TTTCTACCTT	CTCATCCAGT	AACCAGGTAT	CCTGCCCGCT	ATGTGACCAA	TGCTTTCCAC	240
CCACAAAGAT	TGAACGACAT	GCCATGTACT	GCAATGGTCT	GATGGAGGAA	GATACAGTAT	300
TGACTCGGAG	ACAAAAAGAG	GCCAAGACCA	AGAGTGACAG	TGGGACAGCT	GCCCAGACTT	360
CTCTAGACAT	TGACAAGAAT	GAGAAGTGTT	ACCTCTGTAA	ATCCCTGGTC	CCATTTAGAG	420
AGTATCAGTG	TCATGTGGAC	TCCTGTCTCC	AGCTTGCAAA	GGCTGACCAA	GGAGATGGAC	480
CTGAAGGGAG	TGGAAGAGCA	CGTTCGCTCG	AG			512

## (2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 423 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GAATTCGGGC	CTTCATGGCC	TACTCTCATC	TGTATCTGTT	TCCTCTAACT	TTACTGAAAA	60
GATAGAATTC	ATTAAGCATG	AATTCTACCA	TCTTCTCCCT	ACTACAGCTC	TGTCAAAAAG	120
ATGTTGCTCT	CTGAGCCCAA	CTCTCCCTCA	GTCCCCAGGA	TTCTGTCCCT	GTCCACCTTT	180
AATCTTTTCC	TTTCCTGATT	TTATGTTATA	AGTTATTTAG	ATTTCGATGA	GAGATAATCG	240
TACCTAGAGT	ATGGGAGAAC	TATTTAAGGT	TTACAGGTTG	GGTGGAACCC	TTGTATATAC	300
TAGATGGTAC	TGTGAGGGCT	TGCCACACTG	TCAGCCTTCA	TCTGAACAGA	GCAGAAAGTG	360
TTTCTGCATG	TTCACCAAGC	CCTGCTGGAC	TGTATCACTT	TTCTCTGTGG	GCCAAAACTC	420
GAG						423

- (2) INFORMATION FOR SEQ ID NO:824:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 353 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GAATTCGGCC	TTCATGGCCT	AGCGGCCTCA	GATGAATGCG	GCTGTTAAGA	CCTGCAATAA	60
TCCAGAATGG	CTACTCTGAT	CTATGTTGAT	AAGGAAAATG	GAGAACCAGG	CACCCGTGTG	120
GTTGCTAAGG	ATGGGCTGAA	GCTGGGGTCT	GGACCTTCAA	TCAAAGCCTT	AGATGGGAGA	180
TCTCAAGTTT	CAACACCACG	TTTTGGCAAA	ACGTTCGATG	CCCCACCAGC	CTTACCTAAA	240
GCTACTAGAA	AGGCTTTGGG	AACTGTCAAC	AGAGCTACAG	AAAAGTCTGT	AAAGACCAAG	300
GGACCCCTCA	AACAAAAACA	GCCAAGCTTT	TCTGCCAAAA	AGATGATCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:825:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 506 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GAATTCGGCC	AAAGAGGCCT	AGGAGTAAGG	ATGCAGAAAT	GATTGCAGCA	TATTTCATTC	60
TCTACGCAAG	GATGTTCCTC	GGAAATGGAG	GCGACATTGC	TGCCTGCTTT	TTTGAGGGAA	120
TTGATGATGT	TCACTGGAAG	GAAAATGGGA	CATTAGTTCA	AGTAGCAACT	ATATCAGGAA	180
ACATGTTCAA	CCAAATGGCA	AAGTGGGTGA	AACAGGACAA	TGAAACAGGA	ATTTATTATG	240
AGACATGGAA	TGTAAAAGCC	AGCCCAGAAA	AGGGGGCAGA	GACATGGTTT	GATTCCTACG	300
ACTGTTCCAA	ATTTGTGTTA	AGGACCTTTA	ACAAGTTGGC	TGAATTTGGA	GCAGAGTTCA	360
AGAACATAGA	AACCAACTAT	ACAAGAATAT	TTCTTTACAG	TGGAGAACCT	ACTTATCTGG	420
GAAATGAAAC	ATCTGTTTTT	GGGCCAACAG	GAAACAAGAC	TCTTGGTTTA	GCCATAAAAA	480
GATTTTATTA	CCCCTTCAAC	CTCGAG				506

- (2) INFORMATION FOR SEQ ID NO:826:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 337 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GATGGAGCAG	TTCCAGAAGG	AGAAGGAGGA	ACTGGACAGG	GGCTGCCGCG	AGTGCAAGCG	60
CAAGGTGGCC	GAGTGCCAGA	GGAAACTGAA	GGAGCTGGAG	GTGGCCGAGG	GCGGCAAGGC	120
AGAGCTGGAG	CGCCTGCAGG	CCGAGGCACA	GCAGCTGCGC	AAGGAGGAGC	GGAGCTGGGA	180
GCAGAAGCTG	GAGGAGATGC	GCAAGAAGGA	GAAGAGCATG	CCCTGGAACG	TGGACACGCT	240
CAGCAAAGAC	GGCTTCAGCA	AGAGCATGGT	AAATACCAAG	CCCGAGAAGA	CGGAGGAGGA	300
CTCAGAGGAG	GTGAGGGAGC	AGAAACACAA	GCTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:827:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 216 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GAATTCGGCC AAAGAGGCCT	ACAGGTACAG	AATCATATGA	ATGTTTCTTT	CTTTCTTTCT	60
TTTCTTTCCT TCTTTCCTTC	TTTCTTTCTT	TCTTTTTTTG	AGACAGAGTC	TTGTTCTGTT	120
GCCAGACTGG AGTGCAGTGA	CTCAATCTCA	GCTCACTGCA	ACCTCCACCT	CCCAGGTTCA	180
AGCAATTGTC CTCCCTCAGC	GAGGACCTGC	CTCGAG			216

- (2) INFORMATION FOR SEQ ID NO:828:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 386 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

GAATTCGGCC	AAAGAGGCCT	AAAAAAAAGA	AGATGGGTTT	TTTAAGTCCA	ATATATGTTA	60
TTTTCTTCTT	TTTTGGAGTC	AAAGTACATT	GCCAATATGA	AACTTATCAG	TGGGATGAAG	120
ACTATGACCA	AGAGCCAGAT	GATGATTACC	AAACAGGATT	CCCATTTCGT	CAAAATGTAG	180
ACTACGGAGT	TCCTTTTCAT	CAGTATACTT	TAGGCTGTGT	CAGTGAATGC	TTCTGTCCAA	240
CTAACTTTCC	ATCATCAATG	TACTGTGATA	ATCGCAAACT	CAAGACTATC	CCAAATATTC	300
CGATGCACAT	TCAGCAACTC	TACCTTCAGT	TCAATGAAAT	TGAGGCTGTG	ACTGCAAATT	360
CATTCATCAA	TGCAACTCAT	CTCGAG				386

- (2) INFORMATION FOR SEQ ID NO:829:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 293 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GAATTCGGCC AAAGAG	GCCT AGCTGAATCC TAGA	ATTTCAG CTTCTCACTC	AGAATTTAAG 6	0
CTGTTTTCAG TACCAG	AAAT ATTTAAGACT GTT	GTTTAA CTTCTAAGAA	TAGCAGATAA 12	0
AGCGTATAGG TGTTTTC	GAGA TAACCGTATT CATA	AGGAAAA ACAAACATAA	AACTTTCATA 18	10
ATTTTGGGAA GAGTTAG	CACA CAAAAATATC ATCA	ATTGAAT AATTAGTACA	ACAAAAATGC 24	0
ATTTGTTTGT CCTAAAG	GGTT GAAATGAACA GAAT	CATGAT GGGAATACTC	GAG 25	3

- (2) INFORMATION FOR SEQ ID NO:830:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 146 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GAATTCGGCC AAAGAGGCCT	AATTGAATTC	TAGACCTGCC	TATGTCCTAT	TCCCTGTGTC	60
CTGCAAGACC CCCTTTGGTT	TGGTTTTCTT	TTCTTTTCTT	TTTTTCTTTT	TTGAGACTGC	120
GTCTTGCTCT GTCTCCCAGG	CTCGAG				146

- (2) INFORMATION FOR SEQ ID NO:831:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 158 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

GCGATTGAAT	TCTAGACCTG	CCTCTCATCC	ACTATTGTCT	TTCCCCAATT	TTTTTCTAGC	60
CTTATCTTCC	AGAATTCCTC	TCAGACATAG	GTGGCCCTGG	TTGCTTGATC	CTGTCTCTAA	120

158

GTTGGTCTTT CATGTTTTCT CTCCTCAGAT TGCTCGAG

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:	
GAATTCGGCC TTCATGGCCT AGCTGATTTA AATCTAAAAA CTGGATAAGA AGCT TGTAATTAAA AATAGACCTT TATTCACTAG ACCTACAGTT TGCTTTTTTC ATAT AAAAGTTTAA TATCCTGCT. CTCTATTTCA GTTCTAGGGG CACCACTATC AGTT AAAAGATTTCT GTGGGTGAAA CCATTTTGAT TACCATCTTG CTCTGCTGCC AGTT ACCAAACTCT CTTTGTTTCT GGATGCTAAA TCTGTCCACT TGTGCCTTAA CTAC ACTCCCGTCA ACTCGAG	GTTAAG 120 PAACCCT 180 PATGGTA 240
(2) INFORMATION FOR SEQ ID NO:833:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 339 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:	
GAATTCGGCC TTCATGGCCT AGCCCCCGGA GCCCACCACA GTCCCCAGAG TGTG ACAATTTTA TACTTCTTAT CTCTTTCTAG TAGTCTACAT CCCATTCCCA GTCT TCATAAAAAT TTGTAGTTTA TTTAGTTCAC ACTTGAACGT CCTATGAAAC TGTT CTTTTACCTA TCTTGTTTCT TGTCATTATT CTTAAGCCAT TGATACAGAA ATCA AATTTAATAT TGTTGTGGGT ATGAGACAGT TTCTGTCATG TTTTAATTTT TTCC TTTTACTATG TACTTCATAT ATACCGGGCA CTTCTCGAG	TTCCAA 120 TTAAAC 180 GAACCA 240
(2) INFORMATION FOR SEQ ID NO:834:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:	
GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACAC ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTA AAAA ATTAAATTTC TCCTATATTT TATTTCATT ATTTTTTCAG TCATGCTCCT TCT CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTT TTTTATTTAT TTGTTTATTT TTGGAAACAG AGTTTCCTTA TGCTGCCCAC GCTC AGCTCAAGCA ATCTTCACGC CTCAGCCTCC CAAAATTATA GGACTACAGG CATC	AGAGATA 120 STATCTC 180 CCCCTTC 240 GGTCCTG 300
368	
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## (2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 294 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GAATTCGGCC	TTCATGGCCT	ACTTTTACTC	ATGCATAATT	TTGTAAAATC	CTACATTGGT	60
CATTTGGAAA	ATATTGATTC	ACTGAGTAAT	ACAACTCTTC	CAAATGTTGA	ATGTTTCATT	120
CTACAATATC	AGAAACTCAA	TTTGTTAATG	TTACTACTAG	TCTCATCAGA	AATGTCTTTA	180
AGTATTTGTT	AACTGGCAAA	CTCATAGTGA	CGACTACAGG	CTTTCCAGAA	TTTTCATTTT	240
CATTTGAAGT	CTGAATTTTA	TCAACTATAA	ATACTGTCAG	TTGTTTCCCT	CGAG	294

- (2) INFORMATION FOR SEQ ID NO:836:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GAATTCGGCC	TTCATGGCCT	ACTCTGATAC	TAACTGTAGT	CTACATTTAT	ACATTGTGTC	60
TGAATGCTGG	TTTTGTGGCT	TCACTAGCTC	CCTTTTTCTC	TCTCCTTTTT	TATCCTGTCT	120
TTTGCTGCTG	CTTTCCACCT	TCTGTCCAGC	TCCATCTTCA	GACAGCTCCC	TGTATAACGC	180
TCCACTTCCT	GAGTATTCCA	GTTGCCAGCC	TCCTTCAGCA	CCTCCTCCAT	CATACGCTAA	240
AGTCATCTCA	GCTCCAGTGT	CAGATGCCAC	TCCTGATTAT	GCTGTAGTGA	CTGCTTTGCC	300
ACCTACTTCC	ACACCCCCTA	CACCACCACT	GCGACACCCA	GCGACACTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:837:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 355 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GAATTCGGCC	TTCATGGCCT	ACCGGACCTT	GAAAATGGAA	TGTTCAGAAA	CACATGTGCA	60
AGGGAGCTGT	GCCAAGCTCA	TGTTGCGAAC	AGGCCTCCTG	ATGAAGCTTC	TCAGCGAGCA	120
GCAGGAAGCA	AAGGCATTGA	ATGTAGAATG	GGATACGGAC	CAACAAAAA	CAAATTATAT	180
TAATGAGAAC	ATGGAACAGA	ATGAACAGAA	AGAGCAGAAG	TCAAGTGAGC	TCATGAAAGA	240
AGTTCCAGGA	GATGACTATA	AGAACAAACT	CATCTTCGCA	ATATCTGTGA	CTGTAATACT	300
AATAATTTTG	ATTATAATTT	TTTGTCTTAT	AGAGGTGAAT	TCACATATGC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:838:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GAATTCGGCC TTCA	ATGGCCT AAAAATCTA	GTTGAGAAAA	AGAAAGAAAC	CAAGAAGGCT	60
AATCACAAGG GTTC	CTGAAAA TAAAACTGAT	TTAGATAATT	CTATAGGAAT	TAAAAAAATG	120
AAAACCTCAT GTAA	AATTTAA GATAGATTCA	AACATAAGTC	CGAAGAAGGA	TAGCAAAGAA	180
TTTACACAAA AAAA	ATAAGAA AGAGAAAAAA	AACATTGTTC	AACATACTAC	AGACTCTTCT	240
CTCGAAGAAA AACA	AAAGGAC ATTAGACTCA	GGCACCTCTG	AAATTGTGAA	ATCTCCCAGA	300
ATCGAGTGTT CTAA	AGACAAG AAGAGAAATG	CAATCAGTGG	TTCAACTCAT	AATGACAAGA	360
GACAGTGATG GTTA	ATGAAAA CTCAACAGAT	GGTGAAATGT	GTGACAAAGA	TGCTCTGGAG	420
GAAGATTCAG AAAG	GCGTTAG TGAAATAGGA	AGTGATGAGG	AATCTGAAAA	TGAAATTACA	480
AGTGTTGGTA GAGC	CTTCAGG TGATGACGAT	GGAAGTGAAG	ATGATGAAGA	GAAGCTCGAG	540

- (2) INFORMATION FOR SEQ ID NO:839:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 539 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GAATTCGGCC TTCATGGCCT	AGCATTTCAT	CTCTAAATTG	GGGAGAATAG	AAGCATCTAC	60
TTCATGTAGT AGCCAGGATT	AGAAGAGGGA	GGAATAACTG	GGCCCTGGAT	AGAATGTGAT	120
GAATGTATAT TCTTAATGAG	AAGTGGAAAT	AATTTGTGGT	TGAGAGCTGT	GCCTCAGATC	180
AGAGTGACAG GATACATGGC	TAGGCTATAT	TTTCCAGCAG	ATTAAGAGCT	GCAGCCCAAG	240
ACTCTGAAAT ATGAAGAAAA	AAGGAGAAGA	TGACAGCATA	TCTTTTTAAA	GAAATATTTT	300
CCAGCCAAAT GGTGCAGCAG	AGGACTTCCA	GGAATTTGTT	CTTGTTCTGT	ATCAAAGGTG	360
AAGAGTTCGT AGCCTTCAAG	GAAACAAGAA	ACCATGGGAT	GGAGTGAAGG	AAGGTGGCCT	420
GGAACCAGCT GCTGAGCCTC	TCTGAGCCCC	AGTTTCCTCG	TCTCTAAAAT	GGGGCTGATC	480
TCCTCTCCCT CAGACTGTTG	TTGCAGGAAT	TAAAACAGGT	GTTGAGTGGG	CTGCTCGAG	539

- (2) INFORMATION FOR SEQ ID NO:840:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 297 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

TTCCACAGCT	CTGATATTCA	GTAACCCATG	TGGAGAACAA	AAGGATTTTG	CTCCATGAAG	60
TCTAATTGCC	TGCTGAATAA	ATAAATAAAT	AGATGAAGCA	CTGCATGCAT	TAAATGAAAG	120
TAAATATTGA	CCCTGCCACC	ATATGTTTGC	TGGGGTGCTG	GCTGAAGTGT	GCTGGCAGGT	180
CCAATCAGTC	AGAGTCTGCC	AGCCCAGCAA	GCAGGAGAGA	CAGGAATATC	AAAAAGGCGC	240
TCCTGCTTGT	GCCTTAATCT	TTGTCCAACC	CCCAATTCCT	CCACCACAGG	CCTCGAG	297

WO 98/45437 PCT/US98/06956 .

# (2) INFORMATION FOR SEQ ID NO:841:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

GAATTCGGCC TTCA	ATGGCCT ACCTTATTAG	TGATTGGCGA	TTCAGGCCAT	GTCATAGGGC	60
CTTTCAGACA AAAG	GGTTCTT ATCCCAGTCA	GCTGGCCAAA	ACATTAACTT	TGGATTTCTT	120
ACCCTGCTAC AGCA	ATCTTCT AGAAAGGCAG	CAAGATAATA	TTGTGGCAGT	GCACAGATAA	180
CATCAGGGTA GACT	TTGACTG GAGAAAACCA	AATTCTGCGC	TTGCTCCTGT	GTGCCCCCAT	240
CCAGCTGTGC ATGC	CACACAC AGGACACCTT	TCTAGTATGA	AGAACTTGCA	TCATGTCTGC	300
CCTCTATTGA GCAC	CCCCCTT CTAGAAATAC	TTCCAAGTAT	TAGCATGTGA	ACTGTTGACT	360.
CTCGAG					366

- (2) INFORMATION FOR SEQ ID NO:842:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 190 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCTG	ACTTATGAAT	TCTTTCTGTG	TGATCGTAAA	60
AGTGCAGAGT	TTATTGCAAA	GAGAATCTTC	ATCTGAATCC	TCAGCCTGGG	AATCTTCCTC	120
TTCCACCGCC	AACTCCTCCA	CCCAGTCTGA	GTCTACTTCA	ATGGCCCGCT	CTTCCCCATC	180
CGCACTCGAG						190

- (2) INFORMATION FOR SEQ ID NO:843:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 627 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

GAATTCGGGC	TTCATGGCCT	AAGCTCCGCG	AGCCCCCTAC	AACTCGTTTC	CTTCCGTTCA	60
CCTTCGCAGG	GCGGCGACTG	GCGGCGCGAT	GGACCTGACC	GGGCTCCTGC	TGGACGAAGA	120
AGGCACCTTC	TCCCTCGCCG	GCTTCCAGGA	CTTCACGTTC	CTCCCAGGAC	ACCAGAAGCT	180
GAGTGCCCGG	ATCCGAAGGA	GGCTCTACTA	TGGCTGGGAT	TGGGAAGCCG	ACTGTAGCCT	240
GGAGGAGCTC	TCCAGCCCGG	TGGCAGACAT	TGCTGTCGAA	CTGCTCCAGA	AGGCAGCCCC	300
CAGCCCTATT	CGCCGACTCC	AGAAGAAATA	CGTAGCTCAT	GTGTCCCGGG	AGGCATGCAT	360
CTCCCCATGT	GCTATGATGC	TGGCTCTGGT	GTACATTGAA	CGGCTCCGGC	ACCGAAACCC	420
AGACTACTTG	CAGCATGTGT	CATCCTCTGA	CTTGTTCCTG	ATCTCCATGA	TGGTGGCCAG	480
TAAGTACCTC	TATGATGAAG	GGGAGGAGGA	GGAGGTCTTC	AACGACGAAT	GGGGAGCTGC	540
TGGGGGTGTG	GCCGTGCCCA	CTCTCAATGC	CTTGGAGAGG	GGCTTCCTGA	GTGCCATGGA	600

627

TTGGCATCTC TACACTGAAC GCTCGAG

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 305 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:	
GAATTCGGCC TTCATGGCCT ACCTGAGCTG CCGAAGCCGC CGTCCTGCTC TCCCGCGTGG GCTTCTCTAA TTCCATTGTT TTTTTTAGAT TCTCTCGGGC CTAGCCGTCC TTGGAACCCG ATATTCGGCC TGGGCGGTTC CGCGGCCTGG GCCTAGGGGC TTAACAGTAG CAACAGAAGC GGCGGCGGC GCAGCAGCAG CAGCAGCAAT CTCTTCCCGA ACACGAGCAC CACAGGCGCC CGAAGGCCGG AACAGGCGTT TAGAGAAAAT GGCAGACGAT ATTGATATTG AAGCTCTAGC TCGAG	60 120 180 240 300 305
(2) INFORMATION FOR SEQ ID NO:845:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 409 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:	٠
GAATTCGGCC TTCATGGCCT ACCAGAAAAA ACTTACATTG AAGAGAGGAT TCCTTGTTTT GACTATGTGT GTTTCTGCCG TCTTAGGCAG CCAACGTATT GGTTTACATG GATCTGGAGG ATTATGCACA CTAGTGTTGA GTTTCATTGC AGGGACAAAA TGGTCCCAAG AAAAGATGAA AGTCCAAAAAG ATTATTACGA CTGTATGGGA TATTTTTCAA CCACTTCTTT TTGGTTTAGT TGGAGCAGAA GTATCTGTTT CATCGCTTGA ATCAAATATT GTTGGCATAT CTGTTGCCAC TCTAAGTTTG GCATTATGTG TTCGAATTTT AACCACATAT CTATTGATGT GCTTTGCTGG TTTTAGTTTT AAGGAGAAAA TATTTATTGC TTTAGCATGC ATGCTCGAG	60 120 180 240 300 360 409
(2) INFORMATION FOR SEQ ID NO:846:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 370 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:	
GAATTCGGCC TTCATGGCCT AGGCACGGTA CATACGATTA TTATAAACAT CAGCTGCGGT TCTGGGAGTG AGCTTGTGC GTGTTAGTGC CATCTCCCTG ACAAATCTGA CCTGTACCCA CATCTCAGGC TGGGAAGGAG TAGCTGGGCC TCCCTTTAAT GCAGCGGCAC TGGTTTGGGT CACAAGAGCT GGTTTGATCA ACCCCTGACT CCCCCTGGCG GGAGGTGCTC GTCACATCTG GGAGCCTGAG CAGAGGTGCC GGGGCTTGG AAGCTGGAGA AATGATGGAT CTTTCTCCAG GAGAAACAAT TCTTATCTTC ACATCNGCCC CGTGCTCCAA ATGAAGAGCG CGTTTGCATA	60 120 180 240 300 360
372	

370

GCTGCTCGAG

(2) INFORMATION FOR SEQ ID NO:847: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 504 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:847: GAATTCGGCC TTCATGGCCT ACGCGCGGCC GAGCGGAGGC GGAGTCGGCG CCGAGAACAT GGCTGGAGGC AAAGCTGGAA AGGACAGTGG GAAGGCCAAG GCTAAGGCAG TATCTCGCTC 120 ACAGAGAGCT GGGCTACAGT TTCCTGTGGG CCGCATCCAC AGACACTTGA AGACTCGCAC 180 CACAAGCCAT GGAAGGGTGG GTGCCACTGC TGCCGTGTAC AGTGCTGCGA TTCTGGAGTA 240 CCTCACTGCA GAGGTGCTGG AGCTGGCAGG TAATGCTTCT AAGGATCTCA AAGTAAAGCG 300 TATCACTCCG CGTCACTTGC AGCTTGCAAT CCGTGGTGAT GAAGAGTTGG ATTCTCTTAT CAAGGCTACC ATAGCTGGGG GTGGTGTGAT CCCTCACATC CACAAATCTC TGATTGGAAA 420 GAAGGGACAG CAGAAAACTG CTTAGAGGGA TGCTTTAACC AACCTCTTCC TTCCCCGTCA 480 TTGTACTGTA ACTGGGACCT CGAG 504 (2) INFORMATION FOR SEQ ID NO:848: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:848: GAATTCGGCC TTCATGGCCT AAACAAGCAG AGGGACTCCC CAGATAGCTT CATACCCAGT TTAGCTTTAT AACAAGTGTA GTTTTAGGCT CTGTCTTGGC ATACTTGAGA GCACAATGGC 120 TGCTTCAAAA CAGGCATTTG AACTCGCTGT TTAATCAAAT TCTTCTTTAA TCTAAAGTGA GTTTCTCATA GAGAGCATAT ACACTTAACC CTTGAACAAT GTAGGGGTTG GGGTGGGGAG 240 TCAACCCCCT GTGAAGTAAA AATTTGCTAA TAACTTTTGA CTCCCCCAGA ACTTAACTAT AAATAGCCTA CTATTGATTG GAAGTGTTAC CAACAGCATA CACAGTTAAC ATATATTTTG 360 TATGTAATAT GTGTTATCCA CTATATTCTT ACAATAAAGT TAGCAAAAGA AAAAAATGTT 420 ATTAGGAATC CTCGAG 436 (2) INFORMATION FOR SEQ ID NO:849: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 502 base pairs . (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:849: GAATTCGGCC TTCATGGCCT ACATGAGCCC AGGAGTTGAA GGCTATAGCC TGGGTGACAC 60 AACAAGGCCC CATCTCTAAA AAATATATAA ATAAATAAAG TTAAGGATGC TGCGTGGTTT

ATATGTTCAG AAAGAGATTG AGGTAATAAA AGAGTTTTTG GCCAGGCTCT GGCTTACACC

TCGGCCTCCC AGAGTGCTGG GATTACAGGC ATGAGCCACC GCGCCCAGCC GGAAGTAGGT

TTTTTGAAGA GTCAGCTGAA AACAACTGTT GCCGTATTCG GAATTTAAAA TTTTAATTTG

AAAATATTAT AACTGAGAAA TTATTGTATA TATTTATGGT ATACAGCGTG ATGTTATGAT

180

240

300

360

420

ACATGTATAC AATGCAGAAT GATTAAATCA AGCTATTTAA CATAGCTGTC ACCTCAAATA CTATTTTTGT GGTCAGAAAT TTGAAATTTA TTATCTCAGG AATTTTGAAA TGTACAATAC ATTATTATTA ACTGTTCTCG AG 502
(2) INFORMATION FOR SEQ ID NO:850:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:
GAATTCGGCC TTCATGGCCT AGATAAAAAG AAACAAAAAA GAGAAGATAT GATAAGAGAA 60000000000000000000000000000000
(2) INFORMATION FOR SEQ ID NO:851:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 311 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:
GGTTCTGTAT TCTGTTGGTT GGAGTGTTCT ACTATTGTTG GGTGGAGTGT TCTATCTTCT GTTGGGTGGA GTGTTCTGCT GTTGTTGGGT GGCGTGTTCT ATATTCTGTT GTTGGGTGGC 12 GTGTTGTATA TTCTGTTTGTT GGGTGGCGT TTCTATCTTC TGTTGTTGGG TGGATGGATT 18 GTTCTGTATT CTGTTGGGT GCATGTTCTA TCTTCTGTTT TTGGGTGGA CGTTCTATCT CTGTTTGTGGT GGCGCATTCT ATATTCTGTT GTTGGGTGGC GTGTTCTGTA TTCTGTTGTG 30 GGTGGCTCGA G 311
(2) INFORMATION FOR SEQ ID NO:852:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 532 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:
GAATTCGGCC CTTCATGGCC TAGTCTCATC TCAGAGTACT CAGAGAAACT ATTTTTAAT CTCTAGATAT CAATCAATGA ATATTTATTA TTAAATACCT GCTATGTGCC AGATGGTGTT 120
374

AATTATAAGT	TTGTTCTCTT	TTTGTCGTGC	TACTTAGGCT	TTTATCATTT	TGTCCTATCA	180
TTAGGGAAGT	GGCTCCNNNN	CTTACAGCTA	${\bf ATTTTTTTT}$	CAATTTACTA	ATGACTTTTT	240
GTGGAGGTGG	GGATCTCTTC	TGTTCAACAT	TTTCTATGAT	TCATCTCAAT	CCTCCAGTGA	300
AAAATTATT	ACAGTTGCAG	TAAGTTCAGT	CATAGGGGCA	CTGGAATGAG	TCCTTAAAAC	360
TTTATGCTGC	TGCTTTTGCA	ATGATGGATT	GCCTGAGAAT	TAAGGAAAGA	TAACTACTCT	420
CTTGGTCACT	GTATTTCCAA	TCAACCATAT	CCTCCCAGAA	TATGATTTCT	TCCCTCAGGC	480
ATTTTAGAAA	AGAGACAAGA	GACAGATTTT	TTTTTTCAGG	CAATGACTCG	AG	532

- (2) INFORMATION FOR SEQ ID NO:853:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 415 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

GAATTCGGCC	TTCATGGCCT	ACTTTTTGAT	AAGCAACTAG	TGGTCTCATT	ATCAGAGGTC	60
CCTGAGGGGC	CCTACAGGCC	CCCCCAGGTT	CTGCCCCCAA	GATTCTAAGA	GAGACCTTGT	120
GCTAGGGCTC	TAGTCTTGAT	GTTCTTTGCA	TTGTTTGGAT	ATGAAGCCCA	GGATATGTGG	180
GCACAATAAG	GTAAATCATG	AGATGTGAAG	GAGAATGAAG	ATCAGGCCAG	AGGTCACCAT	240
TCATTGAAGA	GCCAGAGAAA	AAGAAAATTA	GTGCACAGAT	TTGTGTAGAT	TTACAGAGAA	300
CTTCTATTTG	CTGCAAGAAC	TTCATCAGGC	GCTGCACCAT	GCCTGATTTG	GAAAGGAGCT	360
TCTTTGGGGC	CTGATAGAAC	TGAATTAATA	TGAAGAAATT	GAAGTGGCTC	TCGAG	415

- (2) INFORMATION FOR SEQ ID NO:854:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 324 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

GAATTCGGCC	TTCATGGCCT	AGTAAAATTA	GCTGAAAAAT	AATTTTCCAA	TGCAAATACT.	60
AATGAGGGTT	ATATGACCGT	TGTCCAAAGC	ATTTGCAGTG	CTGCATGACA	TTTGTCCTAA	120
AACCTGACTC	TTAAAACATT	CCTTGTGAAA	ATAGAAATAT	TCCCATGCCT	AGATTCCAAA	180
TAATAAAAGA	CACTGAGAGT	GTTTTCAAAA	TTAATGGACT	GATTTAAATT	TCACTGGAAA	240
GCAGCTTTTT	AAAACTAAAT	TGTCTGGATG	TGGCCTCCCT	GTGATCACTT	CCAACTGCTT	300
ACTGCCAACT	TCTGGCGGCT	CGAG		•		324

- (2) INFORMATION FOR SEQ ID NO:855:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 616 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

GAATTCGGCC	TTCATGGCCT	AACGGCCTTC	AGATGGAAGG	AGGGCAGGTG	CATATCTGTT	60
AGCAAAATCT	TCACAATCAT	CTTGAGTTTC	TCAGCAAAGT	CGGCCTGGCT	GGAAATTCCT	120
GGCGCTGCCA	TGCTGAAGGT	GACCAGCAAC	ACAGCCCCCA	GGATGGTCAG	TTGTTCCAGC	180
TGCAACTGGA	GCTCGTGGAA	GCGAGACTGG	TCCATTAAAA	CTGTTTCGGG	GAACGGCCTC	240
TGGAGGTGGT	CCCACTTCAG	AAGCTTCAGG	TAAGCGTAAT	TCTGGACAGC	AACAGGGCTC	300
AGCCTGGGCA	TGTCCCCAGA	GCCAGCAGCC	ATTCCCCCCA	CTGGCAGGGC	GTGTTTATAC	360
TTCTGAGTCA	TAAGGTCCTC	TGAGGCTTCT	TCCAGCCACT	GGGTGACAAA	GTCCAGGGAA	420
TTTGGTTGCC	TCTCCAAAAT	CTCTTGAAAC	TTCTTCCTTT	CGTATTCAAC	TGACTGCTGC	480
ATGAGATGAG	GCCTGATGCT	ACTGATAGCA	AAGTTGGCCA	TGTCCACTTT	CATTAGGTCC	540
AACACAGAAA	AAATTTCTCT	GAAAAGGGGC	ACTATTTCCT	TAATGTCCTT	TAGTTTCTTA	600
ACTTCCTCAT	CTCGAG					616

- (2) INFORMATION FOR SEQ ID NO:856:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

GCTCTGGGTG	AAAAGATCTC	ACACCAATGT	ACATAATGTG	GCCATCCTTT	CCATTTTCAA	60
GAAGTTGCCT	TGCTTTGATA	CTGCAAATTC	AGTATTTGTA	CACTGGAATG	ATAAAAAGAT	120
GTTCCACTTT	CTTTTCAGCC	AGAAAGCTTC	CTCGTTGTGT	GTGTGCGTGT	GTGTCCCATC	180
CTATTGCCTG	TTCTTTCTAA	ATCTACATTT	TGTTACCTTA	TCCAATACTT	GCTTTAGCAA	240
GAACATTATG	GGGCCCACCA	TATTCCACAG	GGCCATGCCA	ACCTTTGGAA	AAAAGGTAGG	300
TCAAGGAAGA	AATCAGAACA	AACCCTGTGA	CCATTCCACC	TCCTTGCATC	TTGGGCTTGG	360
GTTTGGAAAC	TGACCAGCAA	GCTGGAGCTG	CCACCACAGA	GAAACATCAA	AGCAAAAGGG	420
TTCCAGGACC	AGAGATTAGG	TAACTAGCTA	CAGGCCAGAG	GAATGCTTCC	CTCTCTAGAT	480
CAACAAGCAC	CCTCGAG					497

- (2) INFORMATION FOR SEQ. ID NO:857:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

GTTCATGGCC	TAGATGCTGG	TTTGTTTTTG	TTTTCGTTTT	TTTGAGACAG	TCTTGCTCTG	60
TGACCCGGGC	TGGAGTGCAG	TGGTGCGATC	TCGCTCATTG	CAACCTCTGC	CTCCCAAGTT	120
CCAGCAAGTC	TCCTGCCTCA	GCCCCCCACC	GAGTAGCTGG	GACTACACGC	AAGTGCCACC	180
ACGCCCAGCT	ACTTTTTGTA	TTTTTAGTAG	AGATGGGGTT	TCACCATGTT	GGCCAGGCTG	240
GACTCGAATT	CCTGACCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:858:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 441 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:858:

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GAAACTATAA TCATCAGTAC TGTAATGAGC AATTATGAGG CCTACAAGCC TTCCACAGGA
                                                                       60
GCTATGGGAG ATCGACTAAC GGCAATGAAA GCAGCTTTCC AGTCACAGTA CAAGAGTCAC
                                                                      120
TTTGTTGCAG CCAGTTTAAG TAATCAGAAG GCTGGAAGTT CTGCTGCTGG GGCAAGTGGG
                                                                      180
TGGACTAGTG CAGGGAGCTT GAATTCTGTT CCAACTAACT CAGCACAACA GGGCCATAAC
                                                                      240
AGTCCTGACA GCCCCGTCAC CAGTGCCGCC AAGGGCATCC CAGGCTTTGG CAATACTGGC
                                                                      300
AACATCAGTG GTGCCCCTGT GACCTACCCG TCTGCCGGAG CCCAAGGAGT CAACAACACA
                                                                      360
GCTTCAGGGA ATAACAGCCG AGAAGGGACT GGGGGCAGCA ACGGGAAAAG AGAGAGATAT
                                                                      420
ACTGAGAACC GGGAACTCGA G
                                                                      441
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- (2) INFORMATION FOR SEQ ID NO:859:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 384 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GAATTCGGCC TTCATGGC	CT ACTGGTCGCC	AATGTGCTGC	AGGTCATGGC	TCCGGAATCA	60
AATTGGGCTC AAACGGGG	SCA AGCTCCAACA	CAGTGGAGCC	TGGCGCTACT	CCCACCTCCA	120
CCTTGCGGAT CTCAGAGG	CTG CAGGATGGCT	CTGCCCACCG	CACCCTGAGC	TGGCCCCGCT	180
TGGGGCTGGC ATTGGGGC	SAC AGTGTGTTCT	GGGCGTCTCT	GCTCCTCTCT	GCTGGTGCCT	240
GTGCCTCTGC TGGCCGCC	CCA CTCATAGATG	TCAGAGCCAC	AGGACGGCCC	CGCAGAATCC	300
CTGCGCCGAC CCTGCCGC	GGG GCTGGCTTTG	GTGCACATGC	AACTCGTCAT	CGTGGTCCCC	360
ATGGGCACCT CTGCTCTT	CT CGAG				384

- (2) INFORMATION FOR SEQ ID NO:860:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 421 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

GAATTCGGCC	TTCATGCCTA	CGTTTCCCGA	GAAACCAAGC	CACAAAAAGT	ACAGGGCCGC	60
CCTGAAGAAG	GAGAAACGAA	AGAAACGTCG	GCAGGAACTT	GCTCGACTGA	GAGACTCAGG	120
ACTCTCACAG	AAGGAGGAAG	AGGAGGACAC	TTTTATTGAA	GAACAACAAC	TAGAAGAAGA	180
GAAGCTATTG	GAAAGAGAGA	GGCAAAGATT	ACATGAGGAG	TGGTTGCTAA	GAGAGCAGAA	240
GGCACAAGAA	GAATTCAGAA	TAAAGAAGGA	AAAGGAAGAG	GCGGCTAAAA	AAACGGCAAG	300
AAGAACAAGA	GAGAAAGTTA	AAGGAACAAT	GGGAAGAACA	GCAGAGGAAA	GAGAGAGAAG	360
AGGAGGAGCA	GAAACGACAG	GAGAAGAAAG	AAAAAGAGGA	AGCTTTGCAG	AAGGGCTCGA	420
G						421

- (2) INFORMATION FOR SEQ ID NO:861:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 271 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

GGATTTCTTT GGAATGGGCA AAGAAGTGGG	GAATCTGCTA	CTGGAAAACT	CACAGCTTCT	60
GGAAACCAAA AACGCCTTGA ATGTGGTGAA	GAATGACCTG	ATTGCCAAGG	TCGACCAGCT	120
GTCCGGGGAG CAGGAGGTGC TGAGGGGCGA	GTTGGAGGCT	GCTAAGCAGG	CCAAAGTCAA	180
GCTGGAAAAC CGTATCAAGG AGCTGGAAGA	GGAACTGAAA	AGAGTGAAGT	CCGAGGCCAT	240
CATCGCCCGC CGTGAACCCA AAGTTCTCGA	G			271

- (2) INFORMATION FOR SEQ ID NO:862:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 288 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear . . .
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

GCGGCTCTTT	GGGAGGTGGT	CAGGGGAAAA	GATGGTCAGT	GCTTTTTCTG	GACAAATCCA	60
GGGGCCAATT	${\tt GAGGTGGGGA}$	GTCTATGAGA	AGGGCCCTGT	CAGCTGAGGC	GAGGGAAAGG	120
GCAGAGGACC	TAGAATAAAA	GGATATGGCC	TCTCTGTGCA	CTAGCAGGAT	GGGTAGGAAA	180
GGGAGATATG	AAAAGACGAA	ATGGGGACCG	GGTGCGGTGG	CTCACGCCTG	CAATCCCAGC	240
ACTCTGGGAG	GCCAAGGCAG	GCAGATCACC	CGAAGTCAGG	AGCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:863:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

GCTCGAGTGG .	AATGGGCCGA	GGAGATGGAT	TTGATTCTCG	TGGCAAACGT	GAATTTGATA	60
GGCATAGTGG .	AAGTGATAGA	TCTTCTTTTT	CACATTACAG	TGGCCTGAAG	CACGAGGACA	120
AACGTGGAGG	TAGCGGATCT	CACAACTGGG	GAACTGTCAA	AGACGAATTA	ACAGAGTCCC	180
CCAAATACAT	TCAGAAACAA	ATATCTTATA	ATTACAGTGA	CTTGGATCAA	TCAAATGTGA	240
CTGAGGAAAC .	ACCTGAAGGT	GAAGAACATC	ATCCAGTGGC	AGACACTGAA	AATAAGGAGA	300
ATGAAGTTGA .	AGAGGCTCTT	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:864:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 546 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

GGAATGGGGA GAGG	GATCTA CCAAGGTNAC	AGCAGTTTTT	TGAGCAGCTG	GCACGTGCCT	60
CTGCTGCCAA CATG	SATGAGG TACAGAACCC	AGCACAGGGA	ATGCTCAGCC	TGTGACTGTG	120
AGCTGGATGT GAGA	GTCTCC TGAGGACCCT	CGGTATACTC	AGAGCATTTC	CTCTCAGGGT	180
GCAGGAAGAG GAAA	GCAGAG GAAGTGGACT	TGAAGGACCA	AAGGTGGGAT	CCTAGCTGGG	240
CCAATCACTG AGAA	GCCATG TGGTCTTGGG	CAAGTCATTC	CCTTCTCTGA	GCCTCAGTTT	300
CCCCATCTGT AAAA	TGGAGG TAATGATACT	ATGCCTACCT	CATCATCATG	CTGTGAAGAT	360
TAAATGAGTT ATGC	CATGGA AGTGCTGTAC	ATTACCCATT	GATAATGTCT	CAGTGGCCTC	420
TCAATGAAAT GGAG	TGTGAC AGAGTGCCAC	ACTCTGAAAC	GGCTCATCCC	CGGTGATGGT	480
GCTGGGACTA GAAC	CCGGGC AACCTCGCAG	TGCCATGCCC	TACTGCATCA	CTACGTCCAC	540
CTCGAG					546

- (2) INFORMATION FOR SEQ ID NO:865:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 808 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

GAATTCGGCC AAAGAGGCCT AAGGATTCAT AGTATAAATC TTTAATTTAT CACAGTCTGT	60
ATTAAGTAAT ACTAAACCAC TTCGCATATA AATACATCAC AACAGTATAC TTCCGTTTAT	120
GCTATCTTGG TCTTTGTACT TTTGTTTTTG TACATTTTAC TTTGGCATAA ATGTCAAAGT	180
ACAGTATTGT TATTTAGCTT TAAATATTCA TTTGCCTCTC TCCTTAATGT AAAAAGGCTT	240
CTTCTCAACT TCCTGACATT TCTTGCTAAA CTATACACGT CTGCCCTGTT TTCCAACAGC	300
ACACTGTTCT GTACTGTCCC TTATTTATTT TTTTTTTTTT	360
GTTCTTTGCC CAGGCCGGAC TGCAGTGGTG CTATTTCGGC TCACTGCAAA CTCTGCTTCC	420
CGGGTTCACG CCATTTTCCG GCTTCAGCTT CCCGAGTAGC TGGGACTACA GGCGCCCGCC	480
ACCACGCCCG GCTAATTTTT TGTATTTTTA GTAGAGATGG GGTTTCTCCG TGTTAGCCAG	540
GATGGTCTTG ATCTCCTGAC CTCGTGATCC GCCCACCTCG GCCTCCCAAA GTGCTGGGAT	600
TACAGGCGTG AGCCACCGCA CCTGGCCTAT TCTGTCCCTT TTTAAAGCAG TTCTCTTTTA	660
AAAAATTGTG GTAAGATATA AATCACATAA AATTTGCAGT TATAACCATT TTAAAGTATA	720
TAATTCCATG GCATTAATTA CAGTCACAGT CTTTTACAAC TATTATTACT ATGTATTCCT	780
AAAGTTTTT TACCCTCCCC CCCTCGAG	808

- (2) INFORMATION FOR SEQ ID NO:866:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 361 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

GAATTCGGCC	TTCATGGCCT	AAAAGAAAAT	GGCTTCAGTA	AGTTAGGATG	AAAAATGAAA	60
ATAAAATATA	AAGAAGAAAA	TCTCGGGGAG	TTTAAAAAAA	ATGCCTCAAT	TTGGCAATCT	120
ACCTCCTCTC	CCCACCCCAA	АСТАААААА	GAAAAAAAGG	TTTTCTAATG	AAAATCTTTA	180
AAAATACTGT	CAGTATTTTA	AAATTTTCAA	CAGTATTATA	AAAACATTGC	ATCTCCCCAC	240
CTCTAATATG	CATATATATT	TTTCCTGCTA	AAATTGGTTT	CTACAATTGA	GTAAATGGCA	300
AATACATGAA	GCAATGTCCC	TAAATTTTAT	AAAGAAATTA	TATTTAATGC	ACATTCTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 880 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

GAATTCGGCC AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCGGC	ACGAGGAAAA	60
CAGTCTTTTA ACCTTTCAAA	ATGCCACAAT	GTGCATTTTA	GATTGCCCTT	AGTTTCCCAA	120
CTCTCAGTAT ATAGAGACTC	AATTAGAAAA	GAAATGGTGC	TAGTAGCTTC	AACCCACTGG	180
TATGTATTTG AGGAACTGTT	CCTGGTAGAA	GGCAGTACCG	TGTCCCTTGG	TATTGCTACT	240
GTGCCTGCTA TGTTACTTCT	TTATGTATAT	GATATGGAAG	TAACTCCTTT	TATACATGTG	300
GAGAAGTTTC ACAGCTTTTT	TTCATAGTCA	TTGCATTAAA	ATGTCTGCTG	AGGCTGGGTG	360
TGGTGGCTTA CGCCGGTAAT	CCCAGCACTT	TGGGAGGCCA	AGGTGGGTGG	ATCACCTGAG	420
GTTGGGAGTT CAAGACCAGC	CTGACCAATA	TGGTGAAACT	CCGTCTCTAC	TAAAAATACA	480
AAAATTAGCT GGGTATGGTG	GCGCACACCT	GTAATTCCAG	CTCCCGCCGG	GCGACTCGAC	540
CAAAGAGGCC GGAATTTGGC	CCTCGAAGCC	AAGAATTCGG	CACGAGGGGT	ATTTTTTTT	600
TTANTINTIC TGTTTCTCTC	TNGAGTGTAT	AGTGTAGAGG	GGGTTTCTGT	CTTGAGTGTA	660
GGCCTGGAGA TTTCCCTTAT	ATGGTACAAA	CCAGCAATGA	ATTAAGAGGT	CTCTTTTCTC	720
CAAGATCTAG TGTTTTGTAC	TAGGAGAACT	CTAAAAAGTA	TCTATTTCAC	TGTAGTGCCA	780
AAGTACAAAT TTATTTGGAT	TTATTTTTTG	CCATCTTATT	TTTTAATATA	TTTCTTTTTC	840
TATGTTGTGC TTCTTTCCCA	CCTCATCTCT	CCTCCTCGAG	•		880

- (2) INFORMATION FOR SEQ ID NO:868:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GAATTCGGCC	TTCATGGCCT	AGTCATGGCT	TTAGAATCTG	GAGAAGAGTC	TGACTCACTT	60
CTTTCCTGAG	GGGATGCACT	GGGTTTCACA	TCAAGTTCTT	GAGAGGATCC	CGAACGACTT	120
. CTCTGCCCCA	GGGGAGTCCG	AGCCACAGTT	TTCTGATCAA	CTGATGATTC	TGACCCGCTT	180
CTTTCTCTCT	GGGGGGTAAG	ACACTTGTTG	TTGAGCTCTG	GGGATGATGG	AGAACGACTC	240
CTCGGCCTAG	GAGTCTGAGG	CAAAGCTTTC	GGTTCTGGGG	AAGAATCACA	TTCGCTTCTC	300
CCTCTAGATG	GCGTTCTAGG	TATATCTTTC	ATTCCAGGAG	AGGACCCAGA	CAGGCTGTGC	360
CTCGAG	•		•			366

- (2) INFORMATION FOR SEQ ID NO:869:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 529 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

GAATTCGGCC	TTCATGCCTA	GAGGATCTTC	TCCTGACCCA	GCATCGCTCA	TCACAATGAA	60
GAACCAAGAC	AAAAAGAACG	GGGCTGCCAA	ACAATCCAAT	CCAAAAAGCA	GCCCAGGACA	120
ACCGGAAGCA	GGACCCGAGG	GAGCCCAGGA	GCGGCCCAGC	CAGGCGGCTC	CTGCAGTAGA	180
AGCAGAAGGT	CCCGGCAGCA	GCCAGGCTCC	TCGGAAGCCG	GAGGGGGCTC	AAGCCAGAAC	240
GGCTCAGTCT	GGGGCCCTTC	GTGATGTCTC	TGAGGAGCTG	AGCCGCCAAC	TGGAAGACAT	300
ACTGAGCACA	TACTGTGTGG	ACAATAACCA	GGGGGGCCCC	GGCGAGGATG	GGGCACAGGG	360
TGAGCCGGCT	GAACCCGAAG	ATGCAGAGAA	GTCCCGGACC	TATGTGGCAA	GGAATGGGGA	420
GCCTGAACCA	ACTCCAGTAG	TCAATGGAGA	GAAGGAACCC	TCCAAGGGGG	ATCCAAACAC	480
AGAAGAGATC	CGGCAGAGTG	ACGAGGTCGG	AGACCGAGAA	GCCCTCGAG		529

- (2) INFORMATION FOR SEQ ID NO:870:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 372 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

GAATTCGGCC	TTCATGGCCT	AATTTGAGCT	TCAAGTCTCC	ATGTGTATAA	TGTGGGGTTG	60
ATGCTGTGGT	GCTCCAAGGT	GTTGGGGGGT	TTTAGGCAGA	GTTCTTATGC	TTAATATAGG	120
ATGGAAAAGT	GTTCGAGCTT	CTTCCCTTTT	CTCTTTCTTC	TCTTCATCTG	ACATGAGCCT	180
GGGGTTCTAC	CTCTTCCAGA	TAATTCATCC	TGGAGCTACT	AATTCTATCT	CCCCATTGAT	240
TTTAGTGTCC	TGTCTGTTTC	TAAATCTACT	GGGCAGTTGG	AGACATTGTC	TTTTGTTCCC	300
TCATCTATCT	TCTGTATCCA	CAGTTGATAA	TTGTCTATGT	TTTTAGTGTG	TTTTAAGGAA	360
ACTAGTCTCG	AG					372
	ATGCTGTGGT ATGGAAAAGT GGGGTTCTAC TTTAGTGTCC TCATCTATCT	ATGCTGTGGT GCTCCAAGGT ATGGAAAAGT GTTCGAGCTT GGGGTTCTAC CTCTTCCAGA TTTAGTGTCC TGTCTGTTTC	ATGCTGTGGT GCTCCAAGGT GTTGGGGGGT ATGGAAAAGT GTTCGAGCTT CTTCCCTTTT GGGGTTCTAC CTCTTCCAGA TAATTCATCC TTTAGTGTCC TGTCTGTTC TAAATCTACT TCATCTATCT TCTGTATCCA CAGTTGATAA	ATGCTGTGGT GCTCCAAGGT GTTGGGGGGT TTTAGGCAGA ATGGAAAAGT GTTCGAGCTT CTTCCTTT CTCTTCTTC GGGGTTCTAC CTCTTCCAGA TAATTCATCC TGGAGCTACT TTTAGTGTCC TGTCTGTTTC TAAATCTACT GGGCAGTTGG TCATCTATCT TCTGTATCCA CAGTTGATAA TTGTCTATGT	ATGCTGTGGT GCTCCAAGGT GTTGGGGGGT TTTAGGCAGA GTTCTTATGC ATGGAAAAGT GTTCGAGCTT CTTCCCTTTT CTCTTCTTC TCTTCATCTG GGGGTTCTAC CTCTTCCAGA TAATTCATCC TGGAGCTACT AATTCTATCT TTTAGTGTCC TGTCTGTTTC TAAATCTACT GGGCAGTTGG AGACATTGTC TCATCTATCT TCTGTATCCA CAGTTGATAA TTGTCTATGT TTTTAGTGTG	GAATTCGGCC TTCATGGCCT AATTTGAGCT TCAAGTCTC ATGTGTATAA TGTGGGGTTG ATGCTGTGGT GCTCCAAGGT GTTGGGGGGT TTTAGGCAGA ATGGAAAAGT GTTCGAGCTT CTTCCTTTC TCTCTTCTC TCTTCATCT ACATGAGCCT GGGGTTCTAC CTCTTCCAGA TAATTCATCT TGGAGCTACT AATTCTATCT CCCCATTGAT TTTAGTGTCC TGTCTGTTC TAAATCTACT GGGCAGTTGG AGACATTGTC TTTTGTTCCC TCATCTATCT TCTGTATCCA CAGTTGATAA TTGTCTATGT TTTTAGTGTG TTTTAAGGAA ACTAGTCTCG AG

- (2) INFORMATION FOR SEQ ID NO:871:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 574 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GAATTCGGCC	TTCATGGCCT	AGGTGGTGGG	TGCCTGTAGT	CCCAGCTACT	TGGGAGGCTG	60
AGGCAGAAGA	ATTGCTTGAA	CCCGGCAGGC	AGAGGTTGCA	GTGAGCTGAG	ATCGTGCCAC	120
TGCACTCCAG	CCTGGGTGAC	AAGAGTGAGA	CTCTGTCTCA	AAGAAAAGAA	ACAAAAAATT	180
ATGTACACAA	ATATGGACAG	CACTGGCAAG	AAGTGTGGCA	AAAACACATG	TGGTTCTCTT	240
GTTTTGGGCT	CAGACATGTG	GCTGTGCCAT	TACAGACCCC	CGGGATTTAG	AATCCTCCTT	300
CTGAAAGGCG	TCCTGTGCAC	TCGTGAGCAC	CAGCCTGAAC	AGATGAAAAG	GCTGAGCTGG	360
AGGGGCTGGG	ACACAGCCCA	CCTTGACGAC	AGCTGCTCCT	GGCTGTGCGG	GGGGGTCTCC	420
AGGAAAGGCC	ATTCTCCCAC	TAGGATCGCC	AGGCCCTACT	GAGGCTCAAG	CTCCTTTGCT	480
GTTTGGAATC	TTCCCTCCCC	AGCCCCCAG	CCTCATCAAA	GGCTGCCTTT	TCCTGTTCAC	540
TGACCACAGC	TGCTTTGACT	CCATTAGCCT	CGAG			574

- (2) INFORMATION FOR SEQ ID NO:872:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 528 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

```
GAATTCGGCG TTCATGGCCT ACCAGACTAC TACGGACTCA TCTAACAAAA CAGCACCGAC
                                                                      60
TCCAGCATCC AGTGTCACCA TCATGGCTAC AGATACAGCC CAGCAGAGCA CAGTCCCCAC
                                                                      120
TTCCAAGGCC AACGAAATCT TGGCCTCGGT CAAGGCGACC ACCCTTGGTG TATCCAGTGA
                                                                      180
CTCACCGGGG ACTACAACCC TGGCTCAGCA AGTCGCAGGC CCAGTCAACA CTACCGTGGC
                                                                      240
TAGAGGAGGC GGCTCAGGCA ACCCTACTAC CACCATCGAG AGCCCCAAGA GCACAAAAAG
                                                                      300
TGCACACAC ACTACAGTTG CAACCTCCAC AGCCACAGCT AAACCTAACA CCACAAGCAG
                                                                      360
CCAGAATGGA GCAGAAGATA CAACAAATTC TGGGGGGAAA AGCAGCCACA GTGTGACCAC
                                                                      420
AGACCTCACA TCCACTAAGG CAGAACATCT GACGACCCCT CACCCTACAA GTCCACTTAG
                                                                      480
CCCCGACAA CCCACTTCGA CGCATCCTGT GGCCACCCCC AACTCGAG
                                                                      528
```

- (2) INFORMATION FOR SEQ ID NO:873:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 611 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GAATTCGGCC TTCATGGCCT	AAGCTGCACA	AAACGTAGAA	AGAAGACATA	GCGCCTGCCA	60
GGGGAATAGG AAATGAGGGC	ACTTACACAT	TAATGTGAAT	TAGTAATTGT	GGTATAGAAA	120
TGTTTTATAG TGAAAGATTC	AAATTTGCTT	TTCAAGAAAA	ATGCCAAAAG	CTATTTAAAT	180
AATTCGAGGT TACATCGTAG	GTTTTGATTT	TTCTCAATTT	AAGATACAGA	AATACAGCAA	240
GCCTTAATAT AAAGTTTCCT	AAAGTTTCTT	CAAGTATTTT	TTAAGGTGGA	GAAATGCAGG	300
AATTGTATAA CCAGAATTGT	TTCTGCCTTT	AGCTTTTCAG	AACTTGAGAT	GTGGCAGCAC	360
TGGACTGGGT TTTTTTAAAT	GTTAGGACTA	GGAATGTTTG	CTCTTGTTAA	TTATGAATTA	420
ATTGATTATT AAGTTTAGAA	TGCATTTTTA	CAAGTATCTA	ACTATCAAAT	TGTGTTTAGT	480
AACTTGAGTG TATGCACAAG	TTTGATCAAC	AGCAAAATAG	AGTTCTGAAT	TTCTTTTAAA	540
GTGATGATAT ATTATTTTGT	GAAACTTTGT	GTTTGAAAAT	GTTTATTTCT	GTTTATGGTG	600
TAATACTCGA G					611

- (2) INFORMATION FOR SEQ ID NO:874:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 303 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

GAATTCGGCC	TTCATGGCCT	ACGAGCGGTG	AAGGAGGAGA	CCAAGGAGGA	TGCTGAGGAG	60
AAGCAATAAA	TCGTCTTATT	TTATTTTCTT	TTCCTCTCTT	TCCTTTCCTT	AAAAATTTTT	120
ATTTTACCCT	GCCCCTCTTT	TTCGGTTTGT	TTTTATTCTT	TCATTTTTAC	AAGGGACGTT	180
ATATAAAGAA	CTGAACTCAA	CATTCAGGTT	GTTTTTTTT	TTGTTTCTAA	GTTTTTGCCC	240
TATTGAAGAT	GACTTCAGAA	AATCCATTCC	CCAGTCATGA	AAATGTACTG	TGCTATTCTC	300
GAG						303

(2) INFORMATION FOR SEQ ID NO:875:

```
(i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 348 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:
GAATTCGGCC TCATGGCCTA ACGGCAGCGG CAGCCTCTGA AAAGAATCGG GGCCCAAGAA
                                                                      60
AAGGCGGTCG TGTTATCGCT CCCAGGAAGG CGCGCGTCGT GCAGCAGCAA AAGCTCAAGA
                                                                     120
AGAACCTAGA AGTCGGAATC CGGAAGAAGA TCGAACATGA CGTGGTGATG AAAGCCAGCA
                                                                     180
GCAGCCTGCC CAAGAAGCTG GCACTGCTGA AGGCCCCAGC CAAGAAGAAA GGGGCAGCTG
                                                                     240
CCGCCACCTC CTCCAAGACA CCTTCCTGAG GACGCTGGCC CCAGTGCAGG CCAACATCCC
                                                                     300
ACCCCCTACC TCCATATGGG ACCTTGCAAG TCATCCCACT TCCTCGAG
                                                                     348
(2) INFORMATION FOR SEQ ID NO:876:
      (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 586 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:
GAATTCGGCC AAAGAGGCCG GAATTTGGCC CTCGAAGCCA AGAATTCGGC ACGAGGAGAC
TATTITCCAT TICACACAG AAATCTITGA TIATTCAGTA AAAAGAGGAA ATATAAGAAA
                                                                     120
AAAAATCAGA CTAGTCTGGC CAACATGGTC TAAAAATACA AAATTAGCCA GGCATGGTGG
                                                                     180
CGGGCGCCTG TAATCCCAGC TACTTGGGAG GCCCAAGCAG GAGAATCGCT TGGACTCGGG
                                                                     240
AGGCGGAGGT TGCAGTGAGC CGAGATCATG CCACTGCACT CCAGCCTGGC AGACAGAGCA
                                                                     300
AGACTCCCTC TCCAAAAAAG TTAAAAAAAA AAAAGAAAAA AAAGGCCGGG TGCAGTGGTT
                                                                     360
CGGCCTCCCA AAGTGCGGGG ATTACAGGCG TGAGCCACCA TGCCCGGCCA CTTTCTGTAT
                                                                     420
TTTTTAATAA ATAAGAAATA CACATTTAGT AGTAGTTACA AAGATCTGTA GGCCGTAGCA
                                                                     480
AATATTCAGT AACTGGAAGA TGCCAATGAA CATTGTTGGG TAGTATTTAA ATAACAAAAT
                                                                     540
GTTCAAATAT TTGACAAGAT TAACAACACT ACACGGCCTT CTCGAG
(2) INFORMATION FOR SEQ ID NO:877:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 445 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:
```

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCGGC	ACGAGGGTAA	60
TTTTAAAAAT	TTATGTATTT	TCTAGCATTT	GCCTCAAGGA	TTGAAATTTT	TTTTTTTACT	120
TGTGTTTACA	GGTAGAATTC	TTTATTTAAA	AAGTCAGTTG	AATATCAAAA	CTATTTGATA	180
TTCTTCAGAC	TGGAATATTA	TTCTCTAGTG	TAGAAGAAAA	CATTTTCTGC	TTACAAAACA	240
AATAGTAAAT	ACTCTAAAAT	AGGGGTTGGC	AAACTTTTCT	TAAATAAAAG	GCCAGATGGT	300
AACTATTTTA	GGTTTTGTGG	GCCATGTGTT	GATAACTATT	TTAGGTTTTG	TGGGCTACGT	360
ATGGGGTCAC	TCTCCCATTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTTTC	420

445

TGTGTGTG AGCGGCGCTC TCGAG

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:	
CTCACAGAAG CCAGCGCGGG TCTCTGCTCA GCACCCCAGC CGGGGCTCTG GACCCAGGGT AACAGCCCCA GTTCATCCCA ACCCCTCTCA GAGCCTCAAG AGGGGTAGCT CGGCTGCCGG AAGAGAGGGG TGCCCTATCC CTGGCAACCC CTCCACGTAG CGTACCCCAG CACCTGCCAC CGCCTTTGCC ATTTCTTTGA GCTTGAAGTT AACTCTCTTA GAGTCTAACT TTGGTTCATT TCTGCACAGG TACAATAGAT GACTTTATTT GTTTAAAATG TTTAATATAT ATACATACAT ATATATATAT TTGTCTGTAA GAATTATGTT TTAAACAGCT GCTGTAGAGT ACCTTTTTT AAGGTAAATCT TACAGTGGAG TATATTTTTT AAAGCACAAA ATTGGTGCCA AGACTGGGTG AGAAATGTAC ATTACCCCCT TATTATTTTG CGTCGGATTC CTCGAG	60 120 180 240 300 360 420 480 540 586
(2) INFORMATION FOR SEQ ID NO:879:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 414 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:	
TAATTATTTT AAAATGAACA TATGAATTT TATTAACTTT TAGTTAAATA CAGATTTTAC AACGAGGTCA GCATAAGCCT AAATCTATAT AGAGGGCTAA CTCAGGCATT GTCTTGTTTA TTTGTAGACT GGATTAAAAA CAACCTGTCC TGTTTTGTCA GTTCCCAGCT TCTTCGTTTA GAATAAATTA GACCAAAAGA AGAAACGTGC TTGTCTCTGT ATACCCGCAG AATGAAGTTA	60 120 180 240 300 360 414
(2) INFORMATION FOR SEQ ID NO:880:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 402 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:	
GAATTCGGCC AAAGAGGCCG GAATTTGGCC TCGAAGCCAA GAATTCGGCA CGAGGGTAAT TTTAAAAATT TATGTATTTT CTAGCATTTG CCTCAAGGAT TGAAATTTTT TTTTTTACTT	60 120
384	

TCTTCAGACT ATAGTAAATA ACTATTTTAG	GTAGAATTCT TTATTTAAAA AGTCAGTTGA ATATCAAAAC TATTTGATAT GGAATATTAT TCTCTAGTGT AGAAGAAAC ATTTTCTGCT TACAAAACAA CTCTAAAATA GGGGTTGGCA AACTTTTCTT AAATAAAAGG CCAGATGGTA GTTTTGTGGG CCATGTGTTG ATAACTATTT TAGGTTTTGT GGGCTACGTA CTCCTATTCT CTCTCTATCA CCTACCCTCG AG	180 240 300 360 402
(2) INFORM	ATION FOR SEQ ID NO:881:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 352 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:881:	
GTTTTTTTT TATTATAAAT TGTACTGTTA TCTTCTAGGT ATTACTTTTA	AAAGAGGCCG GAATTTGGCC CTCGAAGCCA AGAATTCGGC ACGAGGGGCC TTTTTTTTTT TTTTTTCNNG NNAGGCTTTC CCTAGGTGAT TTTTAATTGC AAATATCCAT TTTTCCCATA AAATATTGCT ATATGTTAGT ATATTAATCT CCTTTTTCAA CTCTATTGGT TCTGATAGCT TGTCAGTTGT CTACCTTTCA AAATATTTCT TACAAATAAT GAGATTTGCT CCTACTTTCC AATTTATCTC CTNNTCTTAC TGCACTGGCT AGGACACCAC TACCTTCTCG AG	60 120 180 240 300 352
	ATION FOR SEQ ID NO:882:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 351 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:882:	
TGGTTTTCTT ACTATGTACT ACTAAAGGGA GAGTTTTCTG	TTTTTAACTT AAAAATAGTT GTATTTATAT TCCACAATTT GTTCAAATAC ATAAACTTC TACAGGATGT TTTTAAACAA ATTCTTCACA TTGTGTTTTG TGCGGAATTT CAGGGAAATA GTTCTGTGTA TTTTTAATAG CTTAATTTGT TGGTAGGTGG TCACATGCAG TCCATGTGG ATTCTAACAT GACATTTAGT ATGTGAACA TCCCTTTGAT GCTGAAGGTA ATGCATCTGT TGAAAGAAGT TTGGATTACT GCTCTCTCT TTCTGCTCGA G	60 120 180 240 300 351
(2) INFORMA	ATION FOR SEQ ID NO:883:	
(i)·	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 548 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:883:	
GAAAAAGGTA	TTCATGGCAA GAAGGAGNCT TAGCATCAAA CTTTGGAAAG GGAAGCCAGA GAATGGACAA GTGACACTGT GGACAATGAA CACATGGGCC GCCGTTCATC TGTATTTATG AGAAAACTCG GGCCTTTGGC GAGAGCTCCA CGGAAAGTGA	60 . 120 180

TGAGGAGGAA	GAAGAGGGCT	GTGGCATACA	CACTGTGTAC	GTGGCCACCG	CAAAGGACGG	240
GTTNTGCAAC	CCTAGGACCG	ACCCCCACCA	CCCTTCCCCA	GCTCCTGACC	NTTCCCAGCC	300
CCCTCCAGGG	CCAATGCAGC	ACTAAATCCC	TCTCTCCTCC	AGCATTCCTG	TGTCTGTCTG	360
GCCCTAAATG	TATCCATGTG	GCTACTTCTC	CAGCCCCCTC	CTTCCCTNTC	TTCTGCCTGA	420
TAGAGGGAAG	AGGAAGAGGA	GGACGAACAG	AGATCCTGAA	ATTCTGACTT	GCTGCTATTC	480
CAGAACCCAG	CCTCCTGGGT	TTCCCCAGTC	CTCATTTTTC	CTCCCAATAC	CCACCCTTCT	540
CTCTCGAG						548

- (2) INFORMATION FOR SEQ ID NO:884:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 446 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

GAATTCGGCC	TTCATGGCCT	AAAAAATACA	AAAAATTAGC	CGGGCGTGTT	GGCGGGCGCC	60
TGTAGTCCCA	GCTACTTGGG	AGGCTGAGGC	AGGAGAATGG	CATGAACCTG	GGAGGCGGAG	120
CTTGCAGTGA	GCCGAGATCG	CGCCACTGCA	CTCCAACCTG	GGAGACACAG	CGAGACTCCG	180
TCTCCNAAAA	ааааааааа	AAAAAAACAC	ACTTGTCTTA	CAAAGACTAA	CAAAAGATAC	240
TAAAATAAAA	AACTTTACAG	CATCATTAGA	AAGCGAACAA	AATCCTAAGA	TAGATACATT	300
TATCTTTCTT	GTTTTAGAAC	TTTTTCTGTG	TAATGGAATG	GAAATGCTTA	ATCTTGTTTC	360
AATGTTTTCA	GTGTTTGTGC	TTTGTCAAAT	TGAGGTTGGA	TGTTAAAGCC	CTTACTACTG	420
TATTATACAA	AGCAGCGAAC	CTCGAG				446

- (2) INFORMATION FOR SEQ ID NO:885:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

GAATTCGGCC	TTCATGGCCT	AGCCGGCGCC	GCCGNGTCTT	CCCGGTCTCC	TTTCCCGGCC	60
GCACAGGGTT	TTATAGGATC	ACATTGACAA	AAGTACCATG	GAGTTTTATG	AGTCAGCATA	120
TTTTATTGTT	CTTATTCCTT	CAATAGTTAT	TACAGTAATT	TTCCTCTTCT	TCTGGCTTTT	180
CATGAAAGAA	ACATTATATG	ATGAAGTTCT	TGCAAAACAG	AAAAGAGAAC	AAAAGCTTAT	240
TCCTACCAAA	ACAGATAAAA	AGAAAGCAGA	AAAGAAAAAG	AATAAAAAGA	AAGAAATCCA	300
CAATCCAAAC	CTCCATGAAT	CCGACTCTGA	GAGTGTACCT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:886:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

GAATTCGGCC	TTCATGGCCT	AAAAATCTAA	ATTAACTGAT	GAATAATTTA	AAACAGAATT	60
TCAACATTGA	GACAATGTAG	AGATATATTA	TGGTATAAAA	TGAAGCATTT	GCACGAACTT	120
TTTAGCTAAA	ATTTGTTTCA	AAGAAGTTGC	TTTTGTTTTT	AGTGTACCTT	GAGTTCAACA	180
CAGATGTGAA	TGCCCGCTTT	TTCCAGAAGG	GTTCTTGGGA	GAAAACACTG	GAGAAGTTCT	240
AAGCACTTTT	TTTTTTTTTT	TTTTTTTTT	TTTTTTTAGA	GATGGTTTCT	TACTCTGTTG	300
TTCAGGCTGG	AGTGCAGTGT	TGCAATCATA	GCTCACTGCA	GCCTTGACCT	CCTGGCCTCA	360
AGTGATACCC	CTGTCTCAGC	CTCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:887:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 364 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

GCCCCAGTCT	AAGGCATTTA	AAATTAAACA	GCTCTTCAAC	GCCCCAAGTT	ATTTCATCAG	60
GCTAAGAACT	TCTCCGAGAA	ACGCACAAGA	AGGCAGGCAA	ACAGGTGGGT	AGGTGAGAGG	120
TCACGGGGCT	CCATCTGCAA	GCTCCATCTA	CAAGGCATCA	ATCTGCGTTG	TGGCATCAAC	180
GTTAAAATGT	TCTACAGCTT	AGGGATCTTC	TTGAAGCAAG	GTTCCAAGCA	CAAAACTAGT	240
ATGACCGGAG	GCTCAATTTA	GAAGATGCAG	CATCTGAAAA	CCTTTACCCC	AGGAAAGGAG	300
GGGTGCCTGC	TGGCATTCAT	GGGCTCTGGA	ACAAGCATTT	ATTCAAAGCT	GATGGCCCCT	360
CGAG						364

- (2) INFORMATION FOR SEQ ID NO:888:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 416 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

GCACCCCCAA A	ATGCCAGCCT	CTCCTTTCTT	CCCATCCACC	AGTATACTGC	GGGGCCATTT	60
CTGGTCTTTG T	CCAACAGGA	AACCCATTTC	TGGTGGGATA	TGCCTTCCAG	TGCCACAGGG	120
CCACTCACCC C	CATGCATCTC	TGTCCTGCCC	GTCAGTGCTG	GGACGGACAG	CAAGGGCAAG	180
CCCAGTGTCT C	GCCGGATAGG	TGGGTGGGAA	CAGAGAGGGG	AGAATGCCGT	CCTAAGCTTC	240
TGCTTGGGGA 1	CCCCCACAC	GACCTGGGTA	CTGCCTGGGA	AACCTGTCCT	AAGTAAAACT	300
ATGGACCTCG C	CTCGCCCAC	CGGCCTGCGA	AGCCAGCATC	TCCGTGAAGG	TGGATGGAAG	360
CGCCTTTGTC C	CTCATTTTGA	GCTGCAAGCT	GGGTCAGCGG	CTCTGAAGCC	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:889:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 349 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

GTAGGCCATG	AAGGCCGAAT	GGAAAAAGTC	AGTTAAAGAG	GACTCAGTCC	CCACAGGTGC	60
GGAGGAGAAT	GTGGTGTGTG	AGTCACCAGT	AGAGATTATA	AAGTCCAAGG	AAGTAGAATC	120
AGCCTTACAA	ACAGTGGACC	TCAACGAAGG	AGATGCTGCA	CCTGAACCCA	CAGAAGCGAA	180
ACTCAAAAGA	GAAGAAAGCA	AACCAAGAAC	CTCTCTGATG	GCGTTTCTCA	GACAAATGAC	240
ATCAGACTCC	ACAGAAAAGA	CTATCACACC	GCCAGAGCCT	GAACCAACAG	GAGCACCACA	300
GAAGGGTAAA	GAGGGCTCCT	CGAAGGACAA	GAAGTCAGCA	GCTCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:890:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 719 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

GAATTCGGCC TTCATGGCCT	AGACCTGCCT	CGAGGATGCT	CTGGGTTTGC	TGTAGTCGTC	60
TGTTACTGGT CNTGTTAGGA	GGAGGGCCAG	GGGGACCCCC	ACCTGGGGCA	GTCCCTTCTG	120
TCCCTTCAGC AGGTGGCTGA	GCTGGAGCAG	ACATTTTTCT	GACAGAGAGA	GTGAGGGTCT	180
GTTCCTCTCC GGAGGCTGCG	GCGAGACACC	CGGCGAGGGA	CGCTGCGGCT	GAAGTGGACG	240
GAACTGCCAA GCTCCGCCTC	GCGCCGACTA	CCCCGCGGTC	TAGCTGCGCT	GGGGTTTCAC	300
CATGTTGGCC AGGATGGTCT					360
AAGTGCTGGA ATTACAGGTA	TGAGCCACTG	TGCCTGACAC	CTGTCAAATT	ATTTTACTGT	420
GTTTATTTAC CATGTTTCTT					480
TAACTTCTTT TGTTATTTAG	GAAGGTTTAT	ATTAATATTT	TAATTCTACA	TTGGATAATT	540
CCTATATCAA AACTATTGTT	GACAATCAGT	TACAGATGGA	ACTTCGTCTA	CTCTTTCTCC	600
CCTTCTCACT CCTGCTCTTT	CTCCCTTTCT	CACTCCAGCA	GTTGACTAGT	CTCATTGAAA	660
AAACAAATTG GGGCCGGCCA	GGCATGATGG	CTCATGCCTG	TAATCCCAGA	CAACTCGAG	719

- (2) INFORMATION FOR SEQ ID NO:891:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 453 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GAATTCGGCC	TTCATGGCCT	AGATACTCCG	CTGAAGATCT	GATGTCACCC	CAAATGCATG	60
GCTCCAGCCT	CAGTTCAGCT	TTCCACACTG	CTTGCAGAAA	TTCCTTCATT	TATCTTGAGT	120
TTCTCCTCTC	ACTCCCATGG	TAGCTTTTCC	ATTCCCACTG	CCTCTTCTCA	CATTTCAGTA	180
GATGAGAATA	GAAGCCATAG	GAAGCAAACT	TCCTCAACCT	CCAGCCAACC	GCCGAGCGAT	240
GGGCATCTCT	CGGGACAACT	GGCACAAGCG	CCGCAAAACC	GGGGGCAAGA	GAAAGCCCTA	300
CCACAAGAAG	CGGAAGTATG	AGTTGGGGCG	CCCAGCTGCC	AACACCAAGA	TTGGCCCCCG	360
CCGCATCCAC	ACAGTCCGTG	TGCGGGGAGG	TAACAAGAAA	TACCGTGCCC	TGAGGTTGGA	420
CGTGGGGAAT	TTCTCCTGGG	GCTCAGACTC	GAG			453

- (2) INFORMATION FOR SEQ ID NO:892:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

GAATTCGGCC	TTCATGGCCT	ACCAGCCTCT	GGGCTGAGGC	AAAGACCTCT	GAGGCCCCGT	60
CCACCCAGGA	CCCCTCCACC	CAGGCCTCCA	CTGCGTCCTC	CCCAGCCCCA	GAGGAGAATG	120
CTCCGTCTGA	AGGCCAGCGT	GTGTGGGGTC	AGGGACAGAG	CCCCAGGCCA	GAGAACTCTC	180
TGGAGCGGGA	GGAGATGGGT	CCCGTGCCAG	CGCACACGGA	TGCCTTCCAG	GACTGGGGGC	240
CTGGCAGCAT	GGCCCACGTC	TCTGTGGTCC	CTGTCTCCTC	AGAAGGGACC	CCCAGCAGGG	300
AGCCAGTGGC	TTCAGGCAGC	TGGACCCCTA	AGGCTGAGGA	ACCCCTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:893:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 467 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

AACAGGAGAT	GGACAAGCTG	AAGGAGCAAT	ATGATGCTGA	GTTGCAGGCC	CTGAGGGAGA	60
GTGTGGAAGA	AGCAACCAAG	AATGTCGAGG	TCTTGGCGAG	CAGGAGCAAC	ACTTCAGAGC	120
AAGACCAGGC	GGGGACTGAA	ATGCGCGTGA	AGCTTCTGCA	GGAGGAGAAT	GAGAAGCTGC	180
AGGGAAGAAG	CGAAGAGCTG	GAGCGGAGAG	TTGCTCAGCT	TCAAAGGCAG	ATCGAGGACC	240
TGAAAGGCGA	TGAAGCCAAG	GCGAAGGAAA	CGCTGAAGAA	GTACGAGGGA	GAAATACGAC	300
AGTTAGAGGA	GGCCCTTGTG	CACGCCAGAA	AGGAAGAAAA	AGAAGCTGTG	TCAGCCAGAA	360
GGGCCCTGGA	GAATGAACTG	GAGGCTGCTC	AGGGAAATCT	GAGTCAGACT	ACCCAGGAGC	420
		CTCAAAGAGG				467

- (2) INFORMATION FOR SEQ ID NO:894:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 315 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GAATTCGGGC	TTCATGGCCT	ACTCAGCTTT	CCTGGTCTCC	CATCTGAACT	GCTTCTTTGT	60
GCACCTCTTG	TTCTTTCTCT	TGGCTCCCAG	TCTTGATTCC	TGTGATCACT	CTTGCATCAC	120
TAATTGCACA	AGTGATTTCA	GGTGCAATTC	TGATTAGCCT	GCGTCCACAC	AGTGATCGAT	180
GATCCTATGT	GCCTAGAAAG	GACACTGTGT	GCTGCTCATG	ACCTGCAACA	GGAAAAAAGC	240
CATTTCTTGT	TAGCAGTGTA	AGAACCTTAG	AGCAAAGGAG	TTGACCTTCT	GATTGAATAT	300
AAGCACAACC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:895:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 302 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GGGCTTAGTT A	AGGAGCTATG	GCTAAACATC	ATCCTGATTT	GATCTTTTGC	CGCAAGCAGG	60
CTGGTGTTGC (	CATCGGAAGA	CTGTGTGAAA	AATGTGATGG	CAAGTGTGTG	ATTTGTGACT	120
CCTATGTGCG 7	CCCTGCACT	CTGGTGCGCA	TATGTGATGA	GTGTAACTAT	GGATCTTACC	180
AGGGGCGCTG 7	<b>IGTGATCTGT</b>	GGAGGACCTG	${\tt GGGTCTCTGA}$	TGCCTATTAT	TGTAAGGAGT	240
GCACCATCCA C	GGAGAAGGAC	AGAGATGGCT	GCCCAAAGAT	TGTCAATCTG	GAGGAACTCG	300
AG						302

- (2) INFORMATION FOR SEQ ID NO:896:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 473 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

GAATTCGGCC	TTCATGGNCT	ANTCTCATTT	NAAATATATC	CTTACTGAAA	CATCTGGAAT	60
AACGTCTGAC	CAAATATCTG	GGTACAGTGA	TCCAGCCAAG	TTGAGACATG	AAATTAATCA	120
CCATGGCCTA	CATTTTTATC	TGTTTGGCTG	CAATTCTGTC	AAAGGCTTCT	GCTCTTCATA	180
ACATTTCACT	CACTAGCTCC	ATGAAGCCAT	ATGATACAAA	CCTTGCCTGT	GTAGCCTTCA	240
CTTTTTTCCA	AAAGAAGTCT	ATTAAATGCC	AATCAAGTAT	CTTCTCCTCC	AAGCTCAGTA	300
GCTCGGGCCT	TCAACAGCTG	TTCCCCATTC	CGATCCATCT	CCCTGAGCTA	CCCTGGCATT	360
CTTATCAGGA	CACTGGAGGA	ATCTATGTAT	GTGCCTCTAA	AGATTCAGCA	CCCAAACATG	420
ATAGAAATCA	CTGTGTTCAC	ACTGTATCTC	TATATCTGCC	CATCCCGCTC	GAG	473

- (2) INFORMATION FOR SEQ ID NO:897:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 594 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

GCTCGAGTGA AGTGGTATC	CATTGTGGTT	TGGGTTTTAA	TTTTATAATA	TTTTAATTTT	60
TAAAATCAAA AGAATATAC	r ggggctggg	TGGTGGCTCA	AGCCTGTAAT	CCCAGCACCC	120
TGGGGGGCCA AAGGGGGTG	ACCACCTGAG	TTTATGAGTT	CAAGACCAGC	CTGGCCAACA	180
CGGTGAAACC CCATCTCCA	TAAACATACA	AAACTCAGCC	GGGTATGGTG	GCAGGCACCC	240
GTAATCCCAG CCTCTCAGG	A GGCTGAAACA	GGAGAATCAC	CTGATCCGGG	AGGTGGAGGC	3.00
TGCCATGAGT CAGAATCAC	G TCACTGCACT	CCAGCCTGAG	AGGAGACCCG	TACAAAAAA	360
ΑΑΑΑΑΑΑΑΑ ΑΤΑΤΑΤΑΤΑ	T ATACACACAC	ACACACACAC	ACAAGGATTT	TAGATTTGAA	420
AATGATGTTT TTTACTCAT	T TCAAAATGTA	CTGTAACCTT	TCTTTGGTTC	TTACTGTTTT	480
CATTTAACTT TCTCTGTTT	r caagaaaaat	TGTCTTTATT	GACATTTGTA	AAAAAGAATG	540
TGTTTTGCCC AGTTATTAA	G TATTTTATTT	TTATGCAATT	TCAGAACACT	CGAG	594

- (2) INFORMATION FOR SEQ ID NO:898:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 302 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (b) Torozoor: Times

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

GAATTCGG	CC TTCATGGCCT	ACTGTACATT	TTTTTTAAAG	TTTGTTGAAA	AGAATATTGT	60
CTTATTCT.	AT AAAACATTTC	AAACCTAGTT	AGAGATTTGT	AATCAAAAA	CATTTGCGCA	120
	CA CTTAGGGCTG					180
AATGGCAC	CC TTCTGACATT	CTGAGGCAGC	TGGACTGGCA	GCCAAGTAAA	GGAGAGTGAT	240
GAGGTGGT	GT GGGGAGGGTG	GGGAGGCAGC	GCGAGGGTGC	TCTCCACAGG	GTAGGTCTCG	300
AG						302

- (2) INFORMATION FOR SEQ ID NO:899:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 475 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

GCGGCCTTCA	TGGCCTAGTG	CTTGTCAGTT	TGGAAAGTCA	CAGGGAGTTT	ACCATTCTAT	60
AATTAGAGTA	GGAGGAAAAT	GAGAACCCAC	TGGTAGAAGA	AGAAGCAACA	GTCTTCTAGG	120
	TGATGAGATA					180
AGAACATACG	GCAGAGATTT	GGGAACTCGC	ATGCCTGAAG	CCAGGTTATT	CTTATGTTCT	240
	TGCTCGCAGG					300
GGGGTGCTGG	TCTGCTCCCA	CAAATCTTTA	TCCCAGTCTT	CATCGCAAGG	AGGGCACTGC	360
CAAGTGCTCT	CAGCCAGAGT	CTCTTGTCTA	AGGCTCCTGG	TTTGGTTGAC	AACATCTTGC	420
TCAATACAAC	TTCTGTCATC	ACAGCTTGAG	ATATGATGAC	TAATTTCAGC	TCGAG	475

- (2) INFORMATION FOR SEQ ID NO:900:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 507 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GAATTCGGCC	TTCATGGCCT	ACAGCTGCCT	TTTTCTTTAA	AGGGGTTCTT	GTCTTCTGGA	60
ATTCCCTTTA	CTAGAGGATC	CTCTCCAGAA	CGTTCTTCAA	TATAGTTCTT	TATTTCTTCA	120
GAACATTTAG	ACACTTGTTG	TCTCTGCAAC	TTCACTTCTT	TGCGAAGCTG	CTCAACTTCC	180
ATTTTCAGTT	TTTCCTTCTC	TGGCAAATCT	TCGATGTGAA	GGGCAGGCAT	TTTCGCCCCA	240
GAACCGGGCT	CAGGCTAGCT	CTGGCAGCGG	AGCCGCTGGA	AGAGCGGCGA	AGCTCGGCGC	300
GTCCCGAAAC	AACTGAAGGC	CTGGCCCGCC	GCCCACCCGC	GCAGGATGTG	ACTGCAGCCC	360
TGCTGCGGTC	CCCAGCTCCC	CGAGGGCTTG	GCTTTCTCCG	GGACGCTTGT	CACGCCAGCG	420
TGCCCCAGCT	TCCTAGGACC	TGAGAACTCT	GCCTTTTCTC	AAGTCCCTGC	AACCCAGGAG	480
GCCTGCCCGG	GTGCTAGTAG	GCCATGA				507

(2) INFORMATION FOR SEQ ID NO:901:

PCT/US98/06956 WO 98/45437

(A) LENGTH: 495 base pairs

(i) SEQUENCE CHARACTERISTICS:

```
(B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA -
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:
GAATTCGGCC TTCATGGCCT AGTTTGGATT TTCATATTAG GGATACTCAA CTGGTATTAT
TATTCTGGCC CCTGCAAATT TTTCAGTAGG TCCCCTAGTA TGTCATGCCA GGGACTATGN
                                                               120
GAGTTCCTGG GAATAGCACT GTAANACATT CTTGAGTGGG TCCTTGACTC CATTGAGTTT
ATAATCTCGT AGGAGGAAGG CTATGAAGAA TTCTAATAAA GCAAAGCAAG CAATCACAAC
                                                               240
AAACCTTCCT CTTTAACTTA TCAAAAATGG AAACTTTGAA GAGCTGCTCT TTAATAAATC
                                                               300
ATTGGAAAGC ACCAGGACCC AGGTGTTTTG ACTCAGCCTC ATTTCAGACT GAGATCTGAG
                                                               360
GCCATGATAA CTCATGTGCC TATATATGCT GATAATCACC ATTACCTATA CCATTCTTTA
                                                               420
480
TTTACCGGCC TCGAG
                                                               495
(2) INFORMATION FOR SEQ ID NO:902:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 266 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:
GAATTCGGCC AAAGAGGCCT AGAATTCCAG ACCTAGCTCA ACCCATGCCT CCTTTCCTTC
180
CCTCCCTTCT TTCCTTTCCT CCCTCCCTTC CATTCTTTCC TCCCCCACCC CCCGTTTCTT
                                                               240
CTCTTTGGAG AGATGTACAG CTCGAG
                                                               266
(2) INFORMATION FOR SEO ID NO:903:
    (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 410 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
      (xi) SEQUENCE DESCRIPTION: SEO ID NO:903:
GAATTCGGCC AAAGAGGCCT AAATGAGAGC TGAGTGAAGT GGATGCCCCT TATAAAAACA
                                                                60
TCAGATCTCG TGAGAACTTA CTATCACTAG AATAGCATGG GGGAACCACC CCATGATTCA
                                                               120
GTTACCTGCC CCCAGGTCTC TGCCACCACA CATGGGGATT ATGGGAACTA CAACTCAAGA
                                                               180
TGAGATTTGG GTGGGGACAC AGGCAAATTA TATCAGCTGT TGTGCTCATT AGTTTGTATA
                                                               240
TCATCCTTGG CTCCTTTAGC ACTATAAGGG CAGGATTGAG TCCTTGCAAC AGAAACCATT
                                                               300
CAGCCTGCAA AGCTGAACCT ATTTACTTTC TGACCCTTTA TGGAAAAGTT TACTGATCTC
                                                               360
TGGACTAGAC AGTTTTTTAA AAATGACATC TTATGACCGG GATTCTCGAG
                                                               410
(2) INFORMATION FOR SEQ ID NO:904:
                                392
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(A) LENGTH: 326 base pairs(B) TYPE: nucleic acid

(i) SEQUENCE CHARACTERISTICS:

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(C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:
GAATTCGGCC AAAGAGGCCT AGCCGAGACT CTGTCTCAAA AAAAAGAAAA AAAGCTGCTT
                                                                       60
TGGGTCTTAT GAGGGAGGG ACTGGGAATC TAGGTGTTTC AAGCGCCCCA GGCGATTCTT
                                                                      120
AAGGTCACAC AAGCTTGGGA GACACTTCAT TAAGCAAAAT CTTTTGGCCG TTTTGTTCTG
                                                                      180
GTTGAGCCTC AGTGTCTATT CATTGAGTGG TCACCAAGAG TTTGGGGTGG ACTGATCATC
                                                                      240
AGCATTTACA GGTTTGGAAA TTGAATTTAG TTTTACTACT CAGAGCTTAT TAGACTTGAG
                                                                      300
CAGATTTAAA CGGAAGGACA CTCGAG
                                                                      326
(2) INFORMATION FOR SEQ ID NO:905:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 410 base pairs
              (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:
GAATTCGGCC AAAGAGGCCT AGGAACTGTT TTGACCCTGA AGGCTATTTA ATCCACTGTC
                                                                       60
CCCTACAAGG CCTCACAAGT GCTGGGGGAA AAAAAACAGC AATGAGGATG ATCCTGAGTT
AATGTGTATG CTCCGCAAGA GAGCTTGCCT ATACCTTGAT TATTTCATAA AATCACATGT
                                                                      180
TAATACATTG CTTTCAGAAT GAAATACTGA CTTGATCTGA TAGGAGAAAA TGGTAATATT
                                                                      240
TCATAGTTGT TTTCCAAAGA CAAATTTAAA TGTTGTCTGT TATCTCCTTA CTTAGTTTAA
                                                                      300
GAATTTAGTT TTGAACCCCA TTGACTTTGT CATTTGCAAT TTTAAAAATA TTTGGGACTG
                                                                      360
GGCATGGTCG CTCACGCCTG TAATCCCAGC ACTTTGGGAG GCATCTCGAG
                                                                     410
(2) INFORMATION FOR SEQ ID NO:906:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 498 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:
GAATTCGGCC AAAGAGGCCT ACGCTTCCCG GGTTCAAGCG ATTCTCCTGC CTCAGCCTTT
                                                                       60
TGAGTGGCTG GGACTACAGG TGGATGCCTC CATGCCTGGC TAATTTTTTG TATTTTAGTG
                                                                      120
GAGACAGGGT TTCACCGTGT TGCCCGGGCT GGTCTTGAAC TCGTGAGCTC GGGCAATCCA
                                                                      180
CACTCCTTGG CCTCCCAAAG TGCTAGGATT ACAGGTGTGA GCCACTGCAC CCGGTCGAGG
                                                                      240
TACAGTTTTG AAGTTCATGC AAATCTCATC ATTTGCTCTT CTGCAACAAA ACATTTTCTT
                                                                      300
TCAACTTATT TTGCCTGTGT GAAGCTCAGT GCTTTAACTC ATATATGGAG TTATCTTCTT
                                                                      360
CCCTCAGACT GGAGACGTTG GTGAAATTGG GGCTAGACTG AAGATGTCTA AGGTGGCTTG
                                                                      420
ATTGACAAAG GTCTCTCCTC ATCCCCAAAA TAAATAACAT TTTTTCATTT ATAATAGTAA
TACACCAGTC GACTCGAG
                                                                      498
                                   393
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- (2) INFORMATION FOR SEQ ID NO:907:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GAATTCGGCC	AAAGAGGCCT	AAACTGGTGC	TGGTTTCACA	TCACGACAGC	AACGGGATTC	60
TTTTGCTTTG	AAAATGTTGC	AGTCCACCTG	TCCAACTTGA	TCTTCCGGAC	ATTTGACTTG	120
TTTCTGGTTA	TCCACCATCT	CTTTGCCTTT	CTTGGGTTTC	TTGGCTGCTT	GGTCAATCTC	180
CAAGCTGGCC	ACTATCTAGC	TATGACCACG	TTGCTCCTGG	AGATGAGCAC	GCCCTTTACC	240
TGCGTTTCCT	GGATGCTCTT	AAAGGCGGGC	TGGTCCGAGT	CICTGTTTTG	GAAGCTCAAC	300
CAGTGGCTGA	TGATTCACAT	GTTTCACTGC	CGCATGGTTC	TAACCTACCA	CATGTGGTGG	360
GTGTGTTTCT	GGCACTGGGA	CGGCCTGGTC	AGCAGCCTGT	ATCTGCCTCA	TTTGACACTG	420
TTCCTTGTCG	GACTGGCTCT	GCTTACGCTA	ATCATTAATC	CATATTGGAC	CCAGACTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:908:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 764 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GAATTCGGCC	AAAGAGGCCT	AGAAACAATG	GTTTTCAGAC	ACTGAAAGTT	CATAGTACAG	60
GACTGTGATC	TCTGCGAGAA	GGGGGAATAA	TGAGGTGAGT	CCAGTGATTG	CTCAGGCGAA	120
TGGCCTGGAG	GCAGTTTCTA	GGCAGCAAAG	CAGGGAGAGG	GAAGCCAGAG	ACCAGTGGTC	180
CTGCTGTGTT	GAGGAGATGG	AGATCAGTGT	CACCGGAGGC	CAAGGTGAGT	AAGTGAGAGG	240
AGAGGAGGCA	GCAGCACACA	GACAGAGAGT	GCTGTAGATC	TGCAGTGGGT	CCCCTGGAGT	300
CCTTGGTTGA	GTGAAGGTGT	TAGAAGAAAC	TACTTAAGCC	AAGAAATGAG	TAACTGGAAA	360
TTAGTAGAGC	AAATAATTTA	CAGATCATCT	ATGGGGCTGG	GAAAAGTTTG	TGTTTCCACT	420
AGCCAGAGTA	GAAATAACTC	ATAATGCATG	GGTCATCAGG	TGGAGTCCTC	CAACAGGTGT	480
TGCCTTAGTA	CTGAGGTCAA	ATTGTCCCTA	GACCAAAGGC	TTCTTTGGAC	TTCCCCTAAC	540
AAAGCTTAAA	GACAAGCCTT	GGAAGGATCA	AACTAATTTC	AAGAAACTTA	ACTGTGAATC	600
AGAATAAAAC	CCAATACCAT	TTATAGGAAT	ATAACAAAAT	CCATCAACAN	ACNACATAAC	660
ACTCATAATT	ACCAACATTC	AGTAAAAAAT	TACTGGAAAC	AGAGAAATAT	AAATTATGGC	720
CCATAATTAG	GAAAAAAGGG	TAATCATTAG	AGGTAGAACT	CGAG		764

- (2) INFORMATION FOR SEQ ID NO:909:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 157 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

AATTGCGAAG	ATGAAGGCTC	TGTGGGCCGT	TGTTTCGGAA GCTGTTGGTC		60 120
AGCCGAGGGA	GAGCCGGAGG	TGACAGATCA	GCTCGAG		157
(2) INFORMA	ATION FOR SE	EQ ID NO:910	):		

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 487 base pairs
  - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

GAATTCGCGG CCGCGTCGAC	AGAATAGACC	TGGTTTGTGA	ATTATGGCCT	GGATTTCACT	60
TATACTCTCT CTCCTGGCTC	TCAGCTCAGG	GGCCATTTCC	CAGGCTGTTG	TGACTCAGGA	120
ATCTGCACTC ACCACATCAC	CTGGTGAAAC	AGTCACACTC	ACTTGTCGCT	CAAGTACTGG	180
GGCTGTTACA ACTAGTAACT	ATGCCAACTG	GGTCCAAGAA	AAACCAGATC	ATTTATTCAC	240
TGGTCTAATA GGTGGTACCA	ACAACCGAGC	TCCAGGTGTT	CCTGCCAGAT	TCTCAGGCTC	300
CCTGATTGGA GACAAGGCTG	CCCTCACCAT	CACAGGGGCA	CAGACTGAGG	ATGAGGCAAT	360
ATATTTCTGT GCTCTATGGT	ACAGCAACCA	TTGGGTGTTC	GGTGGAGGAA	CCAAACTGAC	420
TGTCCTAGGC CAGCCCAAGT	CTTCGCCATC	AGTCACCCTG	TTTCCACCTT	CCTCTGAAGA	480
GCTCGAG					487

- (2) INFORMATION FOR SEQ ID NO:911:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 478 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

GAATTCGCGG	CCGCGTCGAC	AGTTACTGAG	CACACAGGAC	CTCACAATGG	GATGGAGCTA	60
TATCATCCTC	TTTTTGGTAG	CAACAGCTAC	AGGTGTCCAC	TCCCAGGTCC	AACTGCAGCA	120
GCCTGGGGCT	GAGCTGGTAA	AGCCTGGGGC	TTCAGTGAAG	TTGTCCTGCA	AGGCTTCTGG	180
CTACACTTTC	ACCAGCTACT	GGATGCACTG	GGTGAAGCAG	AGGCCTGGAC	AAGGCCTTGA	240
GTGGATTGGA	ATGATTCATC	CTAATAGTGG	TAGTACTAAC	TACAATGAGA	AGTTCAAGAG	300
CAAGGCCACA	CTGACTGTAG	ACAAATCCTC	CAGCACAGCC	TACATGCAAC	TCAGCAGCCT	360
GACATCTGAG	GACTCTGCGG	TCTATTACTG	TGCAAGGGAC	AGCTCAGGCT	ACGACTATGC	420
TATGGACTAC	TGGGGTCAAG	GAACCTCAGT	CACCGTCTCC	TCAGCCAAAA	CGCTCGAG	478

- (2) INFORMATION FOR SEQ ID NO:912:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 433 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

PCT/US98/06956 WO 98/45437

GAATTCGCGG CCGCGTCGAC CCAGGATGCC GCGCAGCAGA GCTCTGATTC TGGGGGTCCT CGCCCTGACC ACCATGCTCA GCCTCTGTGG AGGTGAAGAC GACATTGAGG CCGACCACGT AGGCACCTAT GGTATAAGTG TATATCAGTC TCCTGGAGAC ATTGGCCAGT ACACATTTGA ATTTGATGGT GATGAGTTGT TCTATGTGGA CTTGGATAAG AAGGAGACTG TCTGGATGCT TCCTGAGTTT GGCCAATTGG CAAGCTTTGA CCCCCAAGGT GGACTGCAAA ACATAGCTGT AGTAAAACAC AACTTGGGAG TCTTGACTAA GAGGTCAAAT TCCACCCCAG CTACCAATGA GGCTCCTCAA GCGACTGTGT TCCCCAAGTC CCCTGTGCTG CTGGGTCAGC CCAACACCCT CATCATGCTC GAG	60 120 180 240 300 360 420 433
(2) INFORMATION FOR SEQ ID NO:913:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 139 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:	
GAATTCGCGG CCGCGTCGAC GCAAGATGGA TTCACAGGCC CAGGTTCTTA TATTGCTGCT GCTATGGGTA TCTGGTACCT GTGGGGACAT TGTGATGTCA CAGTCTCCAT CCTCCCTGGC TGTGTCAGCA GGAGAGAAG	60 120 139
(2) INFORMATION FOR SEQ ID NO:914:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 166 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:	
GAATTCGCGG CCGCGTCGAC ATCATGGCTA CCCTGCGTGT CCCACTCCTG GTGGCTCTCG TCCTTCTTGC TGTGGCAATT CAGACCTCTG ATGCAGGTCC CTATGGTGCC AATGTGGAAG ACAGTATCTG CTGCCAGGAC TACATCCGTC ACCCTCTGCC ATCACG	60 120 166
(2) INFORMATION FOR SEQ ID NO:915:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 590 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:	
GAATTCGCGG CCGCGTCGAC TTCTTGGGCA GCACAGAAGA CAGAGCCGAT TTTGACCAAG CTATGTTCCC TGTGATGGAG ACCTTCGAAA TCAATGATCC AGTGCCCAAG AAGAGAAATG GGGGGACCTT CTGCATGGCA GTCATGGCCA TCCACCTGAT CCTGCTCACG GCAGGTACTG CACTGCTGCT GATTCAAGTT CTCAATCTGC AGGAGCAGCT CCAGATGCTA GAGATGTGCT GTGGCAATGG ATCACTAGCT ATCGAGGACA AGCCCTTCTT CTCGCTGCAG TGGGCACCCA AAACACACCT GGTACCTAGA GCACAGGGGC TGCAAGCCTT GCAGGCCCAG CTCAGCTGGG	60 120 180 240 300 360

360

TGTTCCAGAT GAATCCCCGG	CCAGGAGCAA CTCCGTCAGC AGTTCAACAA CCTCACTCAA AATCCAGAGT TAAAGGTGAA CGAGGCTCTC CAGGTCCAAA AGGGGCCCCG GGTGCTCCTG GCTGCCTGGG CCAGCTGCTG AGAAGGGAGA AAAGGGGGCT GCAGGTCGTG AGGTGTCCAA GGACCCCAGG GCCCACCAGG AAAACTCGAG	420 480 540 590
(2) INFORM	ATION FOR SEQ ID NO:916:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 592 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:916:	
TTCTATGGCT TCCTGAGAGT CCAACTACTT TTCGTTCAAA CCAAACGTTC TGCTGCAAGT AGTGAAGCCA TCAGGACAGC	CCGCGTCGAC GGAAGAGCAA TGAAAACATA TGCTCCTACA TTATTCATGT GCAGCTGGAT GGGATGAGCC AAGGTGAGCA GGTGGAGCAG CTTCCTTCCA CAGGAGGGA TCCNGTGCCA GCATCAACTG CACTTATGAG AACAGTGCCT CCCTTGGTAT AAGCAAGAAC CTGGAGAGAA TCCTAAGCTC ATCATTGACA TATGGAAAGA AAGCAGACCC AAGGACTCAT CGTTTTACTG GATAAGAAAG TCCCTGCACA TCACAGACAC CCAGCCTGGA GACTCAGCCA TGTACTTCTG GAGAGCACCA ATCACAGCAA ATTAACCTTT GGGGATGGGA CCGTGCTCAC AACATCCAGA ACCCAGAACC TGCTGTGTAC CAGTTAAAAG ATCCTCGGTC ACCCTCTGCC TGTTCACCGA CTTTGACTCC CAAATCAATG TGCCGAAAAC GGAACGTTCA TCACTGACAA AACTGTGCTG GACAATCTCC AG	60 120 180 240 300 360 420 480 540
(2) INFORMA	ATION FOR SEQ ID NO:917:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 166 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:917:	
CTGGATCTCT	CCGCGTCGAC GAATGAGGTG CTCTCTTCAG TTCCTGGGGG TGCTTATGTT GGAGTCAGTG GGGATATTGT GATAACCCAG GATGAACTCT CCAATCCTGT GAATCAGTTT CCATCTCCTG CAGGTCTAGT AAGAGC	60 120 166
(2) INFORMA	ATION FOR SEQ ID NO:918:	
(i) ·	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 200 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:918:	
ACTACAAAGT	CCGCGTCGAC GTCTGAGAGG AACCCTTCTC TGAGGATGGA CACTTCTCAC CCTGTTTGCT GATTCTTCTT GTGGCCCTAC TGTGTGCAGA AAGAGCTCAG GTTACCAGTG CTATGGAGTC CCATTTGAGA CTTCTTGCCC ATCAATTACC	60 120 180

200

TGCCCCTACC CTATAGTGAG

(2) INFORMATION FOR SEO ID NO:919:

<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 231 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:	
GAATTCGCGG CCGCGTCGAC CCAACCTTCC GGAAGCCTCC CCATCAGCAC CATGAACCCA AGTGCTGCCG TCATTTTCTG CCTCATCCTG CTGGGTCTGA GTGGGACTCA AGGGATCCCT CTCGCAAGGA CGGTCCGCTG CAACTGCATC CATATCGATG ACGGGCCAGT GAGAATGAGG GCCATAGGGA AGCTTGAAAT CATCCCTGCG AGCCTATCCT GCCCACGTGT T	60 120 180 231
(2) INFORMATION FOR SEQ ID NO:920:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 115 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:	
GAATTCGCGG CCGCGTCGAC GTTTTGTTAT TGTTACGAAG TAAATGATTC GTATGCTGTA CATAGCTGTT ATAGAAGTGG CGATTAGTGT AATTAGTAGG GCTCAGGCTC TCGAG	60 115
(2) INFORMATION FOR SEQ ID NO:921:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 213 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:	
GTTGAATTCT AGAAATCAAA ATTAATTTGA CAAAGGAAAA GCAGATGCCG GAAACTTCTT CCCAGTCTGT CATACAATTC ACCACTGGCC AGGTGCTGAG AGAAGCATTA GGGAACAGTG TGGGTTGTGT CAGAGTTGGA CGGCTCCATC CCTTTGGCTT CATTATCTTC CTCCTCATGG AGATTCTAAA GCAACCCGTC GACGCGCCG CGA	60 120 180 211
(2) INFORMATION FOR SEQ ID NO:922:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 504 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GAATTCGGCC	AAGAGGCCTA	CTTAGAAGCC	AAAGAAGGAG	ATTTGCACAG	GATAGAAATC	60
CCATTCAAAT	TCCACATGCT	GCATTCAGGG	CTGGTCCACG	GCCTGGCTTT	CTGGTTTGAC	120
GTTGCTTTCA	TCGGCTCCAT	AATGACCGTG	TGGCTGTCCA	CAGCCCCGAC	AGAGCCCCTG	180
ACCCACTGGT	ACCAGGTGCG	GTGCCTGTTC	CAGTCACCAC	TGTTCGCCAA	GGCAGGGGAC	240
ACGCTCTCAG	GGACATGTCT	GCTTATTGCC	AACAAAAGAC	AGAGCTACGA	CATCAGTATT	300
GTGGCCCAGG	TGGACCAGAC	CGGCTCCAAG	TCCAGTAACC	TCCTGGATCT	GAAAAACCCC	360
	ACACGGGCAC					420
TCGGAAAACA	TGTGGAACAC	GGGCAGCACC	TACAACCTCA	GCAGCGGGAT	GGCCGTGGCA	480
GGGATGCCGA	CCACCAGACT	CGAG				504

- (2) INFORMATION FOR SEQ ID NO:923:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 119 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

GAATTCGGCC AAAGAGGCCT ACATTCATCA AGTCATCCAA CTTCTATAGT CAAAGCAGGA
TCATGTGGCG AAGCATATGC TCCACAAGGG TGGATAGCTT TTTTCATGGA ATTCTCGAG
119

- (2) INFORMATION FOR SEQ ID NO:924:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 706 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

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GAATTCGGCC AAAGAGGCCT AAAGAGAGTG GAGGAGGAGG ACAAGATTGA TACTATGAGA
                                                                       60
GTTGGAGGAC ATAATTCATG GATCATAGCT CCAGAAGTGA AAAGGGAGGA AATGTAGACA
                                                                      120
GAGGAAGGCA TTAGCCATTG AGAAGAATAG GGACATATTT TCTTTACTCT CTTGTCAGAG
                                                                      180
GAAGATAGCT GGGGGAGTAT AGACAAGTTG TAAGAATGAA GGAAGGAAGG CAAGAGCAGA
                                                                      240
CTTGTCGGAT GAATTTTATT TTCTCTATGA AGTTTGAGAA TTAAACTTTA TGCTGAGAAG
                                                                      300
GAGGGCAGGA GAGACTGTAT ATGGAATGTA AGGTTTGGGA TAACCAATGT AAGTTTTGGG
AATGAGAAAG CCACCTAGGG ATGAGGAAAA AATATTTAAA ATTTTGTATC CACTGAAAAT
                                                                      420
TCTTCAACAG TGTAAAATGA AGCATGCTCA ACTGGAAATG GTCATATATC TAAAAGAAAA
                                                                      480
TGGATTTATT TTGTTATTTT TCTCTATATT TGTAGTATTT TACAGTAAGC ATGTATTACC
                                                                      540
TTTATAGTGA AAAAGTGTCA TTTTTTTACA TTGGTCAATT TTTTGTTATT AAATTTCATG
                                                                      600
CTTGTTTTTA ATTGTTTCTT GTGTGTATGA TTGCAATATC AGGTATTTGA TGTGGTGATG
                                                                      660
TGTGTGATTC AGAAGTCAGA AGACTTAAGT TCCGACACCC CTCGAG
                                                                      706
```

- (2) INFORMATION FOR SEQ ID NO:925:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 651 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

GAATTCGGCC	AAAGAGGCCT	AGGATTCAAA	TTATTCTGAC	AGACCTGTGT	GGCAGTTCAG	60
GCTGATAGCT	GGAGTTTCTT	GTCTTTTTCT	AÇATGGCCTT	TCATCTTCCA	AGAGTTAGAC	120
TATGATTCTT	CACATCATGA	TGGCTTAGGG	TCCCAAAAAG	AAAAGAGTAG	AACTTGCAAT	180
ACCTCTTAAG	CCCTATGCCC	AAGAACTCAT	ACAGTGATAC	TTCTGCCACC	TTGTGTTAGT	240
CAAAGCAAGT	CACAAGGCCA	GCCAGATTCA	AAAGAATGGA	AAAATAGACT	CAATTTCCTG	300
GTGAGAAGTA	GCAAGGTCAC	ATTGCAAAGG	AGTCTGGACA	TGGGAAGGAG	TTACTCATTT	360
GTGGCCTTTA	TAATAATCTT	CCACAAATGC	CTGTAATTTG	GGCACTGTGC	TTAGTACTGG	420
TGATAGAAGA	TAAGTAGCTT	ATTTCAGTAT	CTTAATTTTG	TTTTATATAT	TTGATAATTT	480
TATGATGCAG	GTTCACTGTG	CACTGGTATC	AATCCCAGGG	GAGGACTGTA	AACACCTTGC	540
CAATACTGTG	TACCAGTA: C	AATCCACTGG	CATGAGTCTG	GTGAGACAGA	ACACACAATA	600
AGTTTAGGGA	AGCAACTTTA	TTACTCACAG	ACAGGCAGCA	AGGGACTCGA	G	651

- (2) INFORMATION FOR SEQ ID NO:926:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 700 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

GAATTCGGCC	AAAGAGGCCT	AAAAAGATGA	AAGGACCAAT	CAAAGATTTA	ATTAAAGCTA	60
AAGGGAAAGA	TTTAGAGACA	GAGAATGAAG	AAAGAAATTC	TAAGTTGGTG	GTGGACAAAC	120
CAGAACAGAC	AGTGAAGACC	TTTCCACTGC	CAGCTGTTGG	TTTGGAAAGA	GCAGCTACTA	180
CAAAGGCAGA	TAAAGACATC	AAGAATCCAA	TCCAACCATC	CTTCAAAATG	TTAAAAAATA	240
CTAAACCAAT	GACTACTTTC	CAAGAAGAAA	CCAAGGCTCA	GTTTTACGCA	TCAGAGAAAA	300
CCCTCCTAAA	AGAGAACTTG	CCAAAGATTT	GCCTAAATCA	GGAGAAAGTC	GATGTAATCC	360
TTCAGAAGCT	GGAGCGTCTT	TACTGGTTGG	CTCAATAGAA	CCTTCTTTGT	CAAATCAAGA	420
TAGAAAATAT	TCCTCAATTC	TACCTAATGA	TGTACAAACT	ACCTCTGGTG	ATCTCAAATT	480
GGACAAAATT	GATCCCCAAA	GACAGGAAAT	TCTAGTAAAA	TTACTAGATG	TGCCTACTGG	540
TGATTGTCAT	ATTTCTCCAA	AGAATGTCAG	TGATGGGGTT	AAAAGGGTAA	GAACATTATT	600
AAGCAATGAG	AGAGATTCCA	AAGGCAGGGA	TCACCTCTCA	GGAGTCCCTA	CTGATGTTAC	660
AGTTACTGAG	ACTCCAGAAA	AGAACACAGA	ATCCCTCGAG			700

- (2) INFORMATION FOR SEQ ID NO:927:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 378 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

GAATTCGGCC	AAAGAGGCCT	AGGGGTGGTG	GAGGCGTGGA	CCCAACGGTG	ACCGTCGGGA	60
TGGAGCAAGG	GCAAGGAGAG	GCTCTGGCCC	AGACACAGCT	TGGAAAAGCT	CATCTCCCTC	120
TGGGGTTTAA	AAACTCAAAG	CAAACGGAGC	AAGCCTGGCG	GCCCTGGGGA	TGGGGCAGGG	180

COMONNOCHO ACHORONOM MOCA COMOCA CARACTA ACCORDANCE	
CCTCTACCTC ACTGTGATCT TCGACCTGGC GACACAGGAC AGCCACACAG AAGCACGCCA ACACACTTAA AGCTTTGCTC CAACTAAATC ATTTAGTTTC CCTTGAAGAA ATAACTGAAA	240
AAAAAAACAA CTGCTGACAT CTATGTCTGT AGCTCGATTT TACAGTCTGC TCTTTGTGAG	300
AAAGGAAAAT CACTCGAG	360
	378
(2) INFORMATION FOR SEQ ID NO:928:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 426 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:	
GAATTCGGCC AAAGAGGCCT AATATTTCAC ATTTCTCTTT TCTAAAAGTG TAAATTTTTC	60
ACTITAAAAT GAAGCAAGAA TIAAATAAAT AGAACAAATA CCATATATCA TCACAGAGTC	120
AATATATTAT GGTCCTGTTC TGACCAAGTG TTGCATTGTA TTTGTGTTAC CAGAACTGCA	180
GGGCTTTCTA TGGCTACATG GTCAGTGCAT GCTCAGACAG CTGTTAAAAT CAAAACCTTC	240
ACTGTGCTGG GTCACCTGGT AACTACTGTC TATCTCACAA GTGCATTCTG CTGACATTCA	300
AGGGTTAAAC TGGTTTCTAG TAAATACTGT GCTTTAAAGT AGTACATACT GTGAGCTGTG	360
TTATTAGAAA CCTGCTTGTC CTTGTGTCTG AAAATAAGGA GGAACACTCT CGCACCAAAT	420
CTCGAG	426
(2) INFORMATION FOR SEQ ID NO:929:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 325 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(iii) NOTECTIVE WARD DAY	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:	
GAATTCGGCC AAAGAGGCCT AGGTAAATGT TAGTGGAAAA TTTTATGAGT ATATGCTGAA	60
AGGAGAGATT AGTTCACATG AACTCAATAA TGTTCAAGAT AATGAAATGC TTAGAAAGGT	120
TACTTTTGAT CCAGAAGTAT TTTTCAACAT ATTACTTCCT CCTATCATAT TTTATGCAGG	180
TTATAGCCTG AAAAGGAGAC ATTTTTTTCG AAATCTTGGG TCTATCCTAG CATACGCTTT	240
TCTTGGAACA GCAATTTCTT GTTTCGTTAT TGGGTCAATA ATGTATGGCT GTGTAACGCT	300
GATGAAGGTA ACGGGACAAC TCGAG	325
(2) INFORMATION FOR SEQ ID NO:930:	
(1) OPOUTNOTE CUADA OPPORT OFFI	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 406 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(al) applying processes and a second	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:	
GAATTCGGCC AAAGAGGCCT ATGGACACCC TGTGCCCCAA GCCGATGGCC CCACCCAGCA	60
GCATCAGCAC AGNTGCCCCC CTTCTCCGCA GAGCAGGCTC TCCTTTACGG GACTCTCCTC	120

TTCCCTCCCA CCTGATGCGC ATCAGCAGCC ACGGGCCTGG CCCTTGAATC TTGTCTAACT GCACTCGCTG CCTGGTGGCC TCATCCCACC CCAAGACCAC TGCACTGATG GCTCCAACCC CAACTTCTCC CTGCACTCAG CTTATGAATA CGACGGCCCT CATTGCATCC ATGCAGAGAC CTCAGAGGCA GCTCAGCTCA	180 240 300 360 406
(2) INFORMATION FOR SEQ ID NO:931:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 246 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:	
GAATTCGGCC TCATGGCCTA CCAGACTGTA AACATTCCAG GTCCTGAAAA AGTGTTGGAC CAGTCTCCTA CTGTTATGTT CTCCAGTTTT AAAAATGTAA AATCAGTTGA AACACTCGAT CAGAAGGCAG ATGAAGTCCT TGACTGTCAG AGTAACCAAA ACAGACCAGA TGAATGCAAA AGTGAAGGTC AGTCAGCCAA GGAGATGCTA AGTAGTGACC AGAGAGAGAC TGTCACCGGA CTCGAG	60 120 180 240 246
(2) INFORMATION FOR SEQ ID NO:932:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 278 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:	
GAATTCGGCC TTCATGGCCT ACTCCATTGT CACGCCAATT TCCCCTAGTC CAAGTTTTT CTTTGCTGAT TCCTTTGTCC ATGTGTGCTT TGAGCCTCTC TCATCTTGTC TTTCCTCCTT TCCTAGGAGC AGCTCCTGAA GCAGCAGCAG CAGCACCAGT GGCAGCAGCA TCAACAGGGC TCTGCCCCTC CTACCCCAGT GCCCCCATCA CCACCACAGC CTGTGACCCT GGGGGCTGTG CCAGCTCCAC AGGCTCCACC CCCGCCCCAC AACTCGAG  (2) INFORMATION FOR SEQ ID NO:933:	60 120 180 240 278
(i) SEQUENCE CHARACTERISTICS:	
<ul><li>(A) LENGTH: 421 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:	
GAATTCGGCC TTCATGGCCT ACGAGTGCGA CCAGCCAGAT GAGCGCCCGG TCCTGGTGAA GAGCATTCAC TACCTCTACT TCTCCATGAT CCTGTCCACG GTCACCCTCA TCACTGTCTC CACCGTGAGC TGGTTCACAG AGCCACCCTC CAAGGAGATG GTCAGCCACC TGACCTGGTT TACTCGTCAC GACCCCGTGG TCCAGAAGGA ACAAGCACCA CCAGCAGCTC CCTTGTCTCT TACCCTCTCT CAGAACGGGA TGCCAGAGGC CAGCAGCAGC AGCAGCGTCC AGTTCGAGAT	60 120 180 240 300

	AACACGTCTA AAACCCACAG CTGTGACATG ACCCCAAAGC AGTCCAAAGT ATCCTGTGGC TCTGTGGAAT ACAGGAGAAG GGCAAGGAAG AGCTCCCGGC	360 420 421
(2) INFORM	ATION FOR SEQ ID NO:934:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 449 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:934:	
TTGCAAATTC AGACACCTGC ATAGCTCACT ATTTTGATGA ATAGCGGTGA GTCATTCTTC GTGAAACTCA	AAAGAGGCCT AAAATAGCAA AGATGGAACA TGGACCTAAA GCAGTGACTA TCCATCAAAG CCTTCAGAAA AGGATTCTGT AGTTTCCCTT GAGTCCCAGA TGACCCAAAA CTGAAAACTC TAAGTCAAAC CAAAAAAAAC AAAGGATCTG CTCTGGTAAC AGTGATGGCG GAGAAGAATT TTGTGAAGAG GAGAAGGAAT TTAGCACAGAA GAAAGGTTTT ACAAGCAGTC TTCCATGTCT GAAGATAGTG CGACTTCTTC ATTGGGAAAG TCAGACGGAC ACGAAAGAAG GAAAGTAGTT AGTTAAGGAA CAAAAACCAC TAGAAAAAAGT GTTTCTTAAA GAAGATACAG TGGGGATACA ACTCTCGAG ATION FOR SEQ ID NO:935:	60 120 180 240 300 360 420 449
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 421 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:935:	
CATTCTACTG AGTCATTTTT AAGTTCATTT TATTTATTCT TTTTGGAAAT	AAAGAGGCCT AAAAATAGTG ATTTTTTGAC TATCTATAGA TATTAGTTGG TAAGGAAAAC TTTCTTTTCT CCTGTACTTA TTCATCGTCC CCCAGGAATC CCAAGGAGAC CTAGTTCCTT TTTGTGAGGA GTTGTTTTTGA GTTCATTTTG GAAGTTTTGA GTTCATTTTA CTATAATCTG CCTAGGTGTG ATTTTCTTTT GCTTAGGATT TGCAGAGATT TTTTTGAACC TGTGGCTTGA TGTCCATCAC TTCTCAGCCA GCATAGTATC TGCAGACTGT GTGTCTGTC CATTTTCTCT TGTAGGACTT CATTCACAAG GATGTTAGAA CTTTTTACCA TGGCTCTCGA	60 120 180 240 300 360 420 421
(2) INFORMA	ATION FOR SEQ ID NO:936:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 648 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:936:	
GAATTCGGCC	AAAGAGGCCT ACAGGTCTAC TGGTAATGAT TTCCTTTACC TTCTAATTAT	60

ATAGAAATGT	CATAATTTCT	CCTTTATTCT	TGAATGATAG	TTTTGTGGGA	TATAGACTTG	120
CTGGATATAG	AATTACTGGA	TATAGAATTG	CCAGATATAA	AATTCTTGGT	TCAAAGTTTT	180
TTTTCTTTGA	GGACTTTGAA	TGTCATCCCA	CTGTCTTCTG	GCCTCCATAG	TTTCTCATAA	240
TAAATCAGCT	GTTAATCTTC	ATTAAGTTTC	CTCTGTACAC	GAAGAGTCAC	TTGTCTCTTG	300
CTGCTTTCAA	ATTTTTCTCA	TTTGCTTTGG	GTTTTCACAC	TTTAATTATA	TGCCTTTCTA	360
TGTGGATCTC	TTTGAGTTTA	TCCTGCTTGG	AGTTCATTGA	GCTTTTTGCA	TCTGTATATT	420
AATTTCTTTC	ATCAGATTTG	GAGATGTTTT	TGGCATTTAT	TTCCTCAAAG	TTCTTTCTGC	480
TTCTTTCTCT	CCTTCTCCTT	CTGGGTCACC	ACAATGCATA	TGTTGGTCTA	CTTGATGATG	540
TCTCACAGGT	TCCTTAGACT	CTGTTTACTT	TTCTTCATAT	TTTTTTCTTT	CTGTTTCTTA	600
AATTTGGATA	ATTTTGGTTG	TCTTATATTC	AAGTTTGCTG	ATCTCGAG		648

- (2) INFORMATION FOR SEQ ID NO:937:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 160 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

GAATTCGGCC	AAAGAGGCCT	AGAGGATGGG	AAGCTTGGGG	AGAGAAGATA	CTGAAATGCT	60
AGAAACTGAG	CCAGTAGAGG	ATGGGAAGCT	TGGGGAGAGA	GGACATGAGG	AAGGATTTCT	120
GAACAACAGT	GGGGAGTTCC	TCTTTAACAA	GCAGCTCGAG			160

- (2) INFORMATION FOR SEQ ID NO:938:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 399 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

GAATTCGGCC AA	AGAGGCCT AGAAAAACT	C AGGAAAGAAA	TTGCAGACTT	CGAACAACAG	60
AAAGCAAAAG AA	TTAGCTCG AATAGAAGA	G TTTAAAAAGG	AGGAGATGAG	GAAGCTACAA	120
AAGGAACGTA AA	GTTTTTGA AAAGTATAC	T ACAGCTGCAA	GAACTTTTCC	AGATAAAAAG	180
GAACGTGAAG AA	ATACAGAC TTTAAAACA	G CAAATAGCAG	ATTTACGGGA	AGATTTGAAA	240
AGAAAGGAGA CC	CAAATGGTC AAGTACACA	C AGCCGTCTCA	GAAGCCAGAT	ACAAATGTTA	300
GTCAGAGAGA AC	CACAGACCT CCGGGAAGA	A ATAAAAGTGA	TGGAAAGATT	CCGACTGGAT	360
GCCTGGAAGA GA	GCAGAAGC CATAGAGAG	C AGCCTCGAG			399

- (2) INFORMATION FOR SEQ ID NO:939:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

GAATTCGGGC	AAAGAGGCTA	GAAGCATCGA	AAGCGTTGGA	GAGGTGTTAC	CGGTAACGGC	60
GGCGAGAAGG	GTGTTCCCGA	ACTAGAGTGG	GGCATACATA	ATCTTGCTGC	TATGCTTCGA	120
AGCTGTAGTC	TGAATCAACC	TAAGTTTTAA	ACAGAAGGTG	AACCTCTGAG	ATAGAAAATC	180
AAGTATATTT	TAAAAGAAGG	GATGTGGGAT	CAAGGAGGAC	AGCCTTGGCA	GCAGTGGCCC	240
TTGAACCAGC	AACAATGGAT	GCAGTCATTC	CAGCACCAAC	AGGATCCAAG	CCAGATTGAT	300
TGGGCTGCAT	TGGCCCAAGC	TTGGATTGCC	CAAAGAGAAG	CTTCAGGACA	GCAAAGCATG	360
GTAGAACAAC	CACCAGGAAT	GATGCCAAAT	GGACAAGATA	TGTCTACAAT	GGAATCTGGT	420
CCAAACAATC	ATGGGAATTT	CCAAGGGGAT	TCAAACTTCA	ACAGAATGTG	GCAACCAGAA	480
TGGGGAATGC	ATCAGCAACC	CCCACACCCC	CCCCTCGAG			519

- (2) INFORMATION FOR SEQ ID NO:940:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

GAATTCGGCC	AAAGAGGCCT	AAGAAATTAT	ACCATTTTAT	GGAATGTCAA	GCTACATCAC	60
CCGAGAAGAC	CAGTACAGCA	AGCCTCCGCA	CAAAAAACTG	AAAGACCGCC	AGATCGATCG	120
CCAGAACCGC	CTCAACAGCC	CTCCTTCTTC	TATCTACAAA	AGCAGCTGCA	CAACAGTATA	180
CAATGGCTAT	GGGAAGGGCC	ATAGTGGTGG	AAGTGGCGGA	GGCGGCAGCG	GTAGTGGTCC	240
CGGAATTAAG	AAAACAGAAG	CGCTCGAG			•	268

- (2) INFORMATION FOR SEQ ID NO:941:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 535 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

GAATTCGGCC	AAAGAGGCCT	AAGCCTCGCC	TTACACTTAA	GTGCACCCGA	TCCTGCCTCT	60
GGCATCTCAC	AAACGTCACT	CCCTGGAACA	AATTTGTGAA	GGCCTCCAGA	CCACAGTGTC	120
CTCATCTGTA	AAATGGGGGT	AGTAGTAATC	CTTGCCTCAT	AAAGTTCTTG	GCAAGGATTA	180
GATGAGCGAG	CATGTGAGTT	TGGCCTCCGT	TTAAACACTC	CATAAAGTTT	CCTTTTAGGA	240
TAACAGCAGG	CCGTTTTAGA	ACCTTCCAGA	GGTTACTTAT	TCAGATATCC	TTAGGTGACG	300
ATTGGGAAGC	TGCCGTTTCT	TGAGAGCCTC	CTGGGTGACA	GATGGAGAGT	GGCCCTGGCG	360
TGACCCTTGA	CCCTATCCTT	GAGGCTTTCC	TGCCCGTCTC	CTGCCTCGAA	TGTGCTCCGC	420
AGCACATGGA	TCAGGATGGG	${\tt GAAGGGGCTG}$	TGTCACTGGA	TACCTTCGGC	CCCTGCCCAC	480
GTCTAGGGCC	TGTGAAAACG	AGGAGGGACA	GCAAAGAAAT	CCCCAAACCC	TCGAG	535

- (2) INFORMATION FOR SEQ ID NO:942:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

GAATTCGGCC	AAAGAGGCCT	AAAATTGTTA	ATTCTAGTCA	CCCTGCAGTG	CTATAGAACA	60
CTGGAACTTA	TTCCTCCTAT	ATCACCGTAT	TTTTGTATCT	ATTAACAAAC	CTCTCCATAT	120
CCTCCCTCCC	TCCTACCCTT	CCCAACCTTT	GGTAATCACT	ATTCTCCTCT	CTACTTCTAT	180
GAGATCAATG	TCTTTATTTA	CTCGAAGTAC	TCTTAAAAGT	TTAGGACTTA	AGTATTTGAA	240
GAAATTCACT	TGCTTTTTGT	TTTTATTCTA	CTCAATACTT	TTTAATATAA	AGATTTACAG	300
TCCCCCCTTA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:943:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 363 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

GAATTCGGCC AAAGAGGCCT	ACAAACTCAA	GATGCCCGAG	TGGATTGGAG	GCGAGAGCGA	60
GCTCAGGAAG TTTCTAAAAC	ATCATTTGCG	ÄGGAAAGAAC	TGTGAACTCC	TGCTGGTGGT	120
ACCAGAAGAG GTAGAGGCTC	ATCAGAGTTG	GAGGACCGAT	GTGTAACAGT	TCTGCCCAAC	180
CTCCCTCTCG CCTCAGCCCC	TTCAGTCCTC	TGTGACGTGC	TGTGGCCTCT	ACAGTGGGTC	240
TGCCCTTGCC ACTTCCCCAA	ACATCTCATC	AAGTTTTTCC	CCTTCAGATC	TGACAGTGCA	300
ATAGGACAGA CGTGTGGACT	GTTATAAGAA	CTACTCAGTG	TTTTGTTCCT	GGGCAAACTC	360
GAG					363

- (2) INFORMATION FOR SEQ ID NO:944:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 324 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

GAATTCGGCC	AAAGAGGCCT	ACTCTGACAG	TGTTTCTGAC	CTTTAGCATT	TCTTTTTGAT	60
TCTTTCTTAG	AATTCTCATC	TTCTGCTTAT	ATACCTGTCT	ATTCTTGCAT	GCTGTCTACG	120
			ATGGTTGTTT			180
TCCAGCATCC	CTGCCACATC	TGAATCTAGT	TCTGATGCTT	GCCCTGTCTC	TTCAAACTCT	240
GTTTTTTTGC	CTTATAATCT	TTTGTTGAAA	GCCGAACATG	ATTCCTGTAC	TGGCTCTTCT	300
GGAGGCTTCT	GCCCTGTTCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:945:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 712 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

GAATTCGGCC	AAAGAGGCCT	ACAGATGACT	TCATTTCTCT	TGGATTCCAC	TTTCTCACGT	60
GTCAGAATGG	GAGAGGAAGG	GAGGTGTTGG	GATAAGTTTC	AGTTCCACTG	TTTGTACTTC	120
TCGTCTGGCT	AACACCCATG	TGGCAAATAG	GTTTCATCAT	TTGTTTCAGC	TTAGATTTGT	180
TGACAGCGGT	TTCCTGGAGT	GCTGTCTTGA	GAACGATTCT	GAGGAGGCTC	AGCAAGAAAG	240
AGTGTTTCAG	TTGATTGGGT	GTGTCTGTCA	TGGAGAAGGA	AGTAAGGAGT	GGGCAGTGCT	300
AGCAAAATTC	CCGGGGCACT	TCTGTCCATT	ATCTCAATAC	CTGGGGTTGA	CATTTCCTGT	360
CTCAGATCAG	GAGTCCTGAC	TACCCTGCCT	CTGACCACTC	GAACTGAGTG	CTGCTTAGCT	420
GTATCGTAGA	CACCGCCTGT	TTGTGAACAG	ACACCCTGCT	TCTTGATAAC	ACAAAGGCCA	480
GCAGGGTCCA	CTGCTGTGTG	GAATGGCCTT	CGGTCATTTC	TGCCCAGAGC	ATAGAGGTCA	540
TTTTCACTAA	TAACATAACT	CTCCTTTTGA	TTGAAAGTGT	TAAAATGTTC	CTCCTAAAAG	600
CACTTATTTT	TTAGGCTCGT	TCTTCAGATT	TGCCCCATAT	CCTAAGCAAA	ATGCCTTCAA	660
TATCAACTCC	ATATTGCTTG	ACCGTAGGGA	GCTTGTCCAT	ACTGTACTCG	AG	712

## (2) INFORMATION FOR SEQ ID NO:946:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GAATTCGGCC T	TCATGGCCT	AGTCTTGAAG	GATAAGACTT	GCCCAAGTGG	ATAAGGGGCG	60
AAAGGCATCC C	CAAGAGGAGA	CAGTAACGTG	TGTATAAATG	AACGAAGGCG	TGAAATAGGA	120
TGGAGTGTTT T	rgaggaacca	CAAGTAGCCT	TCTCTGAGTA	AGAGCATAGG	TTTGTGAGGA	180
GGACCTAGTG T	TGTTTGAAA	AAAGAGAGTG	ATCAATGGAA	GATGAGATAT	CAAGACAGGA	240
GAACCAAGGA A	AGAAAAAGCA	GAGGACAGCT	GGAATGAATC	AAACCGAAGA	ACCAGGATCC	300
TCGAG						305

# (2) INFORMATION FOR SEQ ID NO:947:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

GGGTTTTGTT AATGGA	AAGT TTAAGTAAAT TATATI	rgtaa taaaaaggta gataaacca	T 60
TGTACAACAG TATTCT	AGGC CGCCAACAAA AGTGTC	GACAG ACACACTAAA AGCCCTCCA	A 120
CTTTAACTTG TAACGT	AGCT TCATTCTCAA AGCTGA	ACTCC TTTTTTTTCT TTTTCCTTT	T 180
CTTGAGTGTA GTACAG	TTAA AATTTCAAAC AGCTCO	CTTGA CACTGCTTTT CATGTTCAA	A 240
CCAGCCATTT TGTTGT	ACTT TGGTAAAGGA CCTCTT	CCCC TTCCTCCCCT ACACATACA	G 300
ATACACCCAC CATAAC	rcga g	•	321

- (2) INFORMATION FOR SEQ ID NO:948:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 312 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GAATTCGGCC	TTCATGGCCT	ACAAAAGGCA	ACAAACAAGA	TTAACATGGA	AAAAAAAA	60
TCACTCAATC	CAAAATAAGG	CAGAAGAAGT	GGAAAAGGGA	GATGAAGATC	AGATGGAACA	120
AAGAATATTA	CTAGAAATGA	CTATGTTTTA	TAATGCAAAA	TAGTTCAGTA	CAGGAGAAAG	180
ATACAATAAT	TTGAGTGCAT	ATGAACTTAA	AAGAGAATTT	CAAAATATAT	GAAGCAAAAA	240
TTGACAGAAC	CCAAAAGGCA	ACAAACAAGA	TTAACATGGA	ATTATAAAAA	TCACTCAATC	300
CAATATCTCG	AG					312

- (2) INFORMATION FOR SEQ ID NO:949:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 291 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

GAATTCGGCC	TTCATGGCCT	ATAGGCCATG	AAGGCCGGGA	GCCTCAAGAA	AAATTAGCAG	60
AGGAAAATAA	TAGGTAGTTA	CTATTTAGGG	TAAACTAAAC	TGTTCTAAGG	AATAGAAAAT	120
AAAAATTCCA	TGTCTTCAAA	AATAATTCTT	CCCTCTCAAT	CTCTCTGAAT	ATCTCATAAĠ	180
AGTATTCAGG	CCACAGAAAT	AACTACCATT	TAGCCACTCA	GAGGCTTATA	GTAGTTCTAC	240
TAACTTTAAC	ATTTGGCAAC	CAAAATTACT	CTAAGAATCA	TCACCCTCGA	G ·	291

- (2) INFORMATION FOR SEQ ID NO:950:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 240 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

GAATTCGGCC	TTCATGGCCT	AGATGGGCAT	TCTGTTTATC	TTACTAGTAG	TACGCAGGGT	60
ATGTTGAAAT	CTCCAACTGT	GATGGTGGAC	CTGTCAACTT	CTCCCTGTGG	TTTTATCAGT	120
TTTTCCTGGG	TATTTTGAGG	CTATTCTGAT	AGGTACATAA	AATACAAAAA	TTGCTATATC	180
CTCCTAATTA	ACACTTATTA	TCAAATTGTT	ACTAATGCTT	TCTGTTCCTA	GGCCATGAAG	240

- (2) INFORMATION FOR SEQ ID NO:951:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 404 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

60
120
180
240
300
360
404

- (2) INFORMATION FOR SEQ ID NO:952:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 382 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

GAATTGGCCT	TCATGGCCTA	GAAAAATCAT	GTGGGAAAAC	CACTGCTGAA	AATGGATTTA	60
AATTCAGAAC	AGGCGGAACA	ACTGGAAAGA	ATCAATGATG	CTCTTTCCTG	TGAATATGAG	120
TGCCGCCGAC	GAATGTTAAT	GAAACGATTA	GATGTGACTG	TACAGTCCTT	TGGATGGTCT	180
GATAGAGCAA	AGGTAAAAAC	AGATGATATA	GCAAGAATTT	ATCAGCCTAA	GCGTTATGCT	240
TTGTCACCCA	AGACAACGAT	TACAATGGCA	CATCTACTTG	CTGCTCGTGA	AGATCTATCC	300
AAGATCATTA	GGACAAGTAG	TGGCACCAGC	CGGGAGAAGA	CCGCATGTGC	CATTAATAAG	360
GTGCTGATGG	GAAGGGCTCG	AG				382

- (2) INFORMATION FOR SEQ ID NO:953:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

GAATTCGGCC	TTCATGGCCT	AGTCCCTCTT	CCACTGCATT	TCGGCTTCAT	ACATGCACAT	60
GATGTCCTCC	TCCTTGCACT	CAGTGATGTC	TGGCACGCGG	CGGTACTGCC	GGTGGTAGTA	120
GTAATACCTG	TTCTTTGCGT	GCTGCCGCTC	TATAAATTCT	CTCACGAGGG	TCACGGGTCG	180.
GTCCACGATG	AGGTCGAACG	CTTTCATCAT	GTAGACGATG	GGATTGGGCT	GCACCGGCGT	240
acadececae	GGCTCAGGCT	CGCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:954:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 260 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

60

PCT/US98/06956 WO 98/45437

TGGAATGAGG AAGTGTGAGG AGGGAATCAG TGCCTCTCGG AAGTCGTTTT AATTAGAATG TGATTTTTT TTCTTAAACG TGTCTTCATT GGCTCCCACA TTTGCCGTAG AAACCAAGCA AACTGGGTGC TAAAACAGAA AGGCCCATAG ATTGTACTTT TTGAGCTGTT TGAATTTGTA TACCATATGC ACAACTCGAG	120 180 240 260
(2) INFORMATION FOR SEQ ID NO:955:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 129 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:	
GAATTCGGCC TTCATGGCCT AATCCGAGTG TTTCGCGCAC GTCCTAAGCT GACAGTCCCT CTGGACAGAG TCCCTGGAGT GGAGTCACTG CTCCTTGTCT TTTTTCATA ACATACACTC ACCCGTATG	60 120 129
(2) INFORMATION FOR SEQ ID NO:956:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 404 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:	
GGCTAAACAT GGAAATGAAA GACTGATACT TGCTACCACA AAAANANACT TAAGCACATA GATCATAGAC AGTATAAAGC AATTAGACAA TGAAGTCTAC AAAACAACCA GTTAACAACA CAATGAGAGT ATCAAAATCT TACATGTCAA TACTAACCAT GAATATAAAT GATCTAAGCC CCCCACTTAA AAAGCATAGA GTGGCAAACT GGATAAAGAG ATAAGACCCA ACTGTCTGCT GCCTTTGAGA GACCCATCTT GCATGTAGTG ACACCCACAA GCTGAAAGTA ATGAGATGGA GAAAGATCTA TCATGCAAAA GGAAAACAAA AAAGAGCAAG TATCACTATT CTTATATCAG ATAAGACCAG TTTTAAACCA ACAACTATCA AGAAGAACCT CGAG	60 120 180 240 300 360 404
(2) INFORMATION FOR SEQ ID NO:957:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 283 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:	
GAATTCGGCC TTCATGGCCT AGACTCTCTT TATACAATTC ATCAAGGTTA AACAAAACAT AAAATTCCCT TAAAAATAGG GTAATAAAAT AGATGAAATT TGTATCACTC AATTTGGTGA TACTAGTAAA AACTATAGTT CATATTTATA TACAAATAAT ACAGTCTGTA AAAACAGTCT TAGAATTTAA ATAAGCTATC TAAACGTGTT AAAATTTTAA ATCAGGACCT GATTTGTTTT GCTTTCCATT AAATGTCACA TTGAATTCTA GACCTGCCTC GAG	60 120 180 240 283

### (2) INFORMATION FOR SEQ ID NO:958:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

CTCGAGGACC	TGGTCGTGAC	CAACTATAAG	ATGGGGGGC	GACATTGCCA	ATGGGGTACT	60
TCGGTCCTTG	GTGGACGCAT	CTAGCTCAGG	TGTGTCAGTA	CTGAGCCTGT	GTGAGAAAGG	120
TGATGCCGTG	ATTATGCAAG	AAACAGGGAA	AATCTTCAAG	AAAGAAAAAG	AGATGAAGAA	180
ACGTATTGCT	TTTCCCACCA	GCATTTTGGT	AAATAACTGT	GTATGTCACT	TCTCCCCTTT	240
GAAGAGAGAC	CAGGATTATA	TTCTCAAGGA	AGGTGACTTG	GTAAAAATTA	GGCCTCTTTG	300
GCCGAATTC						309

- (2) INFORMATION FOR SEQ ID NO:959:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 149 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

GAATTCGGCC AA	AGAGGCCT	AGATTGAATT	CTAGACCTGC	CTCGGACTAC	TGCAAGTGCT	60
TAAAGGCATT AT	TTCATAGA	CCTTACAACT	ACCCATATAA	CATTATTATC	TTCATTTTAC	120
AAATGAGGAT AA	TAATGTTA	TATCTCGAG				149

- (2) INFORMATION FOR SEQ ID NO:960:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 455 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

GAATTCGGCC	AAAGAGGCCT	ACACCGTAAT	ACTATAATAC	TATATAATCT	GTTTGTTAAT	60
TTTCTGAGAA	TAATAACTCA	ATGGAGTAAC	TCTTTAATAG	GCATCTTTTC	CTTATAAAAA	120
ATATTGTAGA	TTGGCTCTCT	GCAAGCTAAT	TTCTTTTATA	TGGTTAATAT	TTTAGTGTAC	180
ATTAAGAGCT	TAGAGTTCTT	TTTGTAATCA	AGCTTGCTAC	AGAAGCTGTG	CTTTATTTAT	240
TTCATAGTAA	TTTCCTCTAG	TGGGTCATTG	TATAAACCCT	GATCATTTTT	GTATGTCTAT	300
TCCTTTTCTT	GCGAAGTGGG	CAGCTTGTTT	AGCCATGGTG	TTTTGGCTTC	AATAGTGAGG	360
TCTCTATTTG	GGAATCTCTG	AATTTCACAG	GAATGAGTAG	AACTATATTT	AACAATGAAA	420
AAAATAGTAT	TAGATTTTAG	GGCAGCTGGC	TCGAG			455

- (2) INFORMATION FOR SEQ ID NO:961:
  - (i) SEQUENCE CHARACTERISTICS:

> (A) LENGTH: 207 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

GAATTCGGCC AAAGAGGCCT ACCCTGTCTT TATGCTCCAA TGCTTCTTTC TCCAGATATG 60 AAAGGAGATG CTCTCTATCA AATGGCCCTG TGGTGGACTT TGATGTCTGG TTCTTCTGCC 120 GGAACCCTGC TGGCTTTTTG CTGTAGCTCC ACATTCCTGT GCATTGAGGG GTTAACATTA 180 207 GGCTGGGAAG ATGACAAAAC TCTCGAG

- (2) INFORMATION FOR SEQ ID NO:962:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 247 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

GAATTCGGCC	AAAGAGGCCT	ACTGTAGTAT	TTAAATATCT	GTTACAGGTT	TCCAAGGTGG	60
ACTTGAACAG	ATGGCCTTAT	ATTACCAAAA	CTTTTATATT	CTAGTTGTTT	TTGTACTTTT	120
TTTGCATACA	AGCCGAACGT	TTGTGCTTCC	CGTGCATGCA	GTCAAAGACT	CAGCACAGGT	180
TTTAGAGGAA	ATAGTCAAAC	ATGAACTAGG	AAGCCAGGTG	AGTCTCCTTT	CTCCAGTGGA	240
TCTCGAG						247

- (2) INFORMATION FOR SEQ ID NO:963:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 472 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

GAATTCGGCC	AAAGAGGCCT	ACAAGAACAT	GAAACATCTG	TGGTTCTTCC	TTCTCCTGGT	60
GGCAGCTCCC	AGATGGGTCC	TGTCCCAGGT	GCAGCTGCAG	GAGTCGGGCC	CAGGACTGGT	120
GAAGCCTTCG	GAGACCCTGT	CCCTCACCTG	CGCTGTCTCT	GGTGGCTCCA	TGAATAGTCA	180
CTACTGGAGC	TGGGTCCGGC	AGCCCCCAGG	GAAGGGACTG	GAGTGGATTG	GATATATCTC	240
TGACAGGGGG	AGCACCAACT	ACAACCCCTC	CCTCAGGAGT	CAACTCACCA	TATCACTAGA	300
AACGTCCAAG	AACCAGTTCT	CCCTGAATTT	GTTCTCCGTG	ACCGCTGCGG	ACACCGCCGT	360
ATATTACTGT	TCTCGTGGGA	CATCCCCCCC	CCCCTCCTAC	TACTACTCCA	TGGACGTCTG	420
GGGCAAGGGG	ACCACGGTCA	CCGTCTCCTC	AGGGAGTGCA	TCCACCCTCG	AG	472

- (2) INFORMATION FOR SEQ ID NO:964:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 303 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

GCTCGGCTCG	CTGCAACCTC	TGCCTCCCAG	GTTCGAGCGA	TCTTCCTGCC	TCGGTCTCCC	60
AGGTAGCTGG	GACTACTGGC	GTGCGCGACC	ACGCCCAGCT	AATTTTTTGT	ATTTTTAGTG	120
GAGACGGGGT	TTCACCATGT	TGGCCAGGAT	GGTCTCAATC	TCTTGACCGC	GTGATCTGCC	180
TGCCTCGGCC	TCCCAAAGTG	CTGGGATTAC	AGGCTTGAGC	CACCGCATCC	AGCCAACATT	240
TTTCAAATAG	AAAATCTGAA	GCTAAAATCA	CCCCTAAAGG	ACAAATAACA	GGACTATCTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:965:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 281 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

GAATTCGGCC	TTCATGGCCT	ACTAGATTAT	GGATTTTTTT	ATTTCAATGG	AAGTGAAGTT	60
CAAAGATGCC	AGAGTGGTAC	AGTTCGAACA	AACTGCTTGG	ATTGTCTTGA	TAGAACAAAT	120
AGTGTGCAGG	CATTTCTTGG	CTTAGAGATG	CTAGCTAAAC	AGTTGGAAGC	TCTTGGTTTA	180
GCTGAAAAGC	CTCAGTTGGT	GACTCGCTTT	CAAGAAGTTT	TTCGGTCAAT	GTGGTCCGTG	240
AATGGTGATT	CAATCAGTAA	GATATATGCA	GGAAACTCGA	G		281

- (2) INFORMATION FOR SEQ ID NO:966:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 454 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GAATTCGGCC	TTCATGGCCT	AGACGTGATG	TGTTGAGAGA	AGAATGTTCT	AGGCAGAGGC	60
		GAAGGGGAGA				. 120
		TTCCTAAGGT				180
		AGCAGACCCA				240
		AGAATATGAG				300
		GAGGTTTAGG				360
		TCTGAGGATG				420
				IIINONGGCA	MICGIINO	454
A LUCAL TUGGE	IGAACAGAAA	AGGTGAATCT	CGAG		,	7,72

- (2) INFORMATION FOR SEQ ID NO:967:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 322 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

GAATTCGGCC TTCATGGCCT AGTCATTTAA TTTAACTTAG CAAAACTCCA ATAGTGTAAG	60
TTAACAGATT TTGGAAACTG GTTTTAAGTA GATGTATTAT AACATAAAAC AAAGCTAGCC	120
ATTATCAAGT TATTTCCTTG TTAGCTATTT TTACAGCATG TGCATGTTAG GTAGTCATCG	180
TGAAAGCAAG AATCTTAAGT TAAATACATG TTTTTTTTTT	240
CTGTATAATA CATGATGCTG TTAGCAGCGG AACGTATCAG AGACACGGCA CCAAAGTATG	300
TTACTGTCGG CGAAAACTCG AG	322

- (2) INFORMATION FOR SEQ ID NO:968:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 478 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GAATTCGGCC	TTCATGGCCT	AGACTGCTGG	CATATCCACC	CCACCTGTGC	TGCTGCCCCC	60
GCCAATCCAT	CAGGGCAGCT	CCGACTCCTG	CAGCACCCAC	CGCCCAGGAC	GTCAGCTACT	120
CAGGTTTTCT	GGCTGCTGGG	GTTCCGCACG	AATGGGCCCT	TCTTTTGGGA	AAATGCCAGG	180
			GCTTGTCCCT			240
TATGGCGCAG	GAGGGACAAC	TGGCCCCTGT	GGCCAGCCCC	AGAGAGACGG	GCCCTTTCTT	300
TGGGACCCTG	GCCTCAGAGG	CCTGCGTGTC	ACAGCTCAGG	GTCTGGCTGG	GCAGGGGCAA	360
AACCTGCCTT	ATTTGCCAGA	TGTCCCAGAA	GTACACAGGA	GCAGACGCAC	CACTTCGATG	420
			CATGGTGGCA			478

- (2) INFORMATION FOR SEQ ID NO:969:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

CTCGAGGTCC	CTGTCCTGCT	CAGTTTCTCT	TCAATGTGGA	AGTCCTGGGA	GGTCAGTCTC	60
			TTCTCAGACT			120
CTTGCCAGCT	AGTGGAGTGA	GCAGAACTCC	TCCTGGTTTC	TGTGGCTGTT	CTCAGAATGC	180
CCTAGTTCAC	TTTCCAGTAA	TACTTTTTTG	GGAACATTTT	GTGTTTCTCA	TTTTCTCAGG	240
			CCTCTCACAC			300
TTTGGGGCTG	TTGTTCTGGC	CCACTCCCTG	ATATTTTCTG	GGTTTGTCAC	CTAGTTTTCT	360
TAAAAGTATC	ATCTACATGG	TTTTGGTTTC	ACTATCTATT	CTGTCTTTAT	TTGAACACTA	420
GGGGAAATTC	ATTATGCCAA	TCTCACACAT	TGTGTGATTC	CATTAGGCCA	TGAAGGCCGA	480
ATTC						484

- (2) INFORMATION FOR SEQ ID NO:970:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 540 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GAATTCGGCC	AAAGAGGCCT	AGGCAAAATG	AAAATACTTG	TGGCATTTCT	GGTGGTGCTG	60
ACCATCTTTG	GGATACAATC	TCATGGATAC	GAGGTTTTTA	ACATCATCAG	CCCAAGCAAC	120
AATGGTGGCA	ATGTTCAGGA	GACAGTGACA	ATTGATAATG	AAAAAAATAC	CGCCATCATT	180
AACATCCATG	CAGGATCATG	CTCTTCTACC	ACAATTTTTG	ACTATAAACA	TGGCTACATT	240
GCATCCAGGG	TGCTCTCCCG	AAGAGCCTGC	TTTATCCTGA	AGATGGACCA	TCAGAACATC	300
CCTCCTCTGA	ACAATCTCCA	ATGGTACATC	TATGAGAAAC	AGGCTCTGGA	CAACATGTTC	360
TCCAGCAAAT	ACACCTGGGT	CAAGTACAAC	CCTCTGGAGT	CTCTGATCAA	AGACGTGGAT	420
TGGTTCCTGC	TTGGGTCACC	CATTGAGAAA	CTCTGCAAAC	ATATCCCTTT	GTATAAGGGG	480
GAAGTGGTTG	AAAACACACA	TAATGTCGGT	GCTGGAGGCT	GTGCAAAGGC	TGCACTCGAG	540

- (2) INFORMATION FOR SEQ ID NO:971:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 289 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

GAATTCGGCC	TTCATGGCCT	AGCCAGTCTC	AGCACTTAAA	CAACCAGGTG	TTGAAGGACT	60
ATGTTCCAAA	GAACAGAAGA	GAGTATGGTT	TGCAGATGGT	ATATTGCCCA	ATGGTGAAGT	120
TGCAGATACA	ACAAAATTAT	CATCTGGAAG	TAAAAGATGT	TCTGAAGACT	TTAGTCCTCT	180
CTCACCTGAT	GTGCCTATGG	TAAGGAATTC	AAAGAATACT	TAATTGACTA	AACAAAATTT	240
TATTTCGTAG	ATAATTCCTG	GTGTGATTAT	TAGAGTGCTT	TTTCTCGAG		289

- (2) INFORMATION FOR SEQ ID NO:972:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 418 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

GAATTCGGCC	TTCATGGCCT	AGAGCTTGGG	AGGTTGAGGC	TGCAGTGAGC	TATGAGCTGC	60
ACCACTGTAC	TCCAGCCTGG	GTGACAGGGC	AAGACTCTGT	CTCAAAAAAC	AAAAACAACA	120
ACAAAAACTT	TATTCCTAAA	AAGTGCTGAC	CCAGAGATAA	GAAGCAAGCA	CATGGTTGGT	180
AAAATGACAT	CAGTGAGCTT	GCTTTATGCA	GGGTTGCCCC	AAACCTTCAA	TTTGTAAAAC	240
TCAAAATATC	TGGAAAGCTT	GGTGAGGCGA	GGCGGGACTG	TAACTCAGCA	CTCACCGCAG	300
GGTGAGACCC	TTAGGGCAGC	GGGTGCTACA	CTGAACAAAG	CGGTGAACAG	CCCCCTCGTG	360
AGAGGGGGTT	CTTGGCAGAT	GACGCCAGCA	GCTGACAAAC	AGGCAAGTGC	AACTCGAG	418

- (2) INFORMATION FOR SEQ ID NO:973:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 276 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (2)

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

GAATTCGGCC	TTCATGGCCT	AGATTTGTAA	AAGATTTTCC	TAGATTTACT	GTGTTCTGGA	60
TCTAGCTTGA	ACGTGAATGT	TTGTATAGTA	CGTTTTCTTA	ATATTTTTA	GTATTCATAG	120
TATATAATCA	TACTAAACTT	GAGAAACTGG	AAGAATCAAG	TCTTCCTCAG	TTCTGTTTAG	180
ACTTTCTAGT	TTTTTTTAAG	GATACTTCCA	TATCTTCTGT	AAGCTACACA	GTGAGCTTCA	240
TTTTTGCACA	GTTATAATAC	ACTCTCGAAT	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:974:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 379 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

GAATTCGGCC	TTCATGGCCT	AGGGTTCGAT	GATAAGCACA	GGCGGCAGCT	GGATTGCAAG	60
TGGAGTGGTA	ATGGCCAGAA	CAGCCTCTTT	CTGTTTTGCA	TTTAGTCGAG	GATCCAACTG	120
TTCATCCCAT	TGTCTGTTAG	GACTCCATGG	TATGGTGGGA	GTCATACTGA	TGTCTGGAAA	180
CAAAACCCCA	TTGTCCTTGA	TCCTGTCTAG	TGCATAGTGC	ATTTCACAGA	GGGGTAATCG	240
ATTTAATTGA	AACTGAAGTT	CAACCTGTGT	GTCACAGTCA	GGCCGAAGAT	TAAGTTCTTC	300
ACAGCATTCC	CTAGATAGCC	TTAAAAATAT	ATATTCCTTT	GTTTTTTCTT	CAATAGTAGC	360
TTCCTAGACC	TGCCTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:975:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 417 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

GAATTCGGCC	TTCATGGCCT	AAGAGAAAGA	GAGTGAGAGA	GAGAGAGAAA	GAGAGAGA	60
GATGCTGTTG	AATCAGAAAC	AGATCAACAG	CCCAAAGATT	TTCCTGTCCC	TGGAGTGCCA	120
GCCCCAGGAA	GCTCCAGGGC	TGAGTGGTCA	GGAGCCAGTT	TCTCCAGCCC	CTCCTCCCCA '	180
CAACCCCTAG	TGGGGAGGG	CAGCTGTCCA	TTTGCCCAAA	GTATTAATGC	AACTGAAGCT	240
GTGATATTTC	CAACGACTGT	AGGAGGAAAA	ATTAAGGGGA	GAGAGGAAAA	CAAAACCAAC	300
CAACCCCTAA	AATCATTTTC	TTATTGTACA	TAACGACCTC	ATTCTCCTGT	ATATGCGGAA	360
GATATAACCT	TATATTTGGT	AAGTGTTTCT	TGTGCTATTT	TATCACGCGA	CCTCGAG	417

- (2) INFORMATION FOR SEQ ID NO:976:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 154 base pairs
    - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

GAATTCGGCC TTCATGGCCT ACACAGAAAA ATTTCAACAA TAAAAGTTCT TAATTATGGG 60
AAATAGTTAC ATGTGTGTTA TATCATTTAT GGCTCATTTT GTATTTAT TTAAAAGTAT 120
TAAAATCCCA ACAGTAACAG CAATACAACT CGAG 154

- (2) INFORMATION FOR SEQ ID NO:977:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 252 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

GAATTCGGCC	TTCATGGCCT	AAATTGTTCT	TTGCTCAAAT	AAACTGTTAA	ATTTATCTTG	60
GCAGACTCTA	TTTTGATCCC	CAAATTTGAT	TTAGATTTGG	GGCCATTAAA	TTTCACTATT	120
TAATAATAAC	CCTACTGGAT	GAGAATAAGT	GTTTCTCAAT	TTCTGGTGAT	ATGGTTTGGC	180
TGTGTCCCCA	CCCAGAATCT	CATCTTGAAT	TATATTCCCC	ATAATCCCCA	CGTGTCAACG	240
GCAGGACTCG	AG					252

- (2) INFORMATION FOR SEQ ID NO:978:
  - (i) SEQUENCE CHARACTERISTICS:-
    - (A) LENGTH: 251 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

GAATTCGGCC	TTCATAGCCT	AGTTTAGTTC	TCAGAATTCT	TCATATATTT	TGGCAGCAGT	60
TTTTCCATCA	GATTATTTTG	TAAATATTTT	CTCCCAGTCT	GTGACTTGCŤ	TTTTCCATTC	120
TCTTAACAGT	GTCTTTCACA	CAACAGAAGT	TTTTAATTTT	AATGAGGCTC	AACTTAATTT	180
TTTTTTCATT	AGTAGATTGT	GCTTTTGGTT	TTGTATCTAA	GAAGCCATCA	TTGAACCCAG	240
GATCGCTCGA	G				•	251

- (2) INFORMATION FOR SEQ ID NO:979:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 534 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

60	NCTTTCCATT	CTCAAAACTA	TGAATAATTT	AGAAGGCTTC	TTCATGGCCT	GAATTCGGCC
120	TCTTCTACCA	TTTAGCAATT	TAGATAGGTA	CATAGCACAT	ATTTGATAAA	TNAGTACACG
180	ACATATAAAG	AACAATTTCT	TATGATTTGA	AGGGTTAGAG	GCCCTCACTA	ACTACACTTT
240	GTACCTATGG	TTTCACTTAT	CTGAGACTTC	GTTCACTGAA	TAAGTTTTGT	CATCTTTAAA
300	ATATGTTTTT	ATATGTGTAC	ACTTGCATAC	ATATATACAT	GAGCATACAC	AAGTTAATCT
360	CTCTGGGGAA	ACAGGGACAA	CCTAGACACT	TTAGAATAAA	ACTTTTACCA	TAAGTAAGTN
420	AGTTCACTGA	AGGCAGGTAT	AGGTTGAGGA	ACCCTTCTCT	TGCCTTAACA	CAGGGCGGTC
480	TTGCCTGGTC	TAATCCTGCG	CATCATCTGT	TAAGTCTTCT	GAGGCTGTAG	AGGATGTGAT
534	CGAG	ACTGGCCTCT	CCTCAGCAGC	ACATCTGCTT	AGCTACGTGC	TCACCACCAC

- (2) INFORMATION FOR SEQ ID NO:980:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 223 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

GCTCGAGTGT	CGTGCTATCT	CTAAATTGTG	ATCACTAAGA	ACCGCTGCGG	AAACAGTAAC	60
TGTTTCTTTT	ATTTTTGACA	TTTTAGTTTG	TAATTTATCC	AATTCTTTCT	TCTTTTGATA	120
AGTCTCCATT	CTCTTTACTT	CACGGGTATT	TTCAAATTCA	TTAATCATTT	TATCACAGTG	180
CCACTTGTTA	GACCCTAATG	AACGATGTCA	CCCTCTTATC	AAA		223

- (2) INFORMATION FOR SEQ ID NO:981:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

GAATTCGGCC	TTCATGGCCT	AATTACTTGA	CCCGTAATAG	GGTTGTGGCC	GTTTTCTGAT	60
GCCTAAGTAT	TATACAGAGC	CCACAATGGC	CAGTTTACTA	CCAGAAAGGG	CTTCAGTAAG	120
ATATTCTTGG	ACTTGATACT	TTCTTCAGAT	CCTCTTTGTG	CCAAGATAAT	TTATCCAGTC	180
ATTGGGAATA	GTAAGTTTCT	GTGTAACCCA	TCTCAATTAT	AGAAGCAAGT	TCAGCTTTAT	240
GTATTTGTAT	GGGGAGTTGA	AGATTCAGAT	AGAGGTATTA	AGATGTGTGG	CATTTACTTA	300
AACCATCACA	TTTTTTTCTT	TCTACGCCCC	CTTGCCTGTA	AAACACCTGG	GAAGTTCCAC	360
TGGTGTCATC	CATCCTGATG	CTTCAGACCA	CCCTCCCTTC	TTCACAGACC	GTGTCACTTT	420
GCCTGTGGGT	GGGGGCTAGC	CAGCCACCAC	CCTCTTTTCT	GTGCTGCCAG	CCAATCTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:982:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 293 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

TCCGTGTCCC	CTCCTCCCTC	TGCCCCCAGT	GTTTCTTCTG	ATTTTTTTTT	CCCCTTTCCC	60
TCCCTCCCTC	TCCGCATTCT	TCCCTTGGTT	CAGCACAGGT	AAAACGGTTC	CCCTCCCTCC	120
CTGCCTTCAT	GGATCACCAG	CTCACGTCAT	GTTGCCTTCT	CTTTTCTTTG	TGTGTGTGTT	180
TATTTAAGTT	ATTTTTCTTC	CTCCTCTCCC	TTTTCTTTTT	GGCCCTCCCT	CCCTCCCTCT	240
TCTGCCATGT	AACTGGAGGA	TGTGCTATGA	GTTTGCAAAC	AGCCGGACTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:983:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 334 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GGTGAGGATG	GTGGCTGTGG	TTGTGTTGGT	GGCTGTGATG	GTGAAGGTGG	CTGTGGTGGG	60
GATGGTGACT	CTGATGCTAA	TGTTGGTTGT	GGTGATGGAG	GCAGCTGTGG	CAAGGATGGT	120
GACTTTGGTG	GAGAAGGTGG	CCATGTTGGG	GCTAGTGGCT	GTGGTTGTGG	TGATGGCCAT	180
GGTGAGGATG	GTGTTAAAGG	TGGCTGTGAT	GAAGATGGTG	ACTGGGGTAG	AAATGGTGAC	240
TGTGATGGTA	ATGTTGGCTG	TGGTGATGAA	GGGTAGTTAT	GGTGAGGATG	ATGACTATGG	300
TGGTGAAGGG	GCCATAGTGG	CAACGGCACT	CGAG			334

- (2) INFORMATION FOR SEQ ID NO:984:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 631 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

GAATTCGGCC TTCATGGCCT	AGGGAAAGAG	TAGGGGTGGA	GGGGTAGGAG	GATTTACTCT	60
TCCAGCGAGA GCTACGCGCA	TCCCATCCTC	CCCCTCCCCC	CTACCCGGGC	TCCGGCNTGG	120
AGGCGGGGCG TGGCCGGCCT	GCTTTGGGAG	GGGAGGGGCT	TCCCTTACAG	TGCTGGGCTC	180
TGCCAGGACG GCTGTGGGGT	CGCCTTACCT	CGGGGTATCC	ACTCTGCAGT	CGACCAGTTC	240
CCGCCAGGAG CAAAGGGTAG	GAAGGAGAGC	AGGATCTGCT	GTAGGAACGC	AGCTACCGCG	300
CCACTATCAC GAAGAAACAG	CAGGCTCGGG	GCACGAGACG	AACTGGAGAC	CGCGCTGCCT	360
AGCTGGGTAA CCTGGGAAGC	AGAGGGTAAT	AAGTGGCGCC	TTAAGATAAC	CCTGTAGCAG	420
CAGCAGTGGC GGCCAAAGGA	GGCTGCTCAG	GGAACAAGCG	GCTGTAGTAG	TCTGTGGGGC	480
GACTGGAGTG ACCGAAGCCA	AGGCAGTTTA	GTGCCTCTCG	TGTTCTTATT	TTTTAACCTC	540
TGACTATGCA ATTCTGAAAC	CTCCCCCATT	CGGGGGACCA	GACAGCCTGA	TAGACACCTT	600
CCACTCTCCT TCCTCCCGCC	GTGGTCTCGA	G			631

- (2) INFORMATION FOR SEQ ID NO:985:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 324 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

GAATTCGGCC	AAAGAGGCCT	ACTGCCTCGG	TTTCTACCTT	TGCCAAATGA	GTTGATAGAT	60
TATCGCTTTT	TTTCCAGCTG	TCATACTCTA	GGAGTCTGAA	TTGTAAAATC	AAAGAAGCAT	120
TTCCCAGAAA	AGTTTTTGTC	AAAAATTTGA	TTTACATAAC	CTCAGAAATG	TGTATTGCTT	180
TAAAAATTAT	AAAGTTCATG	GAGCATACCA	AGCAGCCTGT	ATACCATTTC	TAAACCAACT	240
ACTCCCCTGC	AAGATAGATC	TCTTTTTTAT	AGACAGAAAA	TAAATTCAAA	GAGGTTTGTT	300
ACTTGCCCAA	GGCCACCACT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:986:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 239 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GAATTCGGCT	TTCATGGCCT	AAAATGTTTT	TCAATTAAAG	ACTTAAATAT	TACACTTTTA	60
AAACTTTTTA	TTATGGAAAT	СТААААААА	TTCACCAAAT	GAGAGAGAAC	ATTACAATGA	120
ACCACCACAT	ACCCATCACC	CATTTTCAAC	AATTATCAAC	ACATGGCCTA	TCTTGTTTCC	180
TCCATACCTT	CAGACACCCT	CCGTCCACAA	ACTGGGTTAT	TCTGAAGCAA	GCCTTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:987:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 695 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

AAAAGTTCAG	GGACTTTGCA	CCCTGTGGGG	TACTCAGATG	TCCAGCCGCA	CTCTCTACAT	60
TAATAGTAGG	CAACTGGTGT	CCCTGCAGTG	GGGCCACCAG	GAAGTTCCGG	CCAACTTTAA	120
CTTTGCTAGT	GATGTGTNGG	ATCACTGGGC	TGACATGGAG	AAGCTGGCAA	GNGACTCCNA	180
AGCCCACCCC	TGTGGTGGGT	GAATGGGAAA	GGGAAAGAAT	TAATGTGGAA	TTTCAGAGAA	240
CTGAGTGAAA	ACAGCCAGCA	NGCAGCCAAC	TTCCTCTCGG	GAGCCTGTGG	CTTGCAGCGT	300
GGGGATCGTG	TGGCAGTGAT	GCTGCCCNGA	ANGCCTGAGT	GGTGGCTGGN	GATCCTGGGC	360
TGCATTCGAG	CAGGTCTCAT	CTTTATGCCT	GGAACCATCC	AGATGAAATC	CACAGACATA	420
CTGTATAGGT	TGCAGATGTC	TAAGGCCAAG	GCTATTGTTG	CTGGGGATGA	AGTCATCCAA	480
GAAGTGGACA	CAGTGGCATC	TGAATGTCCT	TCTCTGAGAA	TTAAGCTACT	GGTGTCTGAG	540
AAAAGCTGCG	ATGGGTGGCT	GAACTTCAAG	AAACTACTAA	ATGAGGCATC	CACCACTCAT	600
CACTGTGTGG	AGACTGGAAG	CCAGGAAGCA	TCTGCCATCT	ACTTCACTAG	TGGGACCAGT	660
GGTCTTCCCA	AGATGGCAGA	ACATTCCTAC	TCGAG			695

- (2) INFORMATION FOR SEQ ID NO:988:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 314 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

GAATTCGGCC	TTCATGGCCT	ACTCAGAACA	ATCACTGCAT	ATCCCATCTT	AAAGGCAAAA	60
CCCAAACCAG	AAAAACCCCA	CTCAGGTCTT	GCTGACCCAA	CACTACAGTC	ACTGTATTTG	120
AGACCCCTTT	TTCTTGAAAA	AGGGACTTCA	CTTTTTTGAG	CAGCATTCTA	TGGTTCTTTC	180
CACACAGCAA	TTGACGCATC	TCACGGCACT	GCTCTCTGCT	GGGCAGAGAG	CAAACACAGA	240
CAGCCACCAT	CCCCATATTC	GTAGTAAGAG	AAACTCCAGA	AACGCAGCCA	CCGTCCCCCT	300
AGACCTGCCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:989:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 687 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GAATTCGGCC AAAGAGGCCT	AGGAGCTCCC	CCATGGATCA	TGGCGTTAAT	GTTTACAGGA	. 60
CATTTACTAT TCTTAGCATT	ATTGATGTTT	GCTTTCTCTA	CTTTTGAGGA	ATCTGTGAGC	120
AATTATTCCG AATGGGCAGT	TTTCACAGAT	GATATAGATC	AGTTTAAAAC	ACAGAAAGTG	180
CAAGATTTCA GACCCAACCA	AAAGCTGAAG	AAAAGTATGC	TTCATCCAAG	TTTATATTTT	240
GATGCTGGAG AAATCCAAGC	AATGAGACAA	AAGTCTCGTG	CAAGCCATTT	GCATCTTTTT	300
AGAGCTATCA GAAGTGCAGT	GACAGTTATG	CTGTCCAACC	CAACATACTA	CCTACCTCCA	360
CCAAAGCATG CTGATTTTGC	TGCCAAGTGG	AATGAAATTT	ATGGTAACAA	TCTGCCTCCT	420
TTAGCATTGT ACTGTTTGTT	ATGCCCAGAA	GACAAAGTTG	CCTTTGAATT	TGTCTTGGAA	480
TATATGGACA GGATGGTTGG	CTACAAAGAC	TGGCTAGTAG	AGAATGCACC	AGGAGATGAG	540
GTTCCAATTG GCCATTCCTT	AACAGGTTTT	GCCACTGCCT	TTGACTTTTT	ATATAACTTA	600
TTAGATAATC ATCGAAGACA	AAAATACCTG	GAAAAAATAT	GGGTTATTAC	TGAGGAAATG	660
TACGAGTATT CCATGGTCCG	TCTCGAG				687

- (2) INFORMATION FOR SEQ ID NO:990:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 677 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GAATTCGGCC	AAAGAAGGCC	TAGAGCCCTT	CTGTCCCTTC	TACCATGTGT	GGATGCAGTG	60
AGAAGGCACC	GTATCTCTGA	AGCAGAGAGC	CCGCCCTGGA	CACTGGATCT	GCTGGCACCT	120
TGATCTTGGA	CTTCCCAGCC	TCTAGAACTG	TGAGAAATAA	TTTTTTGTTG	TTTACAAATT	180
ACCCAGGCTA	AGGTGTTTCA	TTGTAACCTG	AATGGACCAA	GCTGGTGTGA	CCCTGTTGGA	240
AAACTGGCAG	TATCTACCAA	AAGCCGAACA	TACGTATAAA	CTGATCCAGC	AGTTCCACTC	300
CTGGGTATGT	ACACCACAGA	AAGCTATGTC	CACCGAGACA	TTGGCAAGAA	TGTTTCTAAC	360
CACACGCTGA	CTGTAGCCCC	AAACCTGAAA	CAACCCAAAT	GTCCATCCAC	CAACCCAAAT	420
GTCCATCCAC	AGTTGAAGCT	ACAGTGAAGT	CACAGGGTCG	AATACTACTG	CACAGCAACG	480
AATATGAATG	AAAATATCGC	TATGCACAGC	AACATGGATA	AATTTCACAG	ACATGAGGTC	540
AAGCAAAAGA	GGTCAGAGTC	CTCATCATCA	AGAGAGAATT	CATTGTATGA	TTCTCTTCCT	600
ACAAAAAGTA	CAGAAATAAG	CAAAACTGAT	CCATGGTGTT	AGAAGCCAGG	GGAACAGTTA	660

ACAAGGGAGC ACTCGAG

(2) INFORMATION FOR SEQ ID NO:991:

677

(A) LENGTH: 445 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:	
TAGCAGGTTG CTACTGCCCC GAACCCGCGC TGCAGGGAAC AGCGGGGCAA ACAAAACCAA TAGAGCCATG GCGACTCCCT CTGCTGCCTT CGAGGCCCTT ATGAATGGTG TGACAAGCTG GGATGTACCC GAAGATGCTG TTCCATGTGA ACTGCTTCTT ATTGGAGAGG CTTCATTTCC TGTGATGGTG AATGACATGG GCCAGGTCCT CATTGCTGCC TCCTCCTATG GCCGTGGCCG CCTGGTGGTC GTGTCCCATG AGGACTACTT GGTGGAAGCC CAGCTCACGC CCTTTCTCCT GAACGCAGTG GGGTGGCTTT GCTCTTCCCC TGGGGCTCCC ATTGGTGTAC ACCCATCCCT GGCACCTTTG GCCAAAATCC TCGAG	60 120 180 240 300 360 420 445
(2) INFORMATION FOR SEQ ID NO:992:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 392 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:	
GAATTCGGCC TTCATGGCCT ACTGTGATTT AAAATCTTGC TGTGTGGCTT GGGTTGTTTG TGTTGGTTCC AAACCCTGAA TCTTTTGGGG TCTTCAATTT GTGGGCATGT CAGTGGAAAT TCTAAGCTTT GTTTAATGGT GTGTGTGTT CTGTCTGTCT CTGTGTGAG GTGTTTAGAA ATTGGCTTCT CTGGGTTCCT CGCTCGTCTT CTGGAAGGTG GGGTTATAGA CATGCTGGTG AATTCTGAAT GTTTTATAAA TTAGACTATT AACGGAGTTA AATTGAAGAA ACCTTCTGTC ATAAGACCTT CCAGGAATTC CATTCCAAAT GAGGAAATGC ATAAAGACTT GTCCACTTGG CAAACATTGG GTGTTTGGGA GGTGGACTCG AG	60 120 180 240 300 360 392
(2) INFORMATION FOR SEQ ID NO:993:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 359 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:	
GAATTCGGCC TTCATGGCCT AGGCGGCTCC CTTGGTCCTG GTGCTGGTGG TGGCTGTGAC AGTGCGGGCG GCCTTGTTCC GCTCCAGTCT GGCCGAGTTC ATTTCCGAGC GGGTGGAGGT GGTGTCCCCA CTGAGCTCTT GGAAGAGAGT GGTTGAAGGC CTTTCACTGT TGGACTTGGG AGTATCTCCG TATTCTGGAG CAGTATTTCA TGAAACTCCA TTAATAATAT ACCTCTTTCA	60 120 180 240
422	

TTTCCTAATT GACTATGCTG AATTGGTGTT TATGATAACT GATGCACTCA CTGCTATTGC

CCTGTATTTT GCAATCCAGG ACTTCAATAA AGTTGTGTTT AAAAAGCAGA AACCTCGAG

300

359

(2) INFORMATION FOR SEQ ID NO:994:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 115 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:	
GAATTCGGCC AAAGAGGCCT AGACTGTCAG CTGTGAGTGG CCAGTACAAC AAATGCTTTG GCTTTCAGTT GTCATTCTGA TGTCTTGCAA CATATCATCG TGTTTGATTC TCGAG	60 115
(2) INFORMATION FOR SEQ ID NO:995:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 633 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:	
GAATTCGGCC AAAGAGGCCT AGTGGAGACA AAAGCATGTG ATCCCAATTT GCTGGGATAT CCTCTCCTGC ATTTCAAACA CCTTCACTCA GTGTCAGCCA CAGCGGCCAC CACATAGCAG	60 120
CTGGCCCCGC ACCTTCTCTG GAACAGTCTG GAGATGCAAG GTCAGGGTGG AAGGCCTGGT	180
TCACCCTTGA AAGAAAGGAT GGCTAGGGGT AAACAAGACG AGCAACTCCC TGGAATGCAG	240
GGAGCCAAGA AGGGCAGCCG AGGATAAGGC TCTGCCTCCC CAACGGCGAG GGTTTCCTTT	300
CCTTCTGGTC ATTANAACTG CACAGCCCCC GGGGAGATGT TGAACATGGC AGGGTCGAAT	360
CGCTGGCCTC GGAAGGGAGA ACTTCAGCAT CCCACCCTTC TTCAGCATCT CATGGACTTT	420
CAGCTCATGG CTCTGTGGCT TGCCCTGCAG CTTCTGGTGG TAGTCAAAGG TAAGCCTGTC	480
CAACACCGCC TGTTCCTCCT CATCCACGGT GGCCATGGAG CGCTCCTTGT TGATCTTGTC	540
AATGTCGATG GGCTCTTCTC CCTCCAGGAT GGCGTTCCAC CAATACTCGC CCACCTTGCT CAGGTTCACC AAAACGCACT TCCCGGGCTC GAG	600 633
(2) INFORMATION FOR SEQ ID NO:996:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 462 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:	
GAATTCGGCC AAAGAGGCCT AGTTGATTCT CAGTTCATGG TGGAGTCATT CAAGTTTATT	60
TCTGGCATCT TGGCAGCCCT AGTTGATTCT CAGTTCATGG TGGAGTCATT CAAGTTTATT  TCTGGCATCT TGGCAGCCCT GAGTGCCATG ATCTCTCTAG AAATTCCGCA AGTCAACATC	120
ATGACAAAAA TGGATCTGCT GAGTAAAAAA GCAAAAAAGG AAATTGAGAA ATTTTTAGAT	180
CCAGACATGT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG	240
AAACTGACTA AAGCTATATG TGGACTGATT GATGACTACA GCATGGTTCG ATTTTTACCT	300
422	

TACGATCAGT	CAGATGAAGA	AAGCATGAAC	ATTGTATTGC	AGCATATTGA	TTTTGCCATT	360
CAATATGGAG	AAGACCTAGA	ATTTAAAGAA	CCAAAGGAAC	GTGAAGATGA	GTCTTCCTCT	420
ATGTTTGACG	AATATTTTCA	AGAATGCCAG	GATGTACTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:997:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 548 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

GAATTCGGCC	AAAGAGGCCT	AGCTGGTAAC	ACATGTGAAC	TCAGGTAAAG	TCATCGAGCA	60
TTTTACTGAC	TCTATTCCTC	AATAAAGTAC	TGGGAAAAAA	CTCATAAGAA	TGACAAAAAC	120
AACATACTCA	GGTATGCGAG	CAGAAGCCTC	TGACACAGCT	TGTCTTCGGG	GCTTAACTAA	180
ATGATCTATT	TTAATGAGGG	AATCCGTGGA	AAGGCATGCG	TTTTCAGGCT	CATTTTCTGC	240
TTCGATGCTT	TGTCCAGAGA	GTTGGAATCT	CAACGTGTGT	TTCATGTGAG	GCTCCTTAAG	300
AGGGTGACAT	TCAACATCCC	AAAACTGGGC	ATAATCCCCC	CTACCTCTGG	GCAAAAATGT	360
GATGGAGACT	TTTTGGATCC	CATGGCTTTC	CAGCAGACCA	GAAATAGGAG	AACATCTGAA	420
TGCTGCATAG	GTAGCTCTAA	AAACATCTCC	ACTTTCATCA	ACTCCCTTGA	CATAAGGTGG	480
CACCACAGAC	GTGAAATGGC	ATCTGTCATC	TTTAGCGCCA	CCTTATGTCA	AGGGAGTTGA	540
TTCTCGAG						548

- (2) INFORMATION FOR SEQ ID NO:998:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 572 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

GAATTCGGCC	AAAGAGGCCT	AGTTTCCCTT	TCTGTATTTT	ACTACTAAAT	TAGAAAGCAC	60
TGGTTATGTA	ATAAGTTACT	ACATTGCTTT	GGTTGAGTAA	AAACAAGAGT	ATATATTTTT	120
CTTGTTTCTT	ATTTNCTAAA	CCCTTAACTC	CTGCTGAGGT	CATAACAACC	TCAGTCTAAG	180
CTCTGTGTCC	ATCATACTGT	TAACTTAAAC	AAATGGGTGG	TGGGGGTGGG	AAGGGTAATA	240
CAGTCCTGCC	ATTGCCTACC	AGTAGGAGAG	TCCAAACAGA	ACACTCTTTT	GAGTAGCAAT	300
TATTTAATTT	GCCCAGTCAA	GGCACCGTGT	TTATATACTA	TTTCACATTG	AATTTGATTA	360
TGCCCTACAG	ACCTGGCTGG	TCAAGGATTT	GATATACACA	TATTGGCTTG	GGATTCGAGC	420
TTTCTTTTTT	ATTTAAATAA	AAATTTATAT	ATATATTATA	TATATACATA	TATACATAGC	480
TATATCTGTA	TATATATTGG	GTATGTTTTA	AGGATTTTTT	CGCATGAGCG	CAGCTGTTGC	540
GATAAATTGA	CCGATTGGGA	GGTATTCTCG	AG			572

- (2) INFORMATION FOR SEQ ID NO:999:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 629 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

GAATTCGGCC	AAAGAGGCCT	AGAGGGGAGC	ACGTCTTTTC	CTTGAGTGTA	ATTCACTAAT	60
GACTGTGGTT	CCAAGGAGGT	GCGACCTTTA	AAGGGAATTG	GCCCTTCTTT	GAAGGCAGGT	120
GAGAATCTAG	TCTCAGTGAC	AACCCAGCCT	GATTTGGAAG	GGGGGAGTCA	TAAGGGTTTT	180
CGCCCAGCAC	ACCAGGGTTG	CAGCCTGCGC	AAGACCTTCC	ATAGCTATTT	CTGCCGGCTT	240
GCTTCCTTCC	CTTCCCAGCC	ACGATGAGGC	AGCTGAGGGT	TGCCACGGAA	ACCGGCTCTG	300
TCCTCCCACT	GGAGGCTGCC	AGCTCTGATT	TCCTGCAGAG	TTAAGAAGGA	GGCGGCAGTG	360
GGGGTCACCC	AGGCGTGAAG	ATGGGTTTCC	CTGGGGATAT	CCTGCCTCCT	GCCAATCACA	420
GCGTCTCTCT	GGGAATCCTG	GGGGTGCCTG	GAGGCTGAGG	CCCAGGGAAG	CCCCCAAACC	480
CCAGTGCTGC	TCTGAGAAGA	GACTAGCCTC	TGGGACATTC	AGAGGTCTGG	GGTTCTTTTA	540
TCTCCCTCCA	GCTAAAGCTA	GAGGGACCTC	ATTATGTGTC	TTACAAGATG	TACCCTAAAC	600
CGTCGATTGA	ATTCTAGACC	CGCCTCGAG				629

### (2) INFORMATION FOR SEQ ID NO:1000:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 568 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

GAATTCGGCC	AAAGAGGCCT	ACCTGTATGC	TATTAACACT	CACCACAGCA	GAGAGCTGAG	60
GATTGTGGTT	GCAATTCGGA	ATAAACTGCT	TCTGATCACA	AGAAAACACA	ACAAGCCAAG	120
CGGGGTCACC	AGCACCTCAT	TGTTATCTCC	CCTGTCTGAG	TCACCTGTTG	AAGAATTCCA	180
GTACATCAGG	GAGATCTGTC	TGTCTGACTC	TCCCATGGTG	ANGACCTTAG	TGGATGGGCC	240
AGCTGAAGAG	AGTGACAATC	TCATCTGTGT	GGCTTATCGA	CACCAATTTG	ATGTGGTGAA	300
TGAGAGCACA	GGAGAAGCCT	TCAGGCTGCA	CCACGTGGAG	GCCAACAGGG	TTAATTTTGT	360
TGCAGCTATT	GATGTGTACG	AAGATGGAGA	AGCTGGTTTG	CTGTTGTGTT	ACAACTACAG	420
TTGCATCTAT	AAAAAGGTTT	GCCCCTTTAA	TGGTGGCTCT	TTTTTGGTTC	AACCTTCTGC	480
GTCAGATTTC	CAGTTCTGTT	GGAACCAGGC	TCCCTATGCA	ATTGTCTGTG	CTTTCCCGTA	540
TCTCCTGGCC	TTCACCACCG	AACTCGAG				568

## (2) INFORMATION FOR SEQ ID NO:1001:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

GAATTCGGCC	AAAGAGGCCT	AGTAATACTT	AAAGTGCAAT	TGTTCCAAGG	CTTTTGTTTC	60
CATCATCACA	AATATTATAA	AGAAAGAGCT	ATGTTTAGGG	TGAAGAAGAT	ATGGCACAAG	120
TAATATGTAA	AGAACTTATG	ACTTTCGCAT	CCTCTAGCAA	ACAGTAAGCT	GCCTGTACAG	180
CTGCACACAG	ACGGACTTTA	CACAACAAAC	TCTGGAACTT	CATCATGAGT	GAGATCCAGA	240
GAAAAGTATT	TGCTGGTTCT	TTTGACTGGA	AAAGCATCTT	GGATGTTGAT	GCACTGCTGG	300
GCCAAGCAAC	TGTTGCAATA	GAGGCCTTCC	TCATCCAGTT	CATGGCCACA	TCCAAAGGTG	360
TAACTCTGAG	CAGTGTCCTG	ACACAGACCT	GCAATGCGCA	GGAAGTCTTT	CTGGTAAAGT	420
CTGATGTCAT	CGAGGCTCAA	GCTGTGTCGA	TCAGTGGAGG	TCTTTGGTTT	CCGACATATA	480
GTCTGTGGAA	GAGAATCAGT	ACTCTGGCCA	CGAAGCTTAA	CAACTGTTTC	TGAAGAGCTC	540
GAG						543

- (2) INFORMATION FOR SEQ ID NO:1002:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 592 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GAATTCGGCC	AAAGAGGCCT	AATTCCACTT	ACGAATTAAC	ACTGTGTACA	TGGCACCTTT	60
GGGCCCATCT	TGCCTTGAAA	GTCCCTGTTG	GATGGAACAG	TGGCATTTTC	CTTCCTTTTC	120
TCAGGACTGC	AAACAGACCT	AATATTTGGC	CTTGCCCTTG	CCTGGGAAGC	TGCTGCTGAG	. 180
TCTTGTCTCA	GCCGGGCTGT	GCATTCCGAG	CGGCTGCCCT	GCCCTGCGCT	CAGCAGCTGG	240
AATCAATCTG	CCCACCTCCT	TAAGAAGCCA	CTTCATCAGC	GGTCACCCGG	CAGCTGCTCG	300
CCTCCCAGGG	CTGCCGGGCT	AGGGCTTTAT	CGCATTTTTG	AAATTTCAGA	TTTCTGTGTC	360
TGGGCTATGC	CCCTCGAACA	GTAACAGCAC	CGCTTTGCAG	CAGGGAGGAG	ATTTCACCAG	420
GATATGGAGG	GGACAGGAGA	AAAGCCCTCC	TTCCCAGAGT	CCACTGTCAT	TCAGGATTTG	480
CTCTCAAAGA	GGCAAGAAAT	CTCTAAGAAT	GAAAGGAGGT	GTTTTGTTGT	TGTTGTTGTT	540
TTTTGTATGT	ACTGGGAGGA	AATGGCTAAT	CTTGGGTATG	CACACGCTCG	AG	592

- (2) INFORMATION FOR SEQ ID NO:1003:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 584 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

GAATTCGGCC	AAAGAGGCCT	AGGCTCCGTC	TGTTGGGGGG	CGAACACGCC	GCGGTCCTCG	60
TCGTGTGAAG	TAAGAACTCT	GCTAGAGAGG	AAATGGCTGC	TTCATCATCA	TCCTCCTCAG	120
CTGGTGGGGT	CAGTGGAAGT	TCTGTCACTG	GATCTGGTTT	CAGTGTCTCA	GACCTTGCCC	180
CACCACGGAA	AGCCCTTTTC	ACCTACCCCA	AAGGAGCTGG	AGAGATGTTA	GAAGATGGCT	240
CTGAGAGATC	NTCTGCGAAT	CTGTTTTTAG	CTATCAAGTG	GCATCCACGC	TTAAACAGGT	300
GAAACATGAT	CAGCAAGTTG	CTCGGATGGA	AAAACTAGCT	GGTTTGGTAG	AAGAGCTGGA	360
GGCTGACGAG	TGGCGGTTTA	AGCCCATCGA	GCAGCTGCTG	GGATTCACCC	CCTCTTCAGG	420
TTGATACTGC	CTGGATGGTC	ACCTCTGGTG	CGCAGCAAGT	GCAAAGCCAG	TGGGGGACTT	480
TCTCACAGCT	TACATAGCCA	TCCAGAGATC	CACAGCTACG	TCACTGAATT	GTTAATGCAC	540
ATTTGTACTT	GGTTTCTCTG	TATCTATTCA	CAGGCGAACT	CGAG		584

- (2) INFORMATION FOR SEQ ID NO:1004:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 440 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

426

60

ACTCCAAATG	ATGACATGGT	CTTATTTTAT	CTATTAACCA	TAAGCTTACA	GATTCTAGTG	120
AAGAAAAAAC	TTTAGGAGGC	TACATGGTCT	ATTGGAGAGT	GTAGGCTCTG	CAGTCAGAAG	180
ATCCCTACCC	AGGCTTCTGT	CTTTCTCAGT	AAGACTTGGG	ACCACAGCAA	GGTCCGCAAT	240
CTCCTGAGGC	TCTGTTTTCT	ATGGTTGGGA	TAACATGGTA	AGTTATTTTC	TTCTAAGTAG	300
TCACACATGG	AAATCTTATC	TAAAATTTTA	TACCATTAAC	TTTTATTTCA	CTTATTAACT	360
CATACCATTA	ATACTTTACT	TTAGCTATGT	TTGGTATGCA	TGAGTTGATG	AGTGATTAGA	420
GTACTATGAG	CGATCTCGAG					440

- (2) INFORMATION FOR SEQ ID NO:1005:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 426 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

GAATTCGGCC	TTCATGGCCT	ACTCAGTTGC	AGATTCTGGC	CAACATGGAC	AGCCAGCTAA	60
AAGAGCTACA	GAGTCAGCAT	ACCCATTGTG	CCCAGGACCT	GGCTATGAAG	GATGAGTTAC	120
TCTGCCAGCT	TACCCAGAGC	AATGAGGAGC	AGGCTGCTCA	ATGGCAAAAG	GAAGAGATGG	180
CACTAAAACA	CATGCAGGCA	GAACTGCAGC	AGCAACAAGC	TGTCCTGGCC	AAAGAGGTGC	240
GGGACCTGAA	AGAGACCTTG	GAGTTTGCAG	ACCAGGAGAA	TCAGGTTGCT	CACCTGGAGC	300
TGGGTCAGGT	TGAGTGTCAA	TTGAAAACCA	CACTGGAAGT	GCTCCGGGAG	CGCAGCTTGC	360
AGTGTGAGAA	CCTCAAGGAC	ACTGTAGAGA	ACCTAACGGC	TAAACTGGCC	AGCACCATAG	420
CTCGAG						426

- (2) INFORMATION FOR SEQ ID NO:1006:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 402 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

GAATTCGGCC	TTCATGGCCT	AGAGTAGCCA	GGGAGCTGGA	AGTTCCACAG	ATTGGTTTTA	60
ATAAACAAAC	TCCCTCAATG	ATGAGTGGTC	TTTTGAAGAG	CATGGTTAGA	ACTTGGGATT	120
GTGCTTCTCA	TGACTACAAA	TGTACTTGTA	GCTTAGGTGC	AAAAGGGTAG	GTCAGTGGGT	180
AGCTAACTAC	TGAGGATTGA	TTTTCCTGAC	GCTGGTGTTT	AAGTGTCACC	CAGAACTGGC	240
ATATAAAGTG	GCTCATTCAC	CCAAGTATCT	TCCTTTCCTT	TTTACAAAAT	CCTTGGCTGT	300
TGTGGGGCCT	ACATCTCTTC	ATGATTATTA	TTGCATCTGG	TGTCATGTTT	TTCCAGCTGG	360
TGTACTGCTT	CCCTGTAGGC	TTCTTGATGT	TCACTCCTCG	AG		402

- (2) INFORMATION FOR SEQ ID NO:1007:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 456 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

```
GAATTCGGCC TTCATGGCCT ACTGGTGCCA CGGGAGGCAG ACACCAAGTT CTGGGGTCTC
CAGCTGCAGT GGGTGCCGC CAATTGCTTC TCTCTGTCCA GACTAATGAG AACATGGAGA 120
TCACCAGTGC ACTGCAGTTG GAATAGCACG TAAAGAGGGA GCTGGGAAAG AAGCTGGGCA 180
AGCTAAAGGA CATGGTAACC CTGCCCCATC CAAGAAGAGGC TGGAAGGCGG GCACCAGCCT 240
CTGGGGAGGG GAGGTGGAA GCCAGAGGCA GCTCCAGCCT GGGGGACAGG TGACCCCAGC 300
ACCCTCCAGG GCAGTCCTG GACTGTTTCT TGCTTCCCGC CCTCTGACAT TTAGTGGTGG 360
GTTCGTTCTT CCTAGGTCTG GACATCATCA TCCCAGCTG AGTCATGGAG CCTCCCAAAC 420
ATAGGGAAAG AGATGGTGGT ATAAGAGGCT CTCCAG
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- (2) INFORMATION FOR SEQ ID NO:1008:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 564 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GAATTCGGCC AAAGAGGCC	T AGGATGGCTG	TGTTTGACGG	GTGTTGCTCG	TGACAGTTGG	60
GGTCCTCCTC AGCATCAGT	C TTGACATGGC	TGCAACTGGG	GGGGTCCTCG	GGATCCTCCC	120
GGAATCTCTT CCTCAGCAT	T CGCTCATGAT	AAGGTTTCAG	GTGTCTTGAT	GGTTCAGTCC	180
TGGAGAAACA TAAGCATAA	C CTCTACCCCA	AGTTATTATT	TTACCTATTT	CCCAACTTTC	240
TGTTATCAGG TCTCTCCAG	C AAACCAGTTG	TTCTGCTTCT	GTCTTTGCAG	CTGGTTTCTG	300
TAGATGCTGT TCAGCTGCT	G ATAAGATCCG	GCCTTTAGGC	AGGCTCAAAA	AATTTAAAGT	360
TAATAATGCG ATTCAATTC	C TTATGGGGTG	TCCTGTAGTA	CCTGTTTTCC	CCCTTTTGCT	420
TCTGCAACTG CTGTTTCAC	G GAGAGATTCA	TTCTTTCCAC	TATGGCNTGT	CCTTCAGAAT	480
TATATGGGAT ATCAGTAAT	G TGTTTAATAT	TCCGTATAGA	GAAAAATTTA	GCTAGAGCTT	540
GAGAATTAGG TTCCAATC	T CGAG				564

- (2) INFORMATION FOR SEQ ID NO:1009:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 661 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

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GAATTCGGCC AAAGAGGCCT AGAAAAAGAT GTCATTCCGT AAAGTAAACA TCATCATCTT
                                                                       60
GGTCCTGGCT GTTGCTCTCT TCTTACTGGT TTTGCACCAT AACTTCCTCA GCTTGAGCAG
                                                                      120
TTTGTTAAGG AATGAGGTTA CAGATTCAGG AATTGTAGGG CCTCAACCTA TAGACTTTGT
                                                                      180
CCCAAATGCT CTCCGACATG CAGTAGATGG GAGACAAGAG GAGATTCCTG TGGTCATCGC
                                                                      240
TGCATCTGAA GACAGGCTTG GGGGGGCCAT TGCAGCTATA AACAGCATTC AGCACAACAC
                                                                      300
TCGCTCCAAT GTGATTTTCT ACATTGTTAC TCTCAACAAT ACAGCAGACC ATCTCCGGTC
                                                                      360
CTGGCTCAAC AGTGATTCCC TGAAAAGCAT CAGATACAAA ATTGTCAATT TTGACCCTAA
                                                                      420
ACTITIGGAA GGAAAAGTAA AGGAGGATCC TGACCAGGGG GAATCCATGA AACCITIAAC
                                                                      480
CTTTGCAAGG TTCTACTTGC CAATTCTGGT TCCCAGCGCA AAGAAGGCCA TATACATGGA
                                                                      540
TGATGATGTA ATTGTGCAAG GTGATATTCT TGCCCTTTAC AATACAGCAC TGAAGCCAGG
                                                                      600
ACATGCAGCT GCATTTTCAG AAGATTGTGA TTCAGCCTCT ACTAAAGTTG TCGATCTCGA
                                                                      660
                                                                      661
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(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 316 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:	
CAAAGGCACG TGCAGAGGGA AGTAGGGGTA GAGAGAGGCA AGTTAGCTTC AGAGAGAGTTT  ATTTGCACCC AGTTCTGTTC TACTCAGCCT GACGTTTTAT CATCTTTTTG AAAAGTGGCG  TGAAGTGGTG TGGAACACAT CAGAGGGTGA AGCCGAGCAA ATCTGAAAGA GAGCAGAGGA  TTTCATATGA TATCCTATGT GTGCTTTCCC CTTCCTTCTT AGGAGCTGGA AGAGGCAGAA  3	60 120 180 240 300 316
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 244 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:	
AGTGTAGCCA ACAGTGAGGC AGGCAAAGGT GAGTAAGGTA GATTAGTTCA GGGAAGAAAA 1 CATAACATTA TTTAATCCAT TGTGGGCCAC ATTGCACTAT GATAACACTA TCATGTCATA 1 GAGTCTCACC ATTGTTTAAG ATGTTTAAAT TTTTTAATAC GAATATATTC TCACACCCCT 2	60 L20 L80 240
(2) INFORMATION FOR SEQ ID NO:1012:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 355 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:	
TGGATAAAGA TCTGGGATCT GTGCAGGGAT TTGAAGATAC AAATAAATCC GAGAGAACTG AGAGTCTGGA AGGAGATGAC GAGTCCAAGT TAGATGATGC ACATTCATTA GGCTCTGGTG CTGGAGAAGG ATACGAGCCA ATCAGTGATG ACGAACTAGA TGAAATTCTG GCAGGTGATG CAGAAAAAGAG GGAGGACCAA CAGGATGAGG AGAAGATGCC AGATCCCTTA GATGTGATAG ATGTGGATTG GTCTGGTCTT ATGCCAAAGC ATCCAAAAGA ACAACGAGGC TCGAG  3	60 120 180 240 300 355
(2) INFORMATION FOR SEQ ID NO:1013:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 351 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

GAATTCGGCC	TŢCATGGCCT	ACAGCCTAAA	TGTTTTATTT	CCTGAGAGGC	TGGAATCTGT	60
ATTTGTGGTA	TCAATCAGTC	AACTGAAATT	TATTAAATGC	CTGCTGTGAG	CAAGGCCTAA	120
TGCTGAGGGA	TGTAAAGAAG	AGTGAGAAGC	TAGTCTGGTT	GGGGTNATAT	GACATGGCAA	180
GTCATAGAAT	GAAGAAGCGT	ATTCCTTGTC	ATATGAAAGC	TGCAGATTAG	TGTGGTTCTA	240
AGTAGAGGCC	AGGGTCACTG	GAGTCTAGGA	TTGCAGGGTT	GGCTGGCTTC	CCAGAGGCTA	300
AGAATTTAAT	TTGGATCTTG	AAGATCTGGT	CCAATTCCAA	CANGACTCGA	G	351

- (2) INFORMATION FOR SEQ ID NO:1014:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

GAATTCGGCC	TTCATGGCCT	AGGCCTTGTA	TTTTTTTTTA	TTTTCTGCTA	AATTAGAAAG	60
AAATTTGCTG	TTTCAAATAT	ACTCAAGCTG	TTCAGTTCTT	CAACAAAAAG	TAGGTGACTG	120
AAAACTGTAT	GTTTAACTAT	GCTTAAGTTA	ATATTTATAG	TAATGATAGA	AGCCATTTTA	180
TTGGCAATAT	ATCACTTCCT	GATTTCCACA	CCAGGCATTC	CCACATGCAC	AAACAGGTGT	240
GTGGGAGGAA	GGGAAATGGG	CAAAAATGAT	TTCCTTCAAG	AGGCTACTGA	GAATGAAAAC	300
TCAAAATCTG	CACAAATAGG	GGTGGTGGAA	GGAGAGAAAG	AAAACTCCAT	GCCAGAAATA	360
ACATGCTTAG	CAGAGAGAGA	GAGAGATCTC	GAG			393

- (2) INFORMATION FOR SEQ ID NO:1015:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

GAATTCGGCC	TTCATGGCCT	AACTCAGTTG	GCTTCTAATT	TGCGTAACAA	GATTAAGGTA	60
GTATTTTTGT	ACTATTATTG	GAAGCATGCC	TTCCCTTTTT	CACATTATTA	AATTGTATTT	120
ATATTTGTGC	AATTTTAAAC	TATGTTTTCA	AATAAACTTT	GTCTGCGGCT	TCGAGGTCTT	180
TTCAGGAATC	TTTCAAAATG	GGATTTGGGG	ATCAGAACTC	CTTCTGATCA	AATGGAATCC	240
AATTTGTACT	ACTGGTCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:1016:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

CAGAATGGGA CTCCAAGCCT	GNCTCCTAGG	GCTCTTTGCC	CTCATCCTCT	CTGGCAAATG	60
CAGTTACAGC CCGGAGCCCG					120
CCGTGCGGAC CCTGAGGAAG					180
AAGACTCTCG GAGCTGGTGC					240
CCTGACCCTA GAGAATGTGG	CTGATCTGGT	GAGGCCATCC	CCACTGACCC	TCCACACGCT	300
CGAG					304

- (2) INFORMATION FOR SEQ ID NO:1017:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 355 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

GAATTCGGCC	AAAGAGGCCT	AGTTTAAAGA	AAAAAAAAA	GACCCATCAA	GGGCATAGAA	60
AAGCTTAGGT	GAAGAAACCC	TAAAATGAAT	CCTCATTTAT	CAACTCATTC	ATTTATTGAT	120
TCATTTGTTC	ATTCATTTGT	TCACTCAAGA	AGTATTTGTT	GCCAGACACA	GTACCAACAA	180
AGAAAATAAG	CATCCACTAC	GGCTTTGCAG	AGCTTGGTAC	GCAATGCCTG	GTTCAGAGGA	240
GATATTTGTT	CATCGCTTGC	TTTTAACTGT	ATCACAGCCT	AGGGTGGCAT	GCAGAGGTTT	300
GAATAAGTGC	TGAAACAGGA	CAAGTGAGGT	GCTTATGGAA	ACACACAGGC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:1018:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 502 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

GAATTCGGCC	AAAGAGGCCT	AGAAGGAAAT	TGTCCCGAAT	CCCTGCAGTC	TTTCTGTAGG	60
TTGCGGCACA	ACGCCAGGCA	AAAGAAGAGG	AAGGAATTTA	ATCCTAATCG	GTGGAGGTCG	120
ATTTGAGGGT	CTGCTGTAGC	AGGTGGCTCC	GCTTGAAGCG	AGGGAGGAAG	TTTCCTCCGA	180
TCAGTAGAGA	TTGGAAAGAT	TGTTGGGAGT	GGCACACCAC	TAGGGAAAAG	AAGAAGGGC	240
GAACTGCTTG	TCTTGAGGAG	GTCAACCCCC	AGAATCAGCT	CTTGTGGCCT	TGAAGTGGCT	300
GAAGACGATC	ACCCTCCACA	GGCTTGAGCC	CAGTCCCACA	GCCTTCCTCC	CCCAGCCTGA	360
GTGACTACTC	TATTCCTTGG	TCCCTGCTAT	TGTCGGGGAC	GATTGCATGG	GCTACGCCAG	420
GAAAGTAGGC	TGGGTGACCG	CAGGCCTGGT	GATTGGGGCT	GGCGCCTGCT	ATTGCATTTA	480
TAGACTGACT	AGGGGGCTCG	AG				502

- (2) INFORMATION FOR SEQ ID NO:1019:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 465 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

GAATTCGGCC	AAAGAGGCCT	AATCAAATAG	TAAAGGCTGT	TCTGGCTTTT	TATCTTCTTA	60
GCTCATCTTA	AATAAGTAGT	ACACTTGGAT	GCAGTGCGTC	TGAAGTGCTA	ATCAGTTGTA	120
ACAATAGCAC	AAATCGAACT	TAGGATTTGT	TTCTTCTCTT	CTGTGTTTCG	ATTTTTGATC	180
AATTCTTTAA	TTTTGGAAGC	CTATAATACA	GTTTTCTATT	CTTGGAGATA	TAAATTAAAT	240
GGATCACTGA	TATTTTAGTC	ATTCTGCTTC	TCATCTAAAT	ATTTCCATAT	TCTGTATTAG	300
GAGAAAATTA	CCCTCCCAGC	ACCAGCCCCC	CTCTCAAACC	CCCAACCCAA	AACCAAGCAT	360
TTTGGAATGA	GTCTCCTTTA	GTTTCAGAGT	GTGGATTGTA	TAACCCATAT	ACTCTTCGAT	420
GTACTTGTTT	GGTTTGGTAT	TAATTTGACT	GTGCACGATC	TCGAG		465

- (2) INFORMATION FOR SEQ ID NO:1020:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 243 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

GAATTCGGCC	TTCATGGCCT	AGGATTTCGT	ATGCAAGCTC	TTGTTTCTCA	GGCTGCCTGC	60
AGAAGAAGTC	GCTATAAATT	ATCTGTTGTC	TACATGGTAC	AAGGCCCATT	GACTCATCTG	120
ATGCTTGTTT	TGTTAATTTC	TTTAATATTT	TTATCACGGG	GCAGTGGGAG	GGCTTGGGCT	180
TTTAGCCACA	GCTGTTTTAA	GACTTCTGAT	CTCCTGCCCT	GCAGGAATAG	GTGGCAACTC	240
GAG						243

- (2) INFORMATION FOR SEQ ID NO:1021:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 442 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

CTCCACCGAG A	GCCTGGACA	GTATGAAGGC	TCTGACAGCC	GCCATCGAAG	CTGCAAACGC	60
CCAGATCCAT G	GCCCTGCCA	GTCAACACAT	GGGCAATAAC	ACTGCCACCG	TCACCACCAC	120
GACTACCATA G	CCACCGTCA	CCACGGAGGA	CAGGAAGAAG	GACCACTTTA	AGAAAAATCG	180
ATGCCTGTCT A	TCGGGATAC	AGGTGGATGA	TGCTGAAGAA	CCTGACAAAA	CAGGGGAGAA	240
TAAAGCACCC A	GTAAGTTCC	AGTCCGTGGG	AGTGCAAGTA	GAAGAAGAGA	AGTGCTTCCG	300
CAGGTTCACT C	GATCCAACA	GTGTGACGAC	AGCAGTACAG	GCCGACCTGG	ACTTCCATGA	360
TAATCTGGAA A	ATTCTCTGG	AATCTATAGA	GGACAATTCG	TGTCCTGGCC	CCATGGCCAG	420
ACAGTTCTCC C	GCGATCTCG	AG				442

- (2) INFORMATION FOR SEQ ID NO:1022:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 274 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

60	GGTGTATGTA	ATGGAAATGA	GTTTTTCTGG	AGATGATCAG	TTCATGGCCT	GAATTCGGCC
120	TGTGATTGCA	GATTAATTCT	TTTGTCATGG	CTTTAAAACA	ACCCAGTTCA	TGGATCTATG
180	TGTTTATTAC	TGAGAGTAGG	CCAGCAGAAA	CCCCCTTTGG	CCACCCTCTT	GTAATAGCGG
240	TGCTCGATGC	TCCTTGCTGT	AGTATTCTTC	TTTTGTAGCC	GTGCAGGCTG	CTCAGTGTGG
274			CGAG	GCTCATAACT	TCATCATTTG	ATTCTATTTC
			AGTATTCTTC	TTTTGTAGCC	GTGCAGGCTG	CTCAGTGTGG

- (2) INFORMATION FOR SEQ ID NO:1023:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 196 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

GAATTCGGCC	TTCATGGCCT	ACTITICCAG	AAACCAAGAG	TGGCTCTACT	GTGGCTATAT	60
TATTATTGTT	ATTATTATTA	TTTTGGAGAT	GGGGTCTCAC	TTTGTCATCC	AGGCTGGAGA	120
GCAGTGGCAC	CATCATAGCT	CACTACAGCC	CCAAACTGCT	GTGCTCAAGG	GATCCTCCTG	180
TCTCAGCCTT	CTCGAG				•	196

- (2) INFORMATION FOR SEQ ID NO:1024:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

GAATTCGGCC	TTCATGGCCT	AATCATTTAT	ATAAAGTTTA	AAAACATTTC	AGAACTGAAC	60
TATATATTTT	TAGAAATATC	TGCATATGCC	ACATAAATTT	TTAAAATCAT	AAGAATGCTA	120
AACAGCACAT	TCAGGACAGG	GTGAAGAAAC	AGGCATGCAG	GTTGTGCAGT	AGGAAGCTGG	180
GTAACATTGT	TCCTTATGGC	TTTGTTGTCG	CTTCCAGAAT	TTCATTAAAA	ACTTTTTAAA	240
AAACATGGGC	CCACATTATG	AATTACGTCT	GCTTTTAGAG	TACTAAAAAC	TCCAAGCAAA	300
AACACATGAG	CCACCGGGCA	CGCCTGGCCT	TTATTTTATT	TTTCTACGTT	ATTATTCCTG	360
TTTTCAGAGG	AGGGAATTGT	CAGGGAACTC	TCGAG			395

- (2) INFORMATION FOR SEQ ID NO:1025:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 429 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

GGAGAGCTCT	GGGCCAGCCC	TTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	60
CTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	CTCTGTGTGT	GTATATATAT	ATATATANAC	120
TTTTCCCTTC	TGGATGCAAT	AGAGCTATTT	TTTTCTCTTT	GGAATTGAGT	GACACCACCA	180
AGATACGTTT	TTGGGTTGAA	TATGTGTGTT	TTTCAAAATT	CAGTCTGGCC	TTTTTTGTTG	240
TTGTTGTTGT	TGTTTTCTTT	AGATGGAGTT	TCACTCTTGT	TGCCCAGTCT	GGAGTGCAAT	300
GGCACTATCT	CTACTCACTG	CTACCTCCGC	CTCCCAGGTT	CAAGCAATTC	TCCTGCCTCA	360
GCCTCCCAAG	TAGCTGGGAT	TATAGGCATG	TGCCACCATG	CCCAGGCAGT	TTTTGTATTT	420
AGTCTCGAG						429

- (2) INFORMATION FOR SEQ ID NO:1026:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

GAATTCGGCC	TTCATGGCCT	AGAGAACTGG	AGCCAGCTGT	CAACTGCCCC	CGCCCCACCC	60
AGGCCATTTG	GCTTCTGCTA	CCGGCATGCT	GCTCAGGGCT	CTGCCCAAGG	ACAACGACGA	120
GCCCCCTGTG	TCCTCTCCTG	GGTCATCTTC	CATGACCCTG	AGGCAGCGAA	GACAAGCTCG	180
GCAGCTCCCT	GAGCTGCTTC	ACACCAACTA	CCTATGAGTC	TGAGGCCAGC	ATCCAGGCGC	240
TGCCCAGACC	CTGAGAGTCC	CTGGACCATG	ACGTAGCCTG	TGTGTGAAGG	GAGCAAGACA	300
GCCTTGACAG	AAGCACAGAG	AACGCCACTG	GGATTCTTAA	AGACGCGAAG	GGAAAAAGCA	360
CAGAAGATGC	TGGCGCTGCA	TCTCCTCCAG	CACCGAGAGG	CCTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:1027:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 402 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

GAATTCGGCC	TTCATGGCCT	AAATTAATAT	CCTTATTTTT	GCAGATTAGG	AAACTAAGAC	60
GTACTGAGGC	TGGGTGCCTG	GTTCAAGATC	ATATAGCTAA	CATTATTGGA	CATGCAAATC	120
AAGCCCAGAT	TTGTGACTCT	GAGCTGATGT	TAATTCTGTC	ACAATATTGG	TTCTCAAGAT	180
AAATCTTTCC	AGGTGAGGGG	GAAAGGGAAT	AAATATCTAG	AAGTCCCC'I'T	AAACAGAAGT	240
AATTAATTCG	TTTGCAGAAA	TTGGCAAAAT	TTGGGGTTCC	CTTCTTAAAA	GTTTCCTTCT	300
GTCACTTGGA	AAAAATTTAA	AATATGTGCA	TTAGGTTGAC	AAAGATCAAA	AAAGTTAAAA	360
AAAAACCCTT	TTTGGAATGC	TGTGGAGAAA	GTAGCACTCG	AG		402

- (2) INFORMATION FOR SEQ ID NO:1028:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

GAATTCGGCC	TTCATGGCCT AAGGGGCTGA AAT	TAAGAAT GTGGCTTTTT	TATCCTTTCA	60
	ATTTGGCTGG ATGTGGTGGC TCA			20
	CAGATCACCT GAGGTAAGGA GTT			80
	AAAAATACAA AAAATTAGCC AGG			40
	GGCTGAGGCA GGAGACTCAC TTG.	AACCCGG AGTGTCTCGA		00
GAATTCAATT	AGGCCATGAA		: د	20
(2) INFORMA	ATION FOR SEQ ID NO:1029:		•	
(i)	SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 252 base pa	irs		
	(B) TYPE: nucleic acid			
	(C) STRANDEDNESS: doubl	.e		
	(D) TOPOLOGY: linear	•		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEC	Q ID NO:1029:		
CCACATTTC	GCTCTCATCC CATATCTATT GAG	AATGCTG TAGTTGAGGG	TTGTTAGAAA	60
	ATTAAAATCC CTCCAGGTGA TTC			20
	TTCATAAAGA AAACCTCTGG AGG			80
	TTGAGATCTA GGTTATCTGC CAA			40
AGACAACTCG				52
(2) INFORM	ATION FOR SEQ ID NO:1030:			
(i)	SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 280 base pa	irs		
	(B) TYPE: nucleic acid			
	(C) STRANDEDNESS: doubl	.e		
	(D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEC	Q ID NO:1030:		
GAATTCGGCC	TTCATGGCCT ACCTTATGGC CTA	ATTAAAT ATTAGTAATA	GGTATTCGAT	60
	ATGATTTCTT GTAATAGACT ATT			20
	GTCATGTTAA TGATAAATTT TCT			80
	GGTGGCCTTG GGGGACTTGC AGG			40
	GAACTACAGA GTCAGATGCA GCA			80
		•		
(2) INFORM	ATION FOR SEQ ID NO:1031:			
(i)	SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 291 base page	airs		
	(B) TYPE: nucleic acid			
	(C) STRANDEDNESS: doub	le		
	(D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO:1031:	-	
	·			
	TTCATGGCCT AGAGCAAGTG GTT			60
GACCATTATT	TTTTAATGAC AGAACCTCCA CTC	CAATACAC CAGAAAACAG		L20
GCAGAAATTA	TGTTTGAATC ATTTAACGTA CCA	AGGACTCT ACATTGCAGT	TCAGGCAGTG 1	180

CTGGCCTTGG CGGCATCTTG GACATCTCGA CAAGTGGGTG AACGTACGTT AACGGGGATA

240

GTCATTGACA GCGGAGATGG AGTCACCCAT GTTATCCCAG TGGCTCTCGA G	291
(2) INFORMATION FOR SEQ ID NO:1032:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 277 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	-
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:	
TAAAATAATT TAACTTTTT ATTACATTAA AAAACAGGAC TCTGGGAATT GTCACTTTAT GATCAGCCTT ATATTTTTC CAGACTGTGT CATTGTGTAT GCCTGTGCCA CCCAACGGAT GAGACCACTG ATCATGTTTA GCTCAAATTT ATGTTGGATA GAGGTTATAG GATGGTCCTT ATCTGAATGC AGAAAGGAAT GTTTATTTTG CTGTTATGTT TTATATGGGA TAATACTTTA TAATTGTGTG ACTATCCTAT TCCCCCAACAA ACTCGAG  (2) INFORMATION FOR SEQ ID NO:1033:	60 120 180 240 277
(2) 2.1.1 5.1.1 2.2.1 2.2.1 1.0 1.2.1 2.2.1 1.0 1.2.1 2.2.1 1.0 1.2.1 2.	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 298 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:	
GAATTCGGCC TTCATGGCCT AGGTTACATG TATAAAATAA TCGTAGCTGT TAATCAAACT GATCATTTGC TATTTGTTGT TTCACATGTT TTCATTTATT TGTTCATTCA GCAAACACTT AGTTGTGTGC CAGGAATTAA AATCCAGTGT TGTTCTTTTC TTATTTTTTT TTTGGCTAGT GGAAAATGAA AACCACTGTG ACTTTGTAAA GCTGCGGGAA ATGCTCATTT GTACAAATAT GGAGGACCTG CGAGAGCAGA CCCATACCAG GCACTATGAG CTTTACAGGC ATCTCGAG	60 120 180 240 298
(2) INFORMATION FOR SEQ ID NO:1034:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 339 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:	
GAATTCTGGA AGACACTGAC TGACTGGAAG ACCTGGATTT CTTTCTGGAA GACACTGATT GACTGGAAGAA CCTGGATTC TTTCTGGAAG ACACTGATTG ACTGGAAGAA CTAGATTTTT CTGGAAGAAC TAGATTTACT GGAAGACTTG GATTTGGTGG AAGACGTAGA TTTTTCTGGA AGACACTGAC TGACTGGAAG ACCTGGATTT CTTTCTGGAA GACACTGATT GACTGGAAGA CCTGGATTTC TTTCTGGAAG ACACTGATTG ACTGGAAGAT CTAGATTTTT CTGGAAGAAC TAGATTTACT GGAAGACTTG GTAGGCCATG AAGGTCGAG  (2) INFORMATION FOR SEQ ID NO:1035:	60 120 180 240 300 339
/21 INFORMATION FOR SEQ ID NO: 1015:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:	
GAATTCGGCC AAAGAGGCCT AGCACTGTAA AGATGAAGCT GGCTAACTGG TACTGGCTGA GCTCAGCTGT TCTTGCCACT TACGGTTTTT TGGTTGTGGC AAACAATGAA ACAGAGGAAA TTAAAGATGA AAGAGCAAAG GATGTCTGCC CAGTGAGACT AGAAAGCAGA GGGAAATGCG AAGAGGCAGG GGAGTGCCCC TACCAGGTAA GCCTGCCCCC CTTGACTATT CAGCTCCCGA AGCAATTCAG CAGAGATCTC GAG	60 120 180 240 263
(2) INFORMATION FOR SEQ ID NO:1036:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:	
GAATTCGGCC AAAGAGGCCT AAAGCACCCG CTTCCTCACC ACCCCCACTG TTGGGCCTAT AGTAGCAGGT TAGTGAGTAC CTAGGGCGGC TCAACTCCTC CCACAGCACC AACCCAGCAT GGTCCCACTG AAGTCCTACT ACGCCCTCCC CTCCCCAGCC TTTTCCAGAA ACCATACTGG GCTCAGATCA GAGCTCCGAA GCGGTCAAAG TGAGCTGAGC	60 120 180 240 262
(2) INFORMATION FOR SEQ ID NO:1037:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 285 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:	
GAATTCGGCC AAAGAGGCCT ACGGAGCTGT CAGCCAGGGG AGTGGGGTCA GCCGTCAGCC AGCCCTCCCG TTTCCCGCCC GTGGGCCCTG ACCACACTCC CTTTTCTAGA AGTCAATCCT AAGGTTTCTC TGCTCTGGCT AAGAGGATGT AAATTTGGAT TCTTAGAGGG CATGCACCC CCAGTCCCTG CCCAGATAAA GTAGCACAGT GGCATGCAGC ACCTCTGTCT GTTGCTGACG TTGGGGGGCCT TACACACCCA CCTCATCTCC GTGCACAGAC TCGAG	60 120 180 240 285
(2) INFORMATION FOR SEQ ID NO:1038:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
100	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GAATTCGGCC TT	CATGGCCT .	AGCTCTGCAA	GGAAGAGAGC	TTCACGTCTC	TGGTCAGCCA	60
AGCGAGGCTG TO	CTCTCCAGC '	TCTCAGAGAG	CTCTCGGGGC	TCTCCTGCAG	GAGACCAGGC	120
CAATGCTCCT GT	GCTTCCTG (	GGGCCAGTAG	CAGCACCCTG	AGCTCCCTGC	CACCAGGCAG	180
CTGAAAGGCA TA	AGCGTGAGG '	TGCTTCTCTC	AGTCCCAATT	ATGACAGTGG	CCACCGGAGA	240
CCCAGCAGAC GA	AGGCTGCTG	CCCTCCCTGG	GCACCCACAG	GACGCCTCGA	G	291

- (2) INFORMATION FOR SEQ ID NO:1039:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

GTGGATCCCG GAGTTTCCCC CAAATCCATC TACATCAAAT TTGTAGAAGT AGAGAGGGAT  TTTCTTTCCG CAGGCTCTTT AGTTGAGTGC CTGGAAAAAG CCATTGGATA CCCCTTAAAA  TTTAACAACT GAATGTCATC CTTCATAAGG ATTTGGGCTC TTAGCTCCTT CTTCTCTACT  CACTTCCCAT TACCCGGACC ACCCCTCATC CAGATGCCGC CGTCAGACTC TTCATGGAAA  36	GAATTCGGCC	TTCATGGCCT	AACTCTACAG	CAGTGCTTAT	TTTTACATTT	CCAAGCGAAT	60
TTTCTTTCCG CAGGCTCTTT AGTTGAGTGC CTGGAAAAAG CCATTGGATA CCCCTTAAAA  TTTAACAACT GAATGTCATC CTTCATAAGG ATTTGGGCTC TTAGCTCCTT CTTCTCTACT  CACTTCCCAT TACCCGGACC ACCCCTCATC CAGATGCCGC CGTCAGACTC TTCATGGAAA  36	ACCAAAACCT	TCAGCAAAGA	TTGGGTTGGT	ATTAACGGGT	TTTTGTCTCA	GAACTGTATT	120
TTTAACAACT GAATGTCATC CTTCATAAGG ATTTGGGCTC TTAGCTCCTT CTTCTCTACT CACTTCCCAT TACCCGGACC ACCCCTCATC CAGATGCCGC CGTCAGACTC TTCATGGAAA 36	GTGGATCCCG	GAGTTTCCCC	CAAATCCATC	TACATCAAAT	TTGTAGAAGT	AGAGAGGGAT	180
CACTTCCCAT TACCCGGACC ACCCCTCATC CAGATGCCGC CGTCAGACTC TTCATGGAAA 36	TTTCTTTCCG	CAGGCTCTTT	AGTTGAGTGC	CTGGAAAAAG	CCATTGGATA	CCCCTTAAAA	240
Cheffeet Meedonie Meedelane alonidede edialondi 11andani	TTTAACAACT	GAATGTCATC	CTTCATAAGG	ATTTGGGCTC	TTAGCTCCTT	CTTCTCTACT	300
CCCTTCTC AATTGGGCCA GTACGATCTC GAG 39	CACTTCCCAT	TACCCGGACC	ACCCCTCATC	CAGATGCCGC	CGTCAGACTC	TTCATGGAAA	360
	CCCTTTCTTC	AATTGGGCCA	GTACGATCTC	GAG			393

- (2) INFORMATION FOR SEQ ID NO:1040:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 603 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

GAATTCGGCC AAAGAGGCCT AG	CCCTACTGT GACACACCTA	CCATGCGGAC	ACTCTTCAAC	60
CTCCTCTGGC TTGCCCTGGC CT	TGCAGCCCT GTTCACACTA	CCCTGTCAAA	GTCAGATGCC	120
AAAAAAGCCG CCTCAAAGAC GC	CTGCTGGAG AAGAGTCAGT	TTTCAGATAA	GCCGGTGCAA	180
GACCGGGGTT TGGTGGTGAC GG	GACCTCAAA GCTGAGAGTG	TGGTTCTTGA	GCATCGCAGC	240
TACTGCTCGG CAAAGGCCCG GC	GACAGACAC TTTGCTGGGG	ATGTACTGGG	CTATGTCACT	300
CCATGGAACA GCCATGGCTA CC	GATGTCACC AAGGTCTTTG	GGAGCAAGTT	CACACAGATC	360
TCACCCGTCT GGCTGCAGCT GA	AAGAGACGT GGCCGTGAGA	TGTTTGAGGT	CACGGGCCTC	420
CACGACGTGG ACCAAGGGTG G	ATGCGAGCT GTCAGGAAGC	ATGCCAAGGG	CCTGCACATA	480
GTGCCTCGGC TCCTGTTTGA GG	GACTGGACT TACGATGATT	TCCGGAACGT	CTTAGACAGT	540
GAGGATGAGA TAGAGGAGCT G	AGCAAGACC GTGGTCCAGG	TGGCAAAGAA	CCAGCATCTC	600
GAG				603

- (2) INFORMATION FOR SEQ ID NO:1041:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 292 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

GAATTCGGCC TTCATGGCC	T ATAGAAACAT	CAGTGGGCAC	ATTTACAACC	AGAATGTATC	60
CCAGAAGGAC TGCAACTGC	C TGCACGTGGT	GGAGCCCATG	CCAGTGCCTG	GCCATGACGT	120
GGAGGCCTAC TGCCTGCTG	T GCGAGTGCAG	GTACGAGGAG	CGCAGCACCA	CCACCATCAA	180
GGTCATCATT GTCATCTAC	C TGTCCGTGGT	GGGTGCCCTG	TTGCTCTACA	TGGCCTTCCT	240
GATGCTGGTG GACCCTCTG	A TCCGAAAGCC	GGATGCACAC	ACTGAGCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:1042:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 331 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

GAAGAAAAGC	AGAAAGAACT	GGCAGAAACA	GAACCCAAAT	TCAACAGTGT	GAAAGAGAAA	60
GAAGAACGAG	GAATTGCTAG	ATTGGCTCAA	GCTACCCAGG	AAAGAACGGA	TCTTTATGCA	120
AAGCAGGGTC	GAGGAAGCCA	GTTTACATCA	AAAGAAGAAA	GGGATAAGTG	GATTAAAAAG	180
GAACTCAAGT	CTTTAGATCA	GGCTATTAAT	GACAAGAAAA	GACAGATTGC	TGCTATACAT	240
AAGGATTTGG	AAGACACTGA	AGCAAATAAA	GAGAAAAATC	TGGAGCAGTA	TAATAAACTG	300
GACCAGGATC	TTAATGAAGT	CAAAGCTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:1043:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

GATGGCCACT	TCCCAGGCTG	ACATAGAGAC	CGACCCAGGT	ATCTCTGAAC	CTGACGGTGC	60
AACTGCACAG	ACATCAGCAG	ATGGTTCCCA	GGCTCAGAAT	CTGGAGTCCC	GGACAATAAT	120
TCGGGGCAAG	AGGACCCGCA	AGATTAATAA	CTTGAATGTT	GAAGAGAACA	GCAGTGGGGA	180
TCAGAGGCGG	GCCCCACTGG	CTGCAGGGAC	CTGGAGGTCT	GCACCAGTTC	CAGTGACCAC	240
TCAGAACCCA	CCTGACGCAC	CCCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:1044:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 391 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

GTCATTGCA'	CCAAGATAAT	GAAATATCTA	TAACCCCAAA	AGTTTCCTGT	GTECCCTTGT	60
TATTCATTG	CCTGCCCAGT	ATTCAGGCAA	CACGGATCTG	TTTTCTGTTT	TAGGTTAGTT	120
TGCATTTTC	TTTTTAAAGTCTT	ATGAATGAAA	TAATAAAATG	TGGACTATTT	TCATGGGCCG	180
GGGAGCAGT	G TGGCTTCTTT	CATTTCAAAT	GATTGTTTTG	AAATTCATCC	ACAGCGTTGC	240
ACGTATCAG'	AGTAGATTCC	ATTTGATTGT	TGATTTGTAT	TCTATTGTAT	GCCTGAGTCA	300
AAATTTATT	ATCTCTTTGT	CTGTTGATAG	CCATTTGGGT	TCTTCCAGTT	TGGGGCCATT	360
ACAAATAGA	GTACTATGAA	CTTTTCTCGA	G			391

- (2) INFORMATION FOR SEQ ID NO:1045:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 288 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

GAATTCGGCC	TTCATGGCCT	AATGTGAGCC	ACCGCACCCA	GCCGAATATT	TGTACTTTGT	60
ATAAATTCAT	TGTCTGTTTT	ACAGTTTGAA	TGGCTCTTTT	ACCCTGGCAT	AATTTTGTAA	120
CGTGTGGAGC	ATTTGGAAAA	TTTTTTTTGG	ATTATGCAGA	TATTTTCAAT	GCTGGTATTT	180
CATTATATGA	TAGTAAAAAA	TCACTTTTTG	TTTTGTTTTG	TTTTGTTTAT	TTTTCTTTTT	240
TTTTTGAGGC	AGAGTTTCGT	GCTTGTCGCC	CAGCCGAAGG	CGCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:1046:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 279 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

GAATTCGGCC TTCATGGCCT	AGTAACTTCA	TAACATTGCT	GGTGTTGAGG	TGAATCTTAG	60
TGGTCATCCA GTCCCAAGGC	ATCCTTGCCA	GCCCCTACA	ATACCTGGAT	GGGCGCTTAT	120
CTTCAGGTAG GCCTGAGCCT	TTCTGGTAAA	GAGGAGCTCA	CTATTTCTAA	AGGAAACCTG	180
TGCCATTGGG TTAAAAAAGT	ATTAATTTT	AAACATTGGT	AGTTGTTAAG	CAGTTGTTGA	240
ATATTTTGAG CCAAAATTTG	TTACCTCCCA	TACCTCGAG	•		279

- (2) INFORMATION FOR SEQ ID NO:1047:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

GAATTCGGCC TTCATGGCCT AGCAGCATTC AAGGAATTAA TATTAGTCAC TGAGAACAAA	60
AAGCGAAATT AGAAAATTTC AAGTCACTTC TAGGCTTGTA GGGGAGAAGA CGTGTAGTGA	120
TGAATTCTAT CATTTATGAA GTACCCACTG GATCCCACAC ACTGTGCAAG ACCTTTAGAT	180
CAGGCGCCTC CCTCGGTTTT CTTCACCCTG TGCAGCAGGT GCTGTTATTT CCTTTTTTAA	240
ATTATTATTT ATTATTATTA TTTTTTGAGA CAGGATCTCC CTTTGTCACT CAGGCTGGAA	300
TGCAGAGGCA TGATCACTGC TCACTGCAGC TTCGACCACC CGATCTCGAG	350
(2) INFORMATION FOR SEQ ID NO:1048:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 298 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:	
GAATTCGGCC TTCATGGCCT AAAGCTTTTC AGTACTGTTT ACAAATTTGG TTTTATTGTG	60
TCAACTTAAA AGCATGAGTC TAAATCTATT AGTCATACCA AATTGTTTCA TTTTATTTTA	120
TTTTATAGAG ATGGGGTCTT GCTGTATTGC CCAGGCTGGT CTCAAACGAC TAGGCTCAAG	180
CGATCCTCCC ACCTCAACCT CCCAAAGTGC TGGGATTACA GGTGTAAGCC ACCATACACA	240
GTTCTCAAAT TATTTTATAC AATACAAACA TTTAAAATAT AAATCATGCA CTCTCGAG	298
(2) INFORMATION FOR SEQ ID NO:1049:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 367 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:	
Will beginner belong to no. 1047.	
GAATTCGGCC TTCATGGCCT AGAGCTTTGG TGCTTTTCAC ATAAGGAACT TACTTGGGCT	60
AAAAAGTAAC CTCAGAGAAA CAGTGCTCCC ATTTGGTGGA TAAGGAAACT GAGGTTCCAA	120
ACATGAGATG TAATAGCTTG CCCCAAATCT AGCCAGTGAG CAAGAGAGTA GACTTTTGCC	180
IGTGCCAAAA CAGTAATCAC CATCCACAAG TGGCTATTTA AATTTTAATT ATTACAATTA	240
AATAAAGTTT AAAATCCAGT TCCCCAGTCC CACTGGCAAC TTAACAGCTA CCAGTGACTG	300
IACCATATAT AACAGCATAT ATAGACATAC AGCATATACA ACACATACAT AGGGATTCCC ACTCGAG	360
HC1 COAG	367
(2) INFORMATION FOR SEQ ID NO:1050:	
•	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 367 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:	
GAATTCGGCC TTCATGGCCT ACAATTTTAA AATTAAAATT TTTTCTATTT TTTTCCAATT	60

120

ATCAACCTAA CACATTGAAG AAACTTGGGA AATATAGAAA AAACACACCA AAAAGTATCA

GAGTTACACT	AAAATGTTCA	TAGTCAGTAA	TATAGTCTTT	CAGATTTTTT	TTTCTGTGTC	180
TGTCTGCTGT	CTATGTCCAT	GCCTACCTTA	CTTTCTTCCC	TCTCTCTTCC	CTCCCCACCC	240
TCCCTTCCTT	CCTTCCCTCC	TTCCCACCTT	CCCTGCTTCC	TTCTTGCCTG	CCTCCCTTCC	300
TGCCTGCCTC	CCTTCCTGCC	ACTTACATTC	TGTTAACAAT	GAGAAAAAA	TTCCCCCATC	360
ACTCGAG						367
(2) INFORMA	ATION FOR SE	EQ ID NO:109	51:			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

GAATTCGGCC	AAAGAGGCCT	AAGAAGACCT	CAGCCTTCGC	CTGAAAAAGC	TGACTCACGC	60
TGCCCCCTGC	ATGCTGTTCA	TGAAGGGAAC	ACCTCAAGAA	CCACGCTGTG	GTTTCAGCAA	120
GCAGATGGTG	GAAATCCTTC	ACAAACACAA	TATTCAGTTC	AGCAGCTTTG	ATATCTTCTC	180
AGATGAAGAA	GTTCGACAGG	GGCTCAAAAC	GTACTCTAAT	TGGCCCACCT	ATCCTCAGCT	240
CTATGTTTCT	GGAGAGCTAA	TAGGAGGACT	TGACATAATT	AAGGAGCTGG	AAGCATCAGA	300
AGAGCTGGAC	ACGATCTGTC	CCAAAGCACC	CAATCTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:1052:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

GAATTCGGCC	TTCATGGCCT	ACTATGGACA	GCCACAGNTC	TTCCCAGGAC	AAGACCCTGA	60
CTCACCCCAG	CATGGAAACT	ACCAGGGAGG	GAGGGTCCCC	CATCCTACTA	TGACAACCAG	120
GACTTCCCTG	CCACCAACTG	GGATGACAAG	AGCATCCGAC	AGGCCTTCAT	CCGCAAGGTG	180
TTCCTAGTGC	TGACCTTGCA	GCTGTCGGTG	ACCCTGTCCA	CGGTGTCTGT	GTTCACTTTT	240
GTTGCGGAGG	TGAAGGGCTT	TGTCCGGGAG	AATGTCTGGA	CCTACTATGT	CTCCTATGCT	300
GTCTTCTTCA	TCTCTCTCAT	CGTCCTCAGC	TGTTGTGGGG	ACTTCCGGCG	AAAGCACCCC	360
TGGAACCTTG	TTGCACTGTC	GGTCCTGACC	GCCAGCCTGT	CGTACATGGT	GGGGATGATC	420
GCCAGCTTCA	ACAACACACT	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:1053:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 358 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

WO 98/45437 PCT/US98/06956...

GTGACGTCAG TGACCTCATT TTACTTGATC TATTAGCAGC ATTTCATACA GTTGTTGACT	120
CTTCTCCATT AAAACATTTA CTTTATTTGG CTTCTAGGAA ACATATTTTC CTGCTTTTTC	180
TTCCTATTTC TCTGACTCTT TTCTCAGTTT CCTTTGCTGT TTCCTTTTCT ATCCTCTAAA	240
CATTGAAATA TCCTAAGCCT AGTTTGGGAT TCCCTTGATG GTCTTCATTT CTTTAATGGG	300
AACTGTGCTG GTGACTCAAA TTTATATCTC CAGCCAGAAC CTTTCTCCTG AATTCCAG	358
(2) INFORMATION FOR SEQ ID NO:1054:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 386 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:	
CCTTCATGGC CTACTTCTGG TATTACATCA CACTGATCAT GCTGCTGGTG GCCGTGCTGG	60
CCGGAGCTCT CCAGCTGACG CAGAGCAGGG TTCTGTGCTG TCTTCCATGC AAAGTGGAAT	120
TTGACAATCA CTGTGCCGTG CCTTGGGACA TCCTGAAAGC CAGCATGAAC ACATCCTCTA	180
ATCCTGGGAC ACCGCTTCCG CTCCCCCTCC GAATTCAGAA TGACCTCCAC CGACAGCAGT	240
ACTCCTATAT TGATGCCGTC TGTTACGAGA AACAGCTCCA TTGGTTTGCA AAGTTTTTCC	300
CCTATCTGGT GCTCTTGCAC ACGCTCATCT TTGCAGCCTG CAGCAACTTT TGGCTTCACT	360
ACCCCAGTAC CAGTTCCAGG CTCGAG	386
(2) INFORMATION FOR SEQ ID NO:1055:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 104 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) Totomori. Iliteat	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:	
CGATTGAATT CTAGACCTGC CTGTGCTCCT CGATGGTGTC TCTCCCTCCA GAAAACGCAT	60
GCTTATTGAC CTTGGTTTTG ATCTGCTTGG CCGTGTCGCT CGAG	104
(2) INFORMATION FOR SEQ ID NO:1056:	•
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 650 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	•
(b) Topologi: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:	
CANTINGGOOD ANACAGOTT AGAINAGOTT ANACAGOTT AGAIN	
GAATTCGGCC AAAGAGGCT ACACAAGGCT AAGGGTATTG GATATAACGG AAAGTGGAAG	60
CTATACCTGA CTTCCAGAGA ATGTGGACCG GATATAAGAT CTTAATCTTC TCTTATCTTA	120
CTACAGAAAT CTGGATGGAG AAGCAGTATT TATCTCAAAG AGAAGTGGAC CTAGAGGCTT	180
ATTTCACTAG GAATCACACC GTTTTGCAAG GTACTCGATT CAAAAGAGCC ATTTTCCAAG	240

300

GGCAATACTG TAGAAATTTT GGCTGTTGTG AAGACAGAGA TGATGGCTGT GTCACTGAGT

TCTATGCGGC GAATGCGTTG TGCTACTGTG ATAAATTCTG TGACAGAGAA AATTCTGATT

GCTGTCCTGA CTACAAGTCC TTTTGCCGTG AAGAGAAAGA ATGGCCTCCT CACACACAGC CTTGGTATCC AGAAGGTTGC TTCAAAGATG GTCAACATTA TGAAGAGGGA TCAGTAATTA AAGAAAACTG CAACTCCTGC ACATGCTCAG GACAGCAATG GAAATGTTCC CAGCATGTAT GCCTTGTTCG TCCAGAATTA ATTGAACAGG TCAATAAAGG AGACTATGGA TGGACAGCAC AGAATTACAG CCAATTTTGG GGAATGACTT TAGAAGATGG ACTCCTCGAG	420 480 540 600 650
(2) INFORMATION FOR SEQ ID NO:1057:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 378 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:	
GAATTCGGCC AAAGAGGCCT ACACGTATTG GCCAGGATGG TCTTGATCTC CTGACCTCAT GATCCGCCGG CCTTGGCCTC CCAAAGTGCT AGGATTACAG GCGTGAGCCA TCGCGCCCAG CTGAGAATAG TTTTAAGAAT TGGTTGAGAG GCAGTTGCTT TTTCTTTGAA TATCTAGAAC TGTTCTGGAC TAACGTCAAA GAAACACCAT GGCAACATTA AAGGGAAGAT TATTTGAGAG GCGGGGGATA GTATGGCTTA GGACTTGGGC TGCTACCTTT GACTTTGTAA TTCAAAAGAT TGTAATGTTC CATATTTCA ATCTGATCAT TAAAAATATC TGTGTTACAT GCAAAAAAAA ACCTATAGGC AACTCGAG	60 120 180 240 300 360 378
(2) INFORMATION FOR SEQ ID NO:1058:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 259 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:	
GAATTCGGCC TTCATGGCCT AATTTTACA TTTACATAGA CAATTCATTT GGTGTTTTGT CTCCTAGTTA TTTGGCCCAA TCTCTGATGA TTTCCACTCT GTCTTGGCCA CTCACTCCGT TTGTCATATC TTGGCCATTA TCATCACCTC AAATTGCTCC ATCTTCAAAA TACTTGCATC TTATTTATTG ACCATATTCC TTCCACTTGG TTTATTGAAC TATTCCCTCT ATCATTCTCT GATTTCACTG CAGCCAATG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:1059:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 246 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:	
GAAAAAAACT ACTAACCACT GCAAGCTCTT GTCAAATTTT AGTTTAATTG GCATTGCTTG TTTTTTGAAA CTGAAATTAC ATGAGTTTCA TTTTTTCTTT GAATTTATAG GGTTTAGATT TCTGAAAGCA GCATGAATAT ATCACCTAAC ATCCTGACAA TAAATTCCAT CCGTTGTTTT	60 120 180

TTTTGTTTGT TTGTTTTTC TTTTCCTTTA AGTAAGCTCT TTATTCATCT CTCGAG		40 46
(2) INFORMATION FOR SEQ ID NO:1060:		
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 103 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:		
GAATTCGGCC TTCATGGCCT ACGAGAGTAT ATTGGTAGGG CTGGAATTTC GGTAACTAAC TCTATGTTGA ACATTTTGAG GAGCCCTCTC GAG		5 O
(2) INFORMATION FOR SEQ ID NO:1061:		
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 361 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:	,	
GAATTCGGCC TTCATGGCCT AAAAGGTTAG GCAATCACTG GGACCCGCAT CAAAGAATAG GGTAAAGGAG AGCTGGGAGG GAGCCCTCTC CGTTGGGTGA CCCTTTAGAC AGGCTGGCCT GCCGGTTCCA CAGGGTACAG TTAGGACTTG TTTCTGTTTT GAGTTGGTGA GTGAGTGATA GGGTAACATG GGCCTTCAGG GGAACTGTGC CGAGTTCCTT AAATCTCAGC TGGGATCCTG GACCTGGGAG GGGCCAGCTC TGGAAAAACC TGGGAGTTGA TGCCGGAGGC TGTGGAAGAA G	CTCTTGTGTG 12 AGTCTTTCTT 18 ATGACCCCTT 24 GCCCCTGTGA 30	3 0 3 0 3 0 5 0
(2) INFORMATION FOR SEQ ID NO:1062:		
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:		
GAATTCGGCC TTCATGGCCT AAGAAAAATT GGGAACAAGC TAAGTGCCCA AAAATTACGT TAAATAGATA CACGGTTGCT TTTAAGCTCC ACATACAGCA TTTTATATAT TTGTAGGCAT TAAAGCAATT CCAGGAAGGA TCTAAACCAA CAGGTTGTCT CTCTGGGGAG TGGAGCCACA TGGGATTTCA CTGTTTCTGT CTTATATTAA AACACACATG AACAGAAGAA AAAATAGCCC CAGTATCTCG	CCATAGAGCT 1: ACACTTGACC 1: ATTCTTATTA 24	50 20 80 40 92
(2) INFORMATION FOR SEQ ID NO:1063:		
(i) SEQUENCE CHARACTERISTICS:		

<ul><li>(A) LENGTH: 331 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:	
GAATTCGGCC TTCATGGCCT ACCGTTGTTA CACTTCTGGA CACAAGTTGG GCCGAAGTAA GCCAAGCCCA GTCCTTCCTG TTTCCTTTCT CAGGAAATGT GACCACGTGC ACTGGGAAGC TTTGTTGTAAA GTAGATAGGG GTATGAGCCA ATTGCCCAGC ATTGGTGTTT TGTTTTTTTT TTTTTTTTCACAG AGTCTTGCCC TGTCACCCAG GCTGGAATGC AATGGCGTGA TCTCAGCTTA CTGCAACCTC TGCCTCCCAG GTTCACACAA TTCACCTGCC TCAGCCGCCT GAGTAGCTGT GATTACGGGC ACCGTCTCGA G	120 180 240 300 331
(2) INFORMATION FOR SEQ ID NO:1064:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 136 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:	
CGAGTGTTAC ATTCGTTCTT CCGCTCAAAT CCTGATCTGG TCCATTAAAG AGTGTTCGCA GACAAAGTTT CTGAAAGATT AGAGAAGAAT CCCCCAAGAA TCAATTACAA CCAAAATGGA AAGGGACAAC CTCGAG	60 120 136
(2) INFORMATION FOR SEQ ID NO:1065:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 255 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:	
GAATTCGGCC TTCATGGCCT AGAATAAAGG AAAATTCAGG TCATAGATTG AGTGCTATAT TTGAAGTAAA TACAGACCTT CAAAAAAATA TAATATCAAA AATCACTGCT GAGCTCTCCT GGCCTTCCAT ACTTAGCTCA CCCCGGCACT TGAAATTCC ACTTACTAAT ACAAACTGCT CCTCAGAAGA AGAGATTACT TTAGAAAATC CTGCAGATGT TCCTGTCTAT GTTCAGTTTA TTCCTCTGGC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:1066:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 379 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

GAATTCGGCC	TTCATGGCCT	ACAACCTGCT	TTCCACCTTC	TGTAATCTCC	CATCAGTGAT	60
AAATTACCCA	TCAGCTTTCC	AGATTCCAGA	ATTTTGCTGA	CATCTCCTGT	TGGCTATGTT	120
CTTATTTCCT	TTTCTGTTTA	TTCCTGTGAC	CTTGTGCCCT	TTAATTCTTT	CCCATAATTT	180
GTTGGGACTT	CAGAAGGAAG	TGGAGCTAAA	GGCATGTGTC	TGCCTGCCCC	ATCTTGGCTG	240
GAAGTTGGGA	AGGCCTTCCT	TCCAAGGCAC	CCAGCATAGC	ACCTGGCACA	TGATGGATGC	300
TCAGCAAATG	TCTGTGGGTC	TTCTTTTTAC	TAAACAGGCA	GTTGATTTCA	CCAGAAGTAG	360
TGACCACCTA	AGTCTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:1067:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

GAATTCGGCC	TTCATGGCCT	AACACAGCTC	ACATCAGAAT	ATAATAGTGG	AACTAGGGTG	60
ACTTCACTCC	CTTTCACCTG	ATGTCTATCT	TGGCCTTTTA	GCACCTTGAC	TATCCCTGAA	120
AAGACTGGGT	${\tt CTTTGTTTTC}$	CCAGGGAAAA	AACGAAGTGA	TGTAGATCTA	AGAAATAGTG	180
CCTCTTTAAT	ATTTAATTCT	TACATGACAA	CTAACACACA	GGGAAAAGGC	TATGTTAAGT	240
TGATTATAGC	TCCTCTTAAA	ATGTCCTATG	CTGTCAGTTG	GTCTTAGAGA	CATGGGAATA	300
ACCAAGCAAT	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1068:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

GCGATTGAAT	TCTAGACCTC	ACCTCTGATC	TATCTCTTTT	ACCTCAGCAA	TTTATTTCCC	60
AATTATTATA	TCTACTTTAT	TGTTCTTATG	AGACAATAGA	CTATGATAAT	TTTCCAGAAA	120
TAATTTTGTT	TTCTTCCTCC	CATCTTCTAA	TGTTGAGACC	GTTTCTCTGT	TTTCTTTCAT	180
CTCTACCCCT	CAGTCTCATA	GGTTTATTTC	TCATTTCCAA	TCCAGCGATT	TCAAAACCTG	240
TACAACAAAC	CAACTCAGCA	GCCCTTGGCA	ACTTGAGGAG	ATTTCACAAA	CCACTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:1069:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 256 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

ACGTAGGGAT CTGCGTCTGT	TCCTCGTCTC ATCTTGGAAA CATTGCCAGC AGTGGTTCTG ATTTGGAAGC CACGTGACAC CGTCTGAGC TGTGCCTGC TCTCTTTCTT CCGCAGTGC GTGGGGATGA CGGCAGTGG CCTGGCCATC CTGTGGTATG TTTTCCGTCT	120
GGCCGGGAGA		240 256
(2) INFORMA	ATION FOR SEQ ID NO:1070:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 321 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1070:	
TCTAGACAGA AAGTGCTCAC CCCCTCCTCC TTTCTCTTTA	TTCATGGCCT AGCCATCATG TTTATTAGAA GGTTGGATTT TGGTGTGTGC TACAGAATAA ATACCTGCGC CTTGAGAACA GGAAGTCCAC GATTCATACA TACAGGAAGT TGCTGTGTCA AAATCCAGGC AAGGACCCAA CTCCGGGCAG CTGCTGACCT CAACAAGGGC TGTGCTATTG TTTTTTATTT TATTATTTTA TTATTATTAA TATTATTATT ATTTGCTTTT GCTGTGGTCA CTATCATTGG TTTCCCTCGA G	60 120 180 240 300 321
(2) INFORMA	ATION FOR SEQ ID NO:1071:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 261 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1071:	
CATAGTCAAC AGAATCCAAA AAAATTCCAC	TTCATGGCCT AGGGAGGTAT TTGTCATTGT GAAAAGCTGG GAATCTCAAA TTAACTAAAA AGAAGCTAAT ACAGGTTGAG CATTCCTAAT CCAAAAATCC TTGCTCCAAA ATCTGAAACT TTCTGAATGC TGACCTGATA CTACAAGTAG ATACAAGTAC TTAACACAAA CTTTGTTTCA TGCACAAACT ACTAAAAATA TTAACCTCGA G	60 120 180 240 261
(2) INFORMA	ATION FOR SEQ ID NO:1072:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1072:	
GGTGGCCATG GGCCGAATTT	TTCATGGCCT ACTTGGGCTC ATTTTATTTG GTGAATTTGA TCCTGGCTGT GCCTATGAGG AGCAGAATCA GGCCACCTTG GAAGAAGCAG AACAAAAAGA CAGCAGATGC TCGAACAGCT TAAAAAAGCAA CAGGAAGAAG CTCAGGCAGT TCAGCTGCTT CAAGAGATTT CAGTGGAATA GGTGGGTTAG GAGAGCTGTT	66 120 180 240

CGAG

GGAAAGTTCT TCAGAAGCAT CAAAGTTGAG TTCCAAAAGT GCTAAAGAAT GGAGGTCCCT

300

304

(2) INFORMATION FOR SEQ ID NO:1073:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 397 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:	
GAATTCGGCC TTCATGGCCT AAAAAAGCTA ATGTCATAGG TCTTTATATG TGGGCAGGGT TTATAAGTTG TCTAAGGGC CATCAGGTAG AGTTGGCCTT TTCTGTTGAG GTCCCCTAAA TTTCAGTGGA GGTCTTCTC TTGGGGCCAG TTTCTCTAGA AAACTGGGTC CTGATAGTAG GGTAAGAAAA GACAGCTGAG GACCCCAAGA TTTGTATGAT GACTTTTACT TAATCCCTCT ATCTTCATCC TCTCTCATGC CCATCCGGCC CCACCCCCCA AATCCTCCTC TGGCTGCTGA CCCTCAGGTT CAGTTTTCC TGTCAGTGGA GGTTGAGGGT GGGGCGTAGG CTGGCTGTGG AGAGTAGGGG AGAGGACCTG GGTTCCAGTA GCTCGAG	60 120 180 240 300 360 397
(2) INFORMATION FOR SEQ ID NO:1074:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 309 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:	
GCGATTGAAT TCTAGACCTG CACCACTGCG ATCCCTACGC CTGAGGAAAT GACAAGATTG AGAAGCATGA ACAGACAACT CCAGATAAAT GTTGACTGTA CACTGAAAGA AGTTGACCTC CTTCAATCTA GAGGAAACTT TGATCCAAAA GCCATGAATA ATTTTTATGA CAACATAGAA CCTGGCCCAG TTGTACCACC CAAGCCATCT AAAAAAGACT CCTCAGACCC CTGCACAATT GAGAGAAAAG CCCGAAGAAT TAGCGTGACC TCCAAAGTAC AGGCAGACAT CCATGACACC CATCTCGAG	60 120 180 240 300 309
(2) INFORMATION FOR SEQ ID NO:1075:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 243 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:	
GAATTCGGCC TTCATGGCCT AGAAAACTAA ACATTTGCCT TTTATAAAGA CTGACAAAAT ATAAATCTTT ATTCTAACCC TATCCCCAAA ACTAGCCAGG CCACACCCCA GATGTTCTTA TTGACTATTG GGAAGATAGA AAAGGCGTTG TGTTTTTTGTT TTTTTTGTTG TTGTTGTCAT TGTTGTTTTT TCAGAAGACC AGTGTCTCAG TTCTGTCTTA GTAGTACCAC ACCACGACTC GAG	60 120 180 240 243
449	

- (2) INFORMATION FOR SEQ ID NO:1076:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 598 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

CTCGAGCTGG	GGGCCACTTT	GGCACCTAAC	AAAACCAGAG	AAAACAAGTG	CAACTAAGCA	60
AGCAACTATG	CACATTCCAG	ACATAAAGAT	CATTAATAAA	CGCCTTAATC	TAAGGATCTG	120
TTGGTTCTAA	CGCCAGAAAA	AGAAGTTAAA	TTTTAAAAAA	TATCTAAAAG	AGATTTTAAG	180
TGGGCAAGCA	ATAGAGAAGA	TACCCAACAC	TGAGAAACGG	AAAGGAAAAA	AGACCACCCT	240
AATAACTACT	GCTCATCAAT	ATACATCTAT	AATTCTACCA	GAACAGTATT	AAGAAATGAG	300
AAACGCCAAT	ATTACATAAA	ATAAGGTAAA	AATAACTAAG	CATAGGTTAG	TGTCAGGGGA	360
CCTAGGGTTC	AGACACCCAG	AGTTTTATAT	AAGGATAATT	TGTCCTGAAT	CAAGACCACA	420
CTGTCCTCTC	CTTAAACCTA	ACTGCTACAA	GCAGACACCA	CCTCTTCTGA	CTGGGCTGAA	480
GTGTGGGAAA	CAGTCCAAAA	ATTAGGTATC	ACACCATAAA	CCCTCCACAA	GAGCAACCTT	540
TGCTCTCAAT	TAAGTTGTTG	ACAAAATAAT	TCTCAACTTG	CCTAGGCCTG	CCGAATTC	598

- (2) INFORMATION FOR SEQ ID NO:1077:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 346 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

GAATTCGGCC	AAAGAGGCCT	AGGTGGGTAT	TTGAATGGTT	TTGCTCCAAA	ATTGAACTCA	60
CATTGTTGAT	ATGACATGAA	ACTAGCTGCA	GCAAAAAATC	CAGATACAGT	AGATGAAAAG	120
ACTTGCTTTT	CAGGAGGCAG	CTGGTTGCCA	TTTAAAAAGA	AGATCATTTG	CTTTTCATTC	180
AAGTCTAACA	GAAATCCTAC	TGTATCTCCT	TCTTTCCAGC	ATGGGTGTAT	GTGAGGCTTA	240
CTTCTGGCAT	TGTACCAAAT	CAGCTGCCGG	CAGCCATCAT	ACGCACAGGA	GTATTCATCA	300
TCCCCAATGC	CGTAGCCTTC	ATGATTGAGG	AATTTGCTGT	CTCGAG		346

- (2) INFORMATION FOR SEQ ID NO:1078:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 419 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

GAATTCGGCC	AAAGAGCCTA	GCTCCTGTTA	CCATTATTAT	TATTCATACT	CATATTCATT	60
ACTTCTAACT	TCAAGTGGGC	CATTAGCACT	AACTGGCATA	CCACACTTCT	CTAGTCTATT	120
TATTCTCCTT	GATGACTATT	TCATACCCTT	CCCTCTTTCC	CCAAACTTCC	AACACCTCCT	180
CTTCCCATCA	TTCTCAGCTG	ACGGCCTTGC	TTTCTCCCAT	GATTGGGACT	AGAGAAGCAA	240
TTTGTAGGGA	ATTTCCACAA	GCTCCATCAC	ATGTGGCCAC	TCATCTACAT	CTGGATCCAT	300

CTATTTGGCC TTCCCTATTG TTCTTATACA CTCTCCCTGT CTTACTTTAT CTAAGGTCAA

CATCTCCACT CCACTTATGC ACTAGATCCT GGCATTACAC CAGCAATCCT CACCTCGAG

360

(2) INFORMATION FOR SEQ ID NO:1079:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 261 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:	
GAATTCGGCC TTCATGGCCT AGCTTATTCT TTTTTCTTTT TCTTTTTTTT TTTTTTTTC GAGACAGGGT CTTTCTTTGT CACCACAGGC TGCAGTGCAG	60 120 180 240 261
(2) INFORMATION FOR SEQ ID NO:1080:	•
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 208 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:	
GAATTCGGCC TTCATGGCCT ACATTAACAG ATTAATCCAT CTGTATAGGG CTTTTGCTGT TGGATAGAAT TTAAATTGTC TACATAAATA TTTGTTTTAG GACCCTTAGA TTTTATCTGA ATACACAGAT TAGGCTTTAA AAACAGATAT ATATGTCATT TTTGGCTTAA GGAGTTTGGC TAAGTTAGCT TTTCAACTGG TTCTCGAG	60 120 180 208
(2) INFORMATION FOR SEQ ID NO:1081:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 425 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:	
GAATTCGGCC TTCATGACTC CTGATTCAGG GGTCAGTTTA CTTCATAAAA AATCATTAGA AAAGGAAGAA TTATGCCAAA GACTTAAAGA ACAGTTAGAT GCTCTTGAAA AAGAAACTGC ATCTAAAGCTG TCAGAAATGG ATTCTTTTAA CAATCAACTA AAGGAACTGA GAGAAACCTA CAACACACAG CAGTTAGCCC TTGAACAGCT TTATAAGATC AAACGTGACA AGTTGAAGGA AATTGAAAGG AAAAGATTAG AACTAATGCA GAAAAAGAAAA CTAGAAGATG AGGCTGCAAG GAAAACAAAAG CGACTCCAGG AAGCCAAGAC ACCAGNAAAA ATTCCAAGAA GAGGAACGTC TCGAG	60 120 180 240 300 360 420 425
451	

## (2) INFORMATION FOR SEQ ID NO:1082:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 299 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

GAATTCGGCC	TTCATGGCCT	AAGACTTCTT	GCAGGAAAAA	TGAGTGCATT	GAGGATAGTA	60
ACCTGACTTT	CTGACCTGTG	ATTAAATTAT	GATAGTAGTC	AGTCATTTTA	CTCTCCCAGG	120
GTTTGAGGAA	GTGGCCGGTG	AGGACTTGGA	GCCTAGTGAG	GAGTTAGTAG	AGCTGCCCAG	180
GGTGGAGGAG	GCCACAGAGG	ACAGCCCTGG	TGAAGAGAAC	AGTGAGGCCT	TGGATGTGTT	240
GATATCCAGC	AAGGACCTGG	CACTGTCTAG	TGAGGACGAG	GCCTGCACAG	GATCTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:1083:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

GAATTCGGCC	TTCATGGCCT	AAGTCACTTG	TGTAACGTAG	TTATACTTTG	CTGCATTNTA	60
			GTAAGTTAAA			120
ATGTTTTCCA	TATTTCGTCT	TGATTTACTT	TCTGTATGAG	AACAGCTGTG	TTTTTGATAG	180
GTTTATGGTT	TGCATGAGTT	CATATTTAAA	GTGATCCAGG	CCAATGCATG	GCTATTGCTG	240
TAAATCTTGA	TGTTTATTTC	TGCCTTGTAA	AGTTCTATCA	CGGCCTACCT	GGAATTTAAA	300
ATTCAGTAGA	CAAATTAATT	GGTCCTCTGC	ACAACTTTTT	TAATAAGTAG	ATTATTTTAC	360
AAAGAAATTT	GAACAAATTT	AATTGAATCT	TTTGTTTAGC	TTGCCTCTAA	GAACTTTTCT	420
TAATAAAGCT	CCCAAACACT	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:1084:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

GAGTGAGACT	CCCTCTCAAA	GGAAAAAAAA	AAGTTTTCTA	GGATCAAAAT	AGGAAAACAG	60
TTGTTTCAGA	ACTCATGATA	TGAGTCATGA	CTACAACCCA	CCATATTCAG	TAAAACCTCA	120
CCTTGTCCTG	TTGTCTGACA	TTAAGTGTTC	TACGAGATCC	ATACCTGTGA	AATCAGCTCC	180
TCTGGAATGA	CAGATGCTGG	AATAACTGGC	TGGGGCTGAC	TGCCCAAAAG	CCCAGACCCT	240
CGATCCCGTC	CTGTCCGAAT	AACTCGAG				268

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double .	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:	
GAATTCGGCC TTCATGGCCT ACTTTAAGTG AACAACANCA ACAAAAAAGT TAAGGGTAAG	6
ATGAGGCAGC TTTTCAGTGG AAAATACTTG TCTTGGGGAC AGTATGTCAT GTCCCTATAC	12
CTGGTGCCAT TGATAAGGTT ATTCATTCAA CAATATTTAC TGATCACTGG CATATGCCAA	18
GCACTCTGCC AAGTACTAGG GATATAAACA TTAGAAAGAC AAGTTCCTCC CTTTTCAGTC	24
ACGATCTCGA G	25
(2) INFORMATION FOR SEQ ID NO:1086:	
(1) OPOURING GUADA OMODA OMAGO	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 258 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) Toroboot. Timeat	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:1086:	
(11) 0-10-11-11-11-11-11-11-11-11-11-11-11-11	
GAATTCGGCC TTCATGGCCT AGAGCTTCAC GGAGGCAAGA GGGTAATGGA GTGCCTAAAA	6
AAAGCTCTAA AAATAGCAAA TCAGTGCATG GACCCCTCTC TACAAGTGCA GCTTTTTATA	120
GAAATTCTGA ACAGATATAT CTATTTTTAT GAAAAGGAAA ATGATGCGGT AACAATTCAG	180
GTTTTAAACC AGCTTATCCA AAAGATTCGA GAAGACCTCC CGAATCTTGA ATCCAGTGAA	240
GAAACAGAGC AACTCGAG	25
(2) INFORMATION FOR SEQ ID NO:1087:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 391 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) Toronogi. Iinear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:	
•	
GAATTCGGCC TTCATGGCCT AATAAAAAGA ATTATCAAAG AATTGCAGGG GAAACCCCAT	6
AGAGAAGACT CATTCTTAGA TGAGTATACA ATCCATGGGG GTCTTTAGGA TATTTAACTG	12
ATTTGGGAGA GGTCGGATAA AGAAAAAGGA GCATTAACCT TGACTATGCC TTTAGCTCCA	18
GCCGCCTCTT TAAGAGGAAA TTGTTGGGCA GGTGGGGGGAA GGCTAGTCAT GGAACGAAAC	24
TGTAAGCCAG ATCGGGTGTG AGGAGGGGAG GTGATAAAAG GATTATAGGG TGGGAGAGCA	30
CAGGCTGAGG AAGAATTGGG ACCTGGCTCA GCCTGGCAAG GCACAGCCTG GGGAGGAGGG	36
GAGAGGTCCT GTAGAAAAGG AGGATCTCGA G	39
(2) INFORMATION FOR SEQ ID NO:1088:	
(i) SEQUENCE CHARACTERISTICS:	
(1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 368 base pairs	
(B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (D) TOPOLOGI: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

GAATTCGGCC TTCATGGC	T AGCCTTCNAA	GTTTGAATGG	CCCTTAGGTT	TTAAGTTATC	60
TATGCAAAGA TGAANAAGG	C CTTCACATTC	TCAAAGGTGA	CAACTCATAC	CCAGCCATTT	120
GCTTATTTTT GCCTGCAG	C CTCCAATGGA	AGTCCGGGCA	CATGGCGGAG	AGCCTCACCA	180
ACATGCCACG GCACTCCC	C TACATCATCA	TTGGAGCCCT	CTGCGTGGCC	TTCATCCTTA	240
TGCTGATCAT CCTGATCGT	G GGGATTTGCC	GCATCAGCCG	CATTGAATAC	CAGGGTTCTT	300
CCAGGCCAGC CTATGAGG	G TTCTACAACT	GCCGCAGCAT	CGACAGCGAG	TTCAGCAATG	360
CACTCGAG					368

- (2) INFORMATION FOR SEQ ID NO:1089:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 409 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

GAATTCGGCC	TTATGGCCTA	GTTCATTTAA	CTAATACTTG	TATTAAATCA	CTTCTAAATG	60
CTTATTATAC	CCTGTATTAT	AGTATTATAT	TCTGAGTCTT	AAAGGTGCTT	AATGTGAAGA	120
TTCTCTCTCT	ACATATTCAA	CTCTTACTAA	CTTTTGGCTT	TAGGTAGAAA	TCAGTTAGTG	180
TATTATATGA	TAAAATAGGA	AACTATTTCC	CTAGGGGTAT	AGGTATTCAG	TAGGGAGCTT	240
TGGAGTCTCA	ATGAGCTTCT	TAAAGAAGCA	TTTTTAATGG	TAGGTTTTAG	GGAGAGTTTT	300
TGTAGTAAGA	TAAAGTAGAT	GAGAAAGTGT	TGCCTCTAAA	CAATCAACAA	GCTGGGAATG	360
GGGTGCAGAA	TGAGGAGAAC	CCTAAGCAAT	AGGCAATAAG	AAGCTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:1090:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 359 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GAATTCGGCC	TTGGCCTAGT	GAGAGAGCGT	CAAAAAAACT	TCCATCTCAG	CCAACCACTG	60
ATACTAGTAC	TGACAAAGAA	AGAACTTCAG	AGGACATGGC	TGATAAAGAA	AAATCTACAG	120
CTGACTCTGG	AGGTGAAGGA	CTGGAAACAG	CCCCAAAGTC	TGAAGAGTTC	AGCGACCTCC	180
CCTGTCCAGT	CGAAGAAATT	AAAAATTACA	CAAAAGAGCA	TAATAATTTA	ATTCTGCTAA	240
ATAAGGATGT	TCAACAGGAA	AGCAGTGAGC	AAAAAAATAA	ATCAACAGAC	AAAGGTGAAA	300
AGAAGCCAGA	CAGCAATGAG	AAAGGAGAAA	GAAAGAAAGA	AAAGAAGGAA	AAGCTCGAG	359

- (2) INFORMATION FOR SEQ ID NO:1091:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

GAATTCGGCC TTCATGGCCT	ACATGTTCAT	TCTAAGAAAC	TTAACTCCAT	TTTTAAGCTT	60
TAAGATTCCC CCGATCCCAA	ATAACCTAAC	ACACCAAAAG	CCTTGCCATT	TCACACATGC	120
TGTTCCTTTG CTTAGAACCT	TTTCAATGTC	TAGCTCACTC	TGTTTGGGAC	TTCTTTTTTC	180
TTTTCTTTTT TTTGAGACAG	GGTCTGGCTC	TGTCATCCAG	GCTGGAGTGC	AATGGGGCAA	240
TTTCGGCTCA CTGCAACCTC	CGCCCTTCCA	GGCTCAAGCG			280

- (2) INFORMATION FOR SEQ ID NO:1092:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 443 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

GGAAAATTGA GAAAACCATG	AAAGAAAAAG	AAGAACTGTT	AAAGTTAATT	GCCGTTCTGG	60
AAAAAGAAAC AGCACAACTT	CGAGAACAAG	TTGGGAGAAT	GGAAAGAGAA	CTTAACCATG	120
AGAAAGAAAG ATGTGACCAA	CTGCAAGCAG	AACAAAAGGG	TCTTACTGAA	GTAACACAAA	180
GCTTAAAAAT GGAAAATGAA	GAGTTTAAGA	AGAGGTTCAG	TGATGCTACA	TCCAAAGCCC	240
ATCAGCTTGA GGAAGATATT	GTGTCAGTAA	CACATAAAGC	AATTGAAAAA	GAAACCGAAT	300
TAGACAGTTT AAAGGACAAA	CTCAAGAAGG	CACAACATGA	AAGAGAACAA	CTTGAATGTC	360
AGTTGAAGAC AGAGAAGGAT	GAAAAGGAAC	TTTATAAGGT	ACATTTGAAG	AATACAGAAA	420
TAGAAAATAC CAAGCTTCTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:1093:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 256 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

GAATTCGGCC	TTCATGGCCT	ACCTCCATTG	TATATTAACA	TTTATCATAA	TTATTATTTG	60
CTCATTCAAA	AAATATTGCT	CTGATATGGT	ATTGAATATT	CCTCACATAG	GAAAATATGA	120
ACAGTTTATT	TGCCACCCAG	ATGGTTTGGA	AGCCTATACC	CTCCAAGACA	TTGAGAAAAG	180
AAAAATCTTT	CTCTCAGGAG	AGAGAATGAG	TGCCAAGCAA	TGGGAGAAGC	CCCTTAAAAA	240
ACCATCAGAT	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:1094:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 454 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

GAATTCGGCC	TTCATGGCCT	AAGCTGTTAG	TGATTCTGAC	ACCCTTGGAC	CTCCAGGAGT	60
AGCTCCTCCT	GCCACGAGAG	GACTCTGGCT	TTTCTAATAA	GGAAGGTTCT	GGCCAATCAG	120
TCCAAGAAAG	GCCCGGATTC	TCTTCCAAGG	TGTTGTCTCT	GCAGAAATGT	TCCTCAGGGT	180
GGAAGGTGCT	GCTGCAGCAA	GGGATGTCCC	CTGAGTTTTC	AGGTATGTAG	TCTGTGGCTG	240
CAGCAGGTGA	ACACTCCTCA	CACTCCCATT	TCTTACTGTT	AGATCTAAGA	GAGGAGCAGT	300
CCCTGTGGGT	TCCGTGGGAT	CCGCATGTAG	CACACAGAAT	GAGGCACCAC	CTCCCTTCAT	360
CCTCAAAGCT	GTCTCTGCCT	TGTTCATACA	GACAGATGGG	GGCATCACAG	TGCTGATAGC	420
GCTGATATAA	GTCTGAGAAA	GCCCCTGGCT	CGAG			454

- (2) INFORMATION FOR SEQ ID NO:1095:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 449 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

GAATTCGGCC	TTCATGGCCT	AGTGATCTCA	TCTCTCCGTC	CATGGGCGAA	AAAACAGCCA	60
TCACCAGGCC	ATTCACGCTT	TGTGCTTTTG	TTAGCAGAGC	CCAGGCAGCC	CTGCAGCCCA	120
CATCTAGGGT	ACAAACGGAA	CGGCGGCGTT	TTCCTTGTAT	CATTTAGAGG	AAATTTTTGA	180
GCTGAACAGT	ATTTTTTTC	TCCCTCTCTC	TCTCTCTGAA	ATATTGCTGA	GATTTAAAGG	240
AGGACGAAGA	CAACAGATTC	ATAGCTGGGT	CTTGCTGTTT	TCCTGACGCT	GACCACAGCG	300
GATCTAGTTT	CTCTGCAGAA	GACAGCAAGA	TGCCCCAGGG	AATGTTTGTG	AAAAAGGATG	360
ACTGGATGGG	AAGCAAGCTG	AAGAAAAAGA	AGGAAAGAAA	GAGAGAAATC	AGTAAATCAC	420
CACACAAGAG	GTGGAGAAGA	GGACTCGAG				449

- (2) INFORMATION FOR SEQ ID NO:1096:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 166 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

GACTGGCCGC	AAGGGACGGG	TTGTGAGCAA	TGATGATGGA	AGCATATCTT	ATGAGTCAAG	60
ATCTGAACTT	GATGTGCCTG	TGGAAATACT	AAACATCACA	GAAAAACAAC	GATTTATGGA	120
TGGAGATAAG	AATATTGCTA	TCATCTCAGA	AGCTGCCATG	CTCGAG		166

- (2) INFORMATION FOR SEQ ID NO:1097:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

GAATTCGGCC	TTCATGGCCT	ACATTATTTA	CACCTGTCCC	AGACTTTGAT	TCAGGAACTA	60
ATGCTGCAAA	GCAAGGACTA	TGATGGAAAA	TGCTCACTGC	AAGAATGGTA	GCTGCAGCAA	120
GATCAAGATC	CCAGAAAGCA	GTGGCCAAGG	CACTCACTGT	AGACTTTAGT	GCCTGCAGCA	180
TCTGGTGCAA	GCTACACTGT	CTACGCCCAG	GAACACAGCA	GCAGCATCCG	GCCTGGGCCA	240
ATTCTGTGTA	AGATTTGATG	CGCTGTCCCT	GGCTGCAGTG	CCTGCAGACA	TCTCTCTCTA	300
GCCCTTCTAA	CAATTTCACA	GCAACTCAAC	ATCTTTAAAA	ATTTATTAGC	CAACCAAAAT	360
CAGCTTCTGT	GGCATGCAAG	TAAAAACCCA	GGCTGATATG	TCTGAATACA	GAAGATTTAT	420
ATTAGTTCCT	TAGAGTCAAT	AATCCATACA	GACTCTATTC	TAGCTTCTTT	GTGAAGTGGG	480
TAAGAATTCC	TCTGCCTCGA	G	•			501

- (2) INFORMATION FOR SEQ ID NO:1098:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 282 base pairs
    - (3) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

GAATTCGGCC	TTCATGGCCT	ACTTCAAAAA	CATATATTAA	TATTTTTGTA	CCACGTAAGT	60
TCATCAGAAG	CCTGACTTTA	ATCTCTGATT	TATTATATTT	GAACACTGTG	AAGAAGCAGT	120
TTAACACTGA	ACGAAAGTGT	CGTAATGCAG	CTTTCAAAGT	GGCCATTAAA	GACAGATCTC	180
TGCTTTTCTA	TTAGTACATT	TTCTAAGATG	ACTATCATTG	CCATTGTAGT	CAGCTTTGTG	240
TACCTTTATA	GAGATTCCAG	TATAAACCCA	GAAACGCTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:1099:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 266 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GAATTCGGCC	TTCATGGCCT	AGGAAACTTT	TCAAAGAAGT	AGTCCACGAG	AACTACCTTG	60
AAAGAGCAAA	ACCAGCCAGG	TGCAGTGGCT	CACGCCCATA	ATCCCAGCAC	TCTGGGAGGC	120
CCAGGTGGGT	GGATCTCGTG	AGGTCAGGAG	TTCAAGACCA	GCTTGGCCAA	CATGGTGAAA	180
CCCCATCTCT	GCTGAAAATA	CAAAAGTTAG	CTGAAAATAC	AAAAGTGGCA	CATGCCTGTA	240
ATGCCAGCTA	CCGGGAAAGG	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:1100:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

CTCGAGCGTA	TCCCAGAACT	TAAAGTATAA	TAATAATAAT	AATAATAATA	ATAATAATAA	60
TAATAAAACC	TTCCAACAAG	CTTCCTTTCC	ACCACAGGAA	ATCCTGTTGG	GAGTTCCCCC	120
TGAACCAAAA	AAAAAAAAAG	ATAGAGTATA	AAACATACAC	TTTTCAGGAA	TGCTTATTGG	180
GTAATGTAAG	ATAACACCTC	AAAATGAAAC	TCAGAATTTT	<b>ATTTTATTTT</b>	ATTTTTTGAG	240
ATGGAGTCTC	ACCTAGGCTG	GAGTTCAGTG	TGGTAATCTT	GGCTCACTGT	AGGCCATGAA	300
GGCCGAATTC						310

- (2) INFORMATION FOR SEQ ID NO:1101:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

GCGATTGAAT	TCTAGACCTG	CCTCGAGTGT	ACCTCATTCT	GCCATCTCTG	ATATTATGTC	60
ATCTGATCAA	GAAACTTACT	CTTGTAAACC	TCATGGACGG	ACTCCACTTA	CCTCAGCTGA	120
TGAGCATGTA	CATTCCAAAC	TGGAAGGAAG	TAAAGTAACG	AAATCTAAGA	CTTCTCCGGT	180
GGTATCTGGT	TCATCTAGTA	AATCAACCAC	CCTTCCAAGG	CCACGACCTA	CCAGGACTTC	240
CCTCTTGCGC	AGAGCACGAC	TTGGTGAAGC	TTCAGACAGT	GAACTTGCTG	ATGCTGACAA	300
AGCATCTGTT	GCTTCTGAAG	TATCCACAAC	AAGTTCTACA	TCAAAACCTC	CCACAGGAAG	360
GCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:1102:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 368 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GAATTCGGCC TTCATGGCCT AAGAAAGCAA GAAAGCACGA AAGCAATCAA GCAAGAAAGC	60
AAGCAGGAAA GAAACAAAAG AAAGAAAGAA NGCGAGAAAA CAAGAAAGCA CGAAAGCAA	3 120
CAAGCAAGAA AGCAAGCAAG AAAGAAACAA AAGAAAGA	A 180
GCAAGAAAGC ACGAAAGCAA GCNAGCAAGC AAGAAAGCAA GCAAGAAAGA AACAAAAGA	A 240
AGAAAGAAAG AAAGAAAGAA AAAGAAAACA GGAAAGCAAG AAAGCACGAA AGCAAGCA	3 300
CAAGCAAGAA AGCAAGCATG AAAGAAACGA AAGAAAGAAA GAAAGCAAGA AAACGGGAAA	A 360
GACTCGAG	368

- (2) INFORMATION FOR SEQ ID NO:1103:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GAATTCGGCC TTCTGGC CCCAAGCACA CGATATG AGACACAGAC CCTGTCT ACATCCTCGC ATAGGTG GATACATACA CAGAGTA ACAGGCACAG ACCCCCC	CAC GTGGATACAC GCA CCACAAACAT GAT ACAAGCACAG CCC CCACAAACAC	AGACTTACAA ACCACACACA ACTCACATAC	GCACAGGGCC GCCACACACA ACATATGCGA	ACGTGCAGAC CAGAAGCCAA TACACATATG	60 120 180 240 300 328
(2) INFORMATION FO	R SEQ ID NO:110	)4 :			
(A) I (B) T (C) S	E CHARACTERISTI LENGTH: 246 base 1YPE: nucleic ac STRANDEDNESS: do 1OPOLOGY: linea	e pairs cid ouble			
(ii) MOLECU	LE TYPE: cDNA				
(xi) SEQUEN	CE DESCRIPTION:	SEQ ID NO:	1104:		
GAAAAAACT GAGTTAA TCTGTTTTGC AGTTTAG TAGAACAGAC TCTTTGT AGGCAAGGGT TAAGTTA CTCGAG	ACA CAACTGACCA GGC CCAAAATTAG	GCATTGTTAA CAAATTATAA	AATGGAGATC ATAGAATCTA	ATACGGCTGG AAGCCATCCC	60 120 180 240 246
(2) INFORMATION FO	R SEQ ID NO:110	)5:			
(A) I (B) 7 (C) 5	E CHARACTERISTI LENGTH: 298 base TYPE: nucleic ac STRANDEDNESS: de TOPOLOGY: linea	e pairs cid ouble			
(ii) MOLECU	LE TYPE: cDNA				
(xi) SEQUEN	CE DESCRIPTION:	SEQ ID NO:	1105:		
GAATTCGGCC TTCATGG AGAAGATCAA AAAGCCG GAACAAGATA GAAAATC GAAAGAAGGC GGAGCAG AGAAAACACA GATCTCG	GGA TCGAAAGTCA CAA GGAGAAAGAA AAG TAGAGATCGA	TATAAGCACA AAGAGGGGAT CGAAGAAGCA	GGAGCAAAAG CTGATGATAA GAAGCCATGA	TCGGGACAGA AAAAAGTAGA TCGATCAGAA	60 120 180 240 298
(2) INFORMATION FO	R SEQ ID NO:110	06:			
(A) 1 (B) 7 (C) 5	E CHARACTERISTI LENGTH: 211 bas IYPE: nucleic a STRANDEDNESS: d TOPOLOGY: linea	e pairs cid ouble			
(ii) MOLECU	LE TYPE: cDNA				
(xi) SEQUEN	CE DESCRIPTION:	SEQ ID NO:	1106:		
GAATTCGGCC AAAGAGG TTCTTCAAAA TTGAGTG ACATGATCCT TACTGTC ACACAGTAAA CAATTGC	GGAT GATGCCTTGC	AGAGCCTGAA AGCTGTGTCT	AGCCGTCATT	CACGGGAAAC	60 120 180 211

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 269 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:	
GAATTCGGCC AAAGAGGCCT ACCTGCTTGA ATTGGGGCCC CTTGTGAAGC TGCTGCCGCA TCTCTTCCAT TCGCTGCTTC CGGTACTGCT GCAGAAACTC TTCATCATCT TGGTCCTCAT TCATTATGGC AAACTCCTTC AGAGTCATCT TCCCACTGAT CTTCTCCTGG AGGTCTTTCT GTTTCTGTTG CTCCTCCTCT TCATCCAGAT GGGACCTGCA AGTCATTGAC AGCTTCTTGA TCAGCCTTTC CATCTCCGG CAACTCGAG	60 120 180 240 269
(2) INFORMATION FOR SEQ ID NO:1108:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 133 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:	
GAATTCGGCC AAAGAGGCCT ATGAAAATTG ACTGCAATTA GTAAAGTTGG TATAACGTAC GTTCCCAGTT GTGCTATTTA GAATTATGAT AGTATTATGC TCCTACTTTT CTTTGATATT GAGTAGTCTC GAG	60 120 133
(2) INFORMATION FOR SEQ ID NO:1109:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 123 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:	
GAATTCGGCC AAAGAGGCCT AGCTTTTTCT AATCATAAAT TATATGACCT TTACAGAAAA TTTAGAAAAAT ACAGAAAAAC TGAAAAGTTA CACATGGTAC AACTCACAAC CACAATCCTC GAG	60 120 123
(2) INFORMATION FOR SEQ ID NO:1110:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 240 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
460	

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

GAATTCGGCC	AAAGAGGCCT	AGTGTTCCAG	ATCCTACGGC	TTATGAGGAT	TTTCCGAATT	60
					GAGACACAGC	120
TACCATGAAG	TTGGGCTTCT	GCTTCTCTTC	CTCTCTGTGG	GCATTTCCAT	TTTCTCTGTG	180
CTTATCTACT	CCGTGGAGAA	AGATGACCAC	ACATCCAGCC	TCACCAGCAT	CCCCCTCGAG	240

- (2) INFORMATION FOR SEQ ID NO:1111:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 264 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

GAATTCGGCC AAAGAGGCCT AGGTGGGGAG GG	
ACCGAGAACT CAGCAGCTGC CACCGCAGCT GCC	CTCCTCAG GATCCGGTCG TCGGGGATAG 120
GGAAGGGAGG GGAAAGGGGA ACGGAAAACA AAJ	AAAAAGGG GGAGGAAGG 180
AGTCGGGGAC GGCCTCAAAC TCAGCTCAGA GG	AGTCGCTG CTGCAGCCGC CACTCGGTAC 240
CCGCTGCTAG GCCTCTTTGC CGAG	264

- (2) INFORMATION FOR SEQ ID NO:1112:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GAATTCGGCC	AAAGAGGCCT	AAATATTAGA	AAATGTATAT	TATAGAACAT	GATATATATT	60
TACATTCATC	TCTGTATTCT	CTCAGCTGTT	GTTAGAAGGA	CAGAATGTTA	AACTTTATCT	120
TAATTAGTAT	ACTAGAAAGG	GCAGTATAAT	ACTGTTTTAA	AGTGAAGGCA	TGACTGAAAC	180
			AGAGTAACGT			240
CTTGTACTTA	GTTTTTTCAT	TTAATAATTC	AAACCAACAC	TTTTAAAAAA	ATAATTCAGA	300
			ATATTTCTTA			360
			TGCTTTTTAA			420
ACCTCTTAAA	TTGTGACATG	AAGGTATGTA	ATTAGATTTC	AGAAATTGGT	TTATTAGTGA	480
GGAATTTTTA	TCAATAAATG	TCATGGGGCG	GCGCTCGAG			519

- (2) INFORMATION FOR SEQ ID NO:1113:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 562 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double(D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

GGCCCACCTA	GTTGGTATCC	CAAATTCACA	CATTCAAAAG	CAAAGCCATT	TCTCACCTTC	60
CTCCAAAATA	CTTGTAATTC	CTAATATCCT	GACTCCAATC	CATTCTTTAT	TTTCTATTCC	120
CAAGGCCCTT	CACAGAATCG	AAACTTTTGT	TATGAGCTCT	TACATGGTGT	ATCATCAATA	180
TGTTCACTAG	ACAGGAGTTT	TTTTTAAAAA	AAATCCTCAT	CATTCCTCTT	CAATTCAAGA	240
GCTCTGATGG	CTTCCAGTCT	ATACAAGATA	TATTAAGGCT	CAACTTACAG	TTCCAGTCTC	300
ACCTGCCCCA	CCTCCACCTT	CCCAAACCCT	CTGTATTCTA	GCCAGAGCAT	ACCTGCATTC	360
CCTTAGCTCA	ACATGTGTCC	TTGCTCACAC	TGTCCCTTTG	GTTGACCTAG	CTTCAATTCC	420
TTCCTCATGT	GCAGTTATGT	GTCTACTAAG	CAGCAATGTG	AAATGTCTTT	ATTGTAGGTC	480
TGTCAAAAGC	TAAAGTCATG	GCCCGGTGCA	GTGGCTTGGG	CCTGTAATCC	CAGCACTTTG	540
GTAGGCCTCT	TTGGCCGAAT	TC				562

- (2) INFORMATION FOR SEQ ID NO:1114:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 435 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

GAATTCGGCC	AAAGAGGCCT	ATTATTGCTA	TCGCCCTCCT	TTCCCTTATT	GCCTCCCAGG	60
CAAGCAGCTG	GTCAGTCTTT	GCTCAGTGTC	CAGCTTCCAA	AGCCTAGACA	ACCTTTCTGT	120
AGCCTAAAAC	GAATGGTCTT	TGCTCCAGAT	AACTCTCTTT	CCTTGAGCTG	TTGTGAGCTT	180
TGAAGTAGGT	GGCTTGAGCT	AGAGATAAAA	CAGAATCTTC	TGGGTAGTCC	CCTGTTGATT	240
ATCTTCAGCC	CAGGCTTTTG	CTAGATGGAA	TGGAAAAGCA	ACTTCATTTG	ACACAAAGCT	300
TCTAAAGCAG	GTAAATTGTC	GGGGGAGAGA	GTTAGCATGT	ATGAATGTAA	GGATGAGGGA	360
AGCGAAGCAA	GAGGAACCTC	TCGCCATGAT	CAGACATACA	GCTGCCTACC	TAATGAGGAC	420
TTCAAGCCCC	CTCAG					435

- (2) INFORMATION FOR SEQ ID NO:1115:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 477 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

AGTGCCTAGA	TTGATCGGTA	TAAGGCTCAC	TCTCCCGCCC	60
GAACGAGAAA	AGGGCCATGT	TCGGAGTGTA	TGACAACATC	120
AAAGCACCCC	AAAGAACTGA	TCAGGGGGCC	CATATGGCTT	180
ATTGCAACGT	TGTATCCGAA	AGAGGAAAAT	GGTTGGAAGT	240
GCACAACCTT	AATAAACGCA	TCCGCTATCT	CTACAAACAC	300
TCGATAGAAG	AGAAAGCTGA	GAACTTCGGA	AAAGGCTCAT	360
AACTGTACTT	TTCCCTGTGA	GGAAACGGCT	TTGTATTTTC	420
CTTTGGAATT	TGATAAGCCT	AGGCCTCTTT	GGCCGAA	477
	GAACGAGAAA AAAGCACCCC ATTGCAACGT GCACAACCTT TCGATAGAAG AACTGTACTT	GAACGAGAAA AGGGCCATGT AAAGCACCCC AAAGAACTGA ATTGCAACGT TGTATCCGAA GCACAACCTT AATAAACGCA TCGATAGAAG AGAAAGCTGA AACTGTACTT TTCCCTGTGA	GAACGAGAAA AGGGCCATGT TCGGAGTGTA AAAGCACCCC AAAGAACTGA TCAGGGGGCC ATTGCAACGT TGTATCCGAA AGAGGAAAAT GCACAACCTT AATAAACGCA TCCGCTATCT TCGATAGAAG AGAAAGCTGA GAACTTCGGA AACTGTACTT TTCCCTGTGA GGAAACGGCT	AGTGCCTAGA TTGATCGGTA TAAGGCTCAC TCTCCCGCCC GAACGAGAAA AGGGCCATGT TCGGAGTGTA TGACAACATC AAAGCACCCC AAAGAACTGA TCAGGGGGCC CATATGGCTT ATTGCAACGT TGTATCCGAA AGAGGAAAAT GGTTGGAAGT GGACAACCGT AATAAACGCA TCCGCTATCT CTACAAACAC TCGATAGAAG AGAAAGCTGA GAACTTCGGA AAAGGCTCAT AAACTGTACTT TTCCCTGTGA GGAAACGGCT TTGTATTTTC CTTTGGAATT TGATAAGCCT AGGCCTCTTT GGCCGAA

- (2) INFORMATION FOR SEQ ID NO:1116:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 620 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

GAATTCGGCC	AAAGAGGCCT	AAGATGAAGC	CCAACATCAT	CTTTGTACTT	TCCCTGCTCC	60
TCATCTTGGA	GAAGCAAGCA	GCTGTGATGG	GACAAAAAGG	TGGATCAAAA	GGCCGATTAC	120
CAAGTGAATT	TTCCCAATTT	CCACACGGAC	AAAAGGGCCA	GCACTATTCT	GGACAAAAAG	180
GCAAGCAACA	AACTGAATCC	AAAGGCAGTT	TTTCTATTCA	ATACACATAT	CATGTAGATG	240
CCAATGATCA	TGACCAGTCC	CGAAAAAGTC	AGCAATATGA	TTTGAATGCC	CTACATAAGA	300
CGACAAAATC	ACAACGACAT	CTAGGTGGAA	GTCAACAACT	GCTCCATAAT	AAACAAGAAG	360
GCAGAGACCA	TGATAAATCA	AAAGGTCATT	TTCACAGGGT	AGTTATACAC	CATAAAGGAG	420
GCAAAGCTCA	TCGTGGGACA	CAAAATCCTT	CTCAAGATCA	GGGGAATAGC	CCATCTGGAA	480
AGGGAATATC	CAGTCAATAT	TCAAACACAG	AAGAAAGGCT	GTGGGTTCAT	GGACTAAGTA	540
AAGAACAAAC	TTCCGTCTCT	GGTGCACAAA	AAGGTAGAAA	ACAAGGCGGA	TCCCAAAGCA	600
GTTATGTTCT	CCAAACTGAA					620

- (2) INFORMATION FOR SEQ ID NO:1117:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 158 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

GAATTCGGCC	AAAGAGGCCT	AGACCTGCCA	CATTTGTTAA	CATTTTTCCA	TTTCTAAACC	60
ATCCTTAAAG	AAAATCATAT	ATGGGGTCAC	ACCATCCTCA	CGGTAGTCCA	ATAGAGCAAC	120
CATGCCATCT	GGATTCATGT	TTTCACCAAA	CCCTCGAG			158

- (2) INFORMATION FOR SEQ ID NO:1118:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 410 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

GCACTGCTTC	TGTTAAAGTC	ACTGACCTTA	ACAGTTTAGA	ACTAGATAAA	GGAAATTTTG	60
TGGTTGACCA	AATGTGTGAA	ATAGGTAAGC	CAGAACCATT	GAATGAGGAG	GAAGCAAGGG	120
GTGTGGTTGA	GAATTATAAT	GATGAAGAAG	TGTCAATTAG	AGTTGGTGGA	AATACACAGC	180
CAAGTAAAGT	TTTGAACAAA	AAAAATGTAG	AAGCTATTGG	ACTTCTTGGA	GGACAAAAGA	240
GCAAAGCAGA	TTATGAGCTA	TACAACAAAG	CCTCTAATCC	TGATAAGGTT	GCTAGTACAG	300
CGTTTGCTGA	AAATAGAAAT	TCTGAGACTA	GTGATACTAC	TGGGACCCAT	GAATCTGATA	360
GAAACAAGGA	ATCCAGTGAC	CAAACAGGCA	TTAATATTAG	TGGACTCGAG		410

- (2) INFORMATION FOR SEQ ID NO:1119:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 452 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

GAATTCGGCC	TTCATGGCCT	AGTTGCCCTA	ATTTGCAGCC	GAACTTGGAA	GCCACTGTAT	60
CCAATGGACC	TTTTCTGCAG	CTTTCTTCCC	AGTCTCTTAG	CCATAATGTT	TTTATGTCCA	120
CCAGTCCTGC	ACTTCATGGG	TTATCATGTA	CAGCAGCAAC	TCCGAAGATA	GCAAAATTGA	180
ATAGAAAACG	ATCCAGATCA	GAGAGTGACA	GTGAGAAAGT	TCAGCCACTT	CCAATTTCTA	240
CCATTATCCG	AGGCCCAACA	CTGGGGGCAT	CTGCTCCTGT	GACAGTGAAA	CGGGAGAGCA	300
AAATTTCTCT	TCAACCTATA	GCAACTGTTC	CCAATGGAGG	CACAACACCT	AAAATCAGCA	360
AAACTGTACT	TTTATCTACT	AAAAGCATGA	AAAAGAGTCA	TGAACATGGA	TCCAAGAAAT	420
CTCACTCTAA .	AACCAAGCCA	GGTTATCTCG	AG			452

- (2) INFORMATION FOR SEQ ID NO:1120:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 592 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

GAATTCGGCC TTCATGGCCT	ACATGAATCT	ACTTCTGATC	CTTACCTTTG	TTGCAGCTGC	60
TGTTGCTGCC CCCTTTGATG	ATGATGACAA	GATCGTTGGG	GGCTACATCT	GTGAGGAGAA	120
TTCTGTCCCC TACCAGGTGT	CCTTGAATTC	TGGCTACCAC	TTCTGCGGTG	GCTCCCTCAT	180
CAGCGAACAG TGGGTGGTGT	CAGCAGGTCA	CTGCTACAAG	TCCCGCATCC	AGGTGAGACT	240
GGGAGAGCAC AACATCGAAG	TCCTGGAGGG	GAATGAACAG	TTCATCAATG	CAGCCAAGAT	300
CATCCGCCAC CCCAAATACA	ACAGCCGGAC	TCTGGACAAT	GACATCCTGC	TGATCAAGCT	360
CTCCTCACCT GCCGTCATCA					420
AGCTGCTGGC ACCGAGTCCC	TCATCTCCGG	CTGGGGCAAC	ACTCTGAGTT	CTGGTGCCGA	480
CTACCCAGAC GAGCTGCAGT	GCCTGGATGC	TCCTGTGCTG	AGCCAGGCTG	AGTGTGAAGC	540
CTCCTACCCT GGAAAGATTA	CCAACAACAT	GTTCTGTGTG	GGCTTCCTCG	AG	592

- (2) INFORMATION FOR SEQ ID NO:1121:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

GAATTCGGCT	TCATGGCCTA	AATAATTTTT	ATTCAGAATA	ATAAATCACT	CTTTATCATA	60
GTATCTTCTC	TTCCCTCTTC	CCCTTTAGTT	TGGATAGCCT	AACTCTGAGA	AGTTAACCCT	120
TAAACAGTTT	TCTGGAAGAG	ACTGAATTTC	TGGGTCCTTG	CAGCTGTGAT	GGTTTCAGAG	180
CTCAGACTGA	TCAGGCATCA	AGCTACCCTC	AAGAGTTTCT	GGGCTGGATG	TTTCAGAACA	240
ACATCTACAC	CAGTAAAGTG	TAATAGGTCA	GTTTCAAAAC	GACCAAAAGA	CCCCACCACT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:1122:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 388 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

GAATTCGGCC	TTCATGGCCT	AGTGAAACTC	CATTTTTTTA	CTGCTATTAC	TCTGTGTTTT	60
CAGTTTTATG	ATTTGGAATA	CCATGATGGG	AACATCTATA	CTAAGCATTC	CTTGGGGCAT	120
AAAACAGGCT	GGATTTACTA	CTGGAATGTG	TGTCATCATA	CTGATGGGCC	TTTTAACACT	180
TTATTGCTGC	TACAGAGTAG	TGAAATCACG	GACTATGATG	TTTTCGTTGG	ATACCACTAG	240
CTGGGAATAT	CCAGATGTCT	GCAGACATTA	TTTCGGCTCC	TTTGGGCAGT	GGTCGAGTCT	300
CCTTTTCTCC	TTGGTGTCTC	TCATTGGAGC	AATGATAGTT	TATTGGGTGC	TTATGTCAAA	360
TTTTCTTTTT	AATACTGGTA	ACCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:1123:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 478 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

AGCAATTCCA	TAAACACATC	CTGGTGTCAT	CACAGCCAAG	GTTTTTAGGT	TGCTATACCA	60
ATGGCTTATT	AAATGAAAAT	GGCACTAAAA	GTTTCTTGAG	ATTCTTTATA	CTCTCTGCCT	120
TCAGCAATCA	ATTCCATTCA	TACATCAGCA	CTCTGCTGGT	TCTGTTTGAA	ATATGTTCTG	180
TATTTAAAAC	TCAAATCTTG	TTGGATCTCT	GCAGGGCTTG	TGACCAATGA	AGTCATATTT	240
GTTGATGGTT	GACAAAGCTT	GCTTCACTCC	ATCAGAGAAT	GACTATCAAT	TTTTTTTTAA	300
CTGTCCTATC	ACGTCCTCTC	CTGTCACCCA	TTTTGAAGAG	TGGCAGAACT	TGAAGTTCAA	360
CTTCCTCTGT	AAATATCCAA	GTATAAAGCC	CAGGAACTTC	TAGAATAACC	CAGATGCGCT	420
TTAATTTTTT	TTAATATGTT	TTGATCACAG	AACTCCTTAG	GCCTCTTTGG	CCGAATTC	478

- (2) INFORMATION FOR SEQ ID NO:1124:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 450 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

GAATTCGGCC	AAAGAGGCCT	AGGAATTCAG	TGCAAACACT	ACTTTGAACT	GTGGTTCCTA	60
ATTTCCACGA	AAGTTTTTCT	CTGTTCTTCT	ATTATGGCAC	TTTTCAGGGT	CTCCCTTGTA	120
CATTTTAGTT	TTTGTGTTTT	TCAGTAAGTG	CCTTGAGATC	AGGGACCGGT	TCTACTGGTC	180
TGTTCCAACC	ATAGTTCCTT	AAACATTGTG	TTCCATTAAT	ATTGGGTGAA	TTGAAATGAA	240
TTTATAGGAA	GCTCCTTAAC	CTGGGGTCCT	CAGACCTCTA	TGGGGTCCAT	GGACAGAATT	300
TGAAGTGGGA	AGGATATATG	AACTTGGATG	GAGGAAAATT	ACTTATTTGT	TTTTTACCAA	360
CCTCTCCTTT	GTAATTTAGC	CATTTGTTCA	ATTATAATGT	AGGCAAATAA	TAAAAAAAA	420
AAAATAAAA	TAAAGGCAGC	TTAGGCCTCT				450

(2) INFORMATION FOR SEQ ID NO:1125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 550 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

GAATTCGGCC AAAGAGGCC	T ATCCTTAGTG	GATTCCGACT	TCCATGGCCA	CCGTCCTGCT	60
GTCTATATCA ACCAACACC					120
CCGGCGTTCG GTTCATCCC					180
TCGCATTCCA CGCCCGGCT					240
GAATAGGTTG AGATCGTTT					300
TGCGTGGCGG GGGTGCGTC					360
GGGAACCAGC TACTAGATG					420
GATTTGCACG TCAGGACCG	C TACGGACCTC	CACCAGAGTT	TCCTCTGGCT	TCGCCCTGCC	480
CAGGCATAGT TCACCATCT	T TCGGGTCCTA	ACACGTGCGC	TCGTGCTCCA	CCTCCCCGGC	540
GCGGCGGCG					550

- (2) INFORMATION FOR SEQ ID NO:1126:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 381 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

GAATTCGGCC	AAAGAGGCCT	AGTTTGCAGG	AAGAAGGCAT	GGGATAGTCT	GAGAACAAAC	60
AGGCACTAAA	TGGAGCAACA	TCATCTTGAG	GTGTCAAGCA	GGAGCTGGGA	GACCAGCAGA	120
GACTCCCAAG	GCCTTGCTGC	TGTTGGTCTG	CAGGCAGCTC	TGTAGGGCAG	GCTGTTGTCA	180
TTTTGCAAGT	GAGCAAGCAG	AAGCCCAGGC	AGGTGAGTCA	TTCACTCCAC	AGTTCATAAC	240
TTGGATTGTG	GGTTAGTTAC	ACCTGACTCC	AAAACTTGAC	TTTTTACTAC	TCAGCTATAC	300
TGGCCTCTCA	AGAAAGGCTA	GGCCCTAATT	TCTAGACTCT	CTTTTACCAA	TAATACCTGT	360
TGCCACGAAG	TAGGCCTCTT	T				381

- (2) INFORMATION FOR SEQ ID NO:1127:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 361 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GAATTCGGCC	AAAGAGGCCT	ACTCTCAAGG	TGGGCATATG	CAAAACATAA	TCTCTAAATT	60
CTTCAATACT	AAGAAATACC	TTTGTTTTAC	CCCTAAAATC	AAATGCCATT	TTGGCTGGAT	120
ATAGGATTCT	AGGATTAAAG	CCTTTTTCCA	GCAGAACTTT	GAAGACATTG	CTCCATTTAC	180
TTCTAGCATC	CAGTGTGTCC	AGTGATAAGT	CTGCTGTCAA	CCTGATTCTT	GTTCCTTGGT	240
AGGTAATTTC	TCTTCTCTCT	CTAGAAGCCC	TTATTATTTT	CTCTTTATCA	CTAGAATTCC	300
AAAATTTCAC	CAAGATGTGT	CTAGGAGTCA	GTCTCTTTTC	ATCAATTTTA	CTAGGTACTC	360

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 359 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:	
GCAGCCAATG GCGGCGCAG AGGGGAAACN GAGCCTTGCT NACGGGCCCA ACGCTGGGGA GCAGCCAGGC CAGGTGGCGG GCGCAGACTT CGAGAGCGAG GACGAGGGCG AGGAATTTGA TGACTGGGAG GACGACTACG ACTATCCCGA AGAGGAGCAG CTCAGTGGTG CCGGCTACAG AGTATCAGCC GCTCTTGAAG AAGCCGACAA GATGTTTCTG AGAACAAGAG AACCAGCCCT GGATGGCGGG TTTCAGATGC ATTATGAGAA GACCCCGTTT GATCAGTTAG CTTTTATCGA AGAGCTTTTT TCACTGATGG TTGTCAATCG TCTGACCGAA GAACCCGGCT GCTCTCGAG	60 120 180 240 300 359
(2) INFORMATION FOR SEQ ID NO:1129:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 274 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:	
GATGGCACCC TCCTCAGAAA GCAGCGTCCC CTCTCACAGT ATGTCCTCCC GACGGGACAC AGACTCGGAT ACCCAGGATG CCAATGACTC AAGCTGTAAG TCATCTGAGA GGAGCCTCCC GGACTGTACC CCTCACCCCA ACTCCATCAG CATCGATGCC GGTCCCCGGC AGGCCCCCAA GATTGCCCAG ATCAAGCGCA ACCTCTCCTA TGGAGACAAC AGCGACCCTG CCCTAGAGGC GTCCTCGCTG CCCCACCCG ACCCCTGGCT CGAG	60 120 180 240 274
(2) INFORMATION FOR SEQ ID NO:1130:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:	
GGCTTTCCAC CTTCCCTGCG GAGATGAGGG TGGTGGCCTC CCTTTTTGTC ACCCTTCCAA GGGTCATGCT CGTCTGCTGG CTTTTCTCCA AGATGCTGCC AAAAATGATC TTAA1AAGAC ACAAGCCTGG TTGTGATATT TTCCTGATTC AAGTGTCTCT GTGGTTCTTG GTTGCCTTCA GGAGAGAGGTT CAAGCCTCTT ATGGTGGTTT GTGAGGCCAG GCCTGAACTA GCCCCATCGT CTGTTCATTC ACCACCCCAG TATCCCTGCT GCAGGTTTTT AAAGATCTCA TGTCCCTGAT TGCCTGTCAC TGTGTCTGAC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:1131:	

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(i) SEQUENCE CHARACTERISTICS:
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- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

TCACATCACG GCCTCCATAT GCAGGATCCT CAGGGCCTCG GAGATCTGCG CGCTGGGGTC 12	30
CATCTGGCCG TACATGCCCA CCAGGAAGGC CCGGTGGAGC AGCACAGCCG CGTGCTCTTG 18	_
GCACAGGAGA GCGTACTCAG GCAGGTTCCG GAGGGCCGTC TGCACCACCT CAAAGTCCTG 24	0
GCTGCCCAGG CAGTACATGA ACGTNGGGCA GGAAAGCGGC TGCAATGCNG GGGGCTGTCT 30	0
GCATGGAGCG CAGGGCCAGG CTGAAGGCGA GGTTGCGGCA ACACTCCTCG GCCGAGCTCA 36	0
TCAGCCGCTG CAGGTTGGTC GAGAAGAAGC TCAGGATCTC GGGTCTCCGC CGGGACATCT 42	20
CGTCTATGTC ACTCAGAACC TCCAGCAGAT CCTCCACCGT TTGGCCCCGG GAAAGCCGTT 48	0
TCATGTAGGG GGCCATCTCG GCCGCGGTCA GAGGGGTGAA CAGGGAGACG CTGACCAGGG 54	0
GCAAGGAGCC GGCTGAGCTC TCCTCCTCGC CCTCTTCGTC CAGGCCTCGG TCGGTCCTGT 60	0
CGTCCCTGCT GGGCAGGCTG AGCCCTGCAA GGAGGGATC 63	9

- (2) INFORMATION FOR SEQ ID NO:1132:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 448 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GGTCTGTGGT	CTTGGAGGCT	TAAATTGTAA	AATACATCCC	TTATGGAATC	CTAAATTCCT	60
			TTGTGAGCTA			120
TTCCTATCTG	GCATTTCCAT	CTTGCCCCTG	GTACACAAGT	CACTGGCCTG	GAACTCAGCC	180
TTGATTCACT	GTCCGTCTTC	ACGGATTAGC	TGTGCTGTTA	TGTTGTCTGT	GCTGCAGATT	240
GGCCCATGTG	GGAAGTCGGG	GGGGACCTGA	TTTCCTGCTT	GGAAGACTTG	GGGGACTGCC	300
GAGCATATCA	AAGTGTTTAT	AGTCACCAAG	TGAACTGCAG	CACAACCATC	TCCTCTCCAG	360
CAAGCCCTGA	AGTCAGTAGT	GCCTGCAGGT	GAAACCAACC	AGCCCTGTGT	TAGAGGAGGA	420
AAAGCGGAGA	TGACGTGGAA	GTCTCGAG				448

- (2) INFORMATION FOR SEQ ID NO:1133:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 372 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

GAATTCGGCC	TTCATGGCCT	AGGGCTATGG	CCGGAGCTTG	AGATACGCCG	CTCTGAATCT	60
TGCCGCCCTG	CACTGCCGCT	TCGGTCACTA	TCAACAGGCA	GAGCTCGCCC	TGCAGGAGGC	120
AATTAGGATT	GCCCAGGAGT	CCAACGATCA	CGTGTGTCTC	CAGCACTGTT	TGAGCTGGCT	180
TTATGTGCTG	GGGCAGAAGA	GATCCGATAG	CTATGTTCTG	CTGGAGCATT	CTGTGAAGAA	240

CAACATCTCG AG

(2) INFORMATION FOR SEQ ID NO:1134:

GGCAGTACAT TTTGGGTTAC CGAGAGCTTT TGCTGGGAAG ACGGCAAACA AGCTGATGGA

TGCCCTAAAG GACTCCGACC TCCTGCACTG GAAACACAGC CTGTCAGAGC TCATCGATAT

300

360

<b>(i)</b>	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 452 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1134:	
TTTTTAGTGC CCCATTTACA CATAGAAAAC AAGAAGGAAC TTTTATTCTG TATAACACAG CTTAGGTCCT	TTCATGGCCT AGCTGGTTCT TTTATTTTGG TGTCTCAGGG ATGTAAAAGA ATAATATAA ATGGCAAAAT CAAATTTCCC AACAATATAC AAAATAAAAT	60 120 180 240 300 360 420 452
(1)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 283 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1135:	
AGAGGAGGTA CTTATTTAAC GGTAGCCGTC TCAAGGTAAA	TTCATGGCCT AGGAGGAGGG AAGGATTGGG AGCAGTGGGG TGTGAGTGGG GGGAACCAGA TGGGGAGAAT CGAGCCAAGT TCTGGGTTGG AGGAAACTTT TGAGCTGGTG GGTTACATAT CTAATGTTGC AGGTGATGAA TACAGGCTGG TAAATCCACC GAAAGAAGTA AATGAAAGTG GTTTCTTGTA GGTCGAAAGG TGGCTGGTTT TTAGGAAACA ACTGATCCTC GAG	60 120 180 240 283
(2) INFORMA	ATION FOR SEQ ID NO:1136:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1136:	
TGGATGAAAT CATACTGCAC	TTCATGGCCT ACTGGAGACT TGTAATTAGT CTAAGCATAA TATGATTAGG ATTTTGGAGT TTGGTTTTGT TTTAAATGTA AATACTCATG AAAAGTAAAA TGTGTCCCTG GGAATATTTT TGTTATCTTT AAAATACTCA GTATTATAGG CACAGCCTTA CATTTGCCCG GTTTGACCTG GAGGCCGAAA TGAATTGTGA	60 120 180 240
	469	

264

CTTATGTCCC AGCTGGGTCT CGAG

(2) INFORMATION FOR SEO ID NO:1137:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 653 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137: GAATTCGGCC TTCATGGCCT ACCACGTTTC CTCACCTGTA AAATGGACAC TGCAGCTATG 60 TCTGCTGTTC CACATTGTTG ATAGAACTGG ATGCTGTGGT GACATTTGGG ACACTATCAT 120 GGTGCCTGGG GTGGGTGGGT GCCCAGGCCT GTGGGCTTCT GTCTTTCATC AAAGAACTTC 180 AGATCCCAGA AAATTAAGAT TCTCAAAACA TAACTGTCGG AAAGGGCTTT TGAATCCACC 240 TTGGTGGCCT CTTCCTGCCT CCAGGGCTCA TGAGATAGGC TGACTTCATA TGAAAGTTTT 300 GAGGATGAGG AAGTCTCTCT CCTCTTCAGA TACTGACCCT CTCTCTCTT ATTTCCTTGG 360 TGCCCAGAAT AGGGCTTTGG TTATCTTGAA TGAATGAATA TAAACTCACA GGTGTGATCT GAGCCACCTA AAGCCCTCTT TGGGTTCTGC TCAGCTTGAG GGCATCACCT AAAGGCCACT 480 GGCTGCATTT TCCAGGAGGT GTTTTCTAAG CTGTATCTAT ATAGGAATGG GGAGGAAAGC 540 TAAGTCATTG TAGACTGAGA GAAAGGGAAT AAGAGTCTGT TCCAGACCAG CTAGGGCTGA 600 CAAGCTTAGG CAGCTGGGGG CAGAGGGCAC TGAGAATGAG GCCCTAGCTC GAG 653 (2) INFORMATION FOR SEQ ID NO:1138: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138: GAATTCGGCC TTCATGGCCT ACAAAAGGTT CTTGATGACC ACCACAATCC TCGCTTAATC 60 AAAGATCTTC TGCAAGACCT AAGCTCTACC CTCTGCATTC TTATTAGAGG AGTAGGGAAG 120 TCTGTATTAG TGGGAAACAT CAATATTTGG ATTTGCCGAT TAGAAACTAT TCTCGCCTGG 180 CAACAACAGC TACAGGATCT TCAGATGACT AAGCAAGTGA ACAATGGCCT CACCCTCAGT 240 GACCTTCCTC TGCACATGCT GAACAACATC CTATACCGGT TCTCAGACGG ATGGGACATC 300 ATCACCATTC TCGAG (2) INFORMATION FOR SEQ ID NO:1139: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139: 60 AACTCGCAAA CTTCCAGCAT TTGTCTAAAT CTACTCAATA TATTCCAGTA CATCAGATAA 120

TGACTTGATG	TCATCCTCCT GAAAAACTCT TTTCCAGTGT ATCCTGACCT GCTCTAATTT CTTTCTGTAT CTGGTGCACA GCTGTTACCT TGGAATCTTC CCTTCATCAT GTTTCTGTAG TTTTCTCTT GCATTGGATT TTGTGCTTCC TGAATCCTCT	180 240 300 304
(2) INFORM	ATION FOR SEQ ID NO:1140:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 303 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1140:	
TTAAGATTTT TTTTAGGAAA TATTCCTTTA	AAAGAGGCCT AGGGTTTGT TTGGTTTGGT TTTAGTTTTT TGTGGGAGAA TTAAGAGATA TTTTCAGATT TTTCTGTTGT CAGTTTTGGT AATTTGTGTC ATTTCATTC ATCCAAGTTG TTGGATTATT TGGCATAAAA TTTTTCAGAA ATATCCTTCT AATGTCTGTA GAATCTAATC TGTATTGCAG TCTCTTCATA GTGTTTTTTC TATTTTTCC TGGATCAGTC AGTCTAGCTG GGGAGAACTC	60 120 180 240 300 303
(2) INFORMA	ATION FOR SEQ ID NO:1141:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1141:	
TACTCTCTCC ATGGAAGTAT CTCTGCTCCA GCTTCATTTC	AAAGAGGCCT AGTAGCTTAG TTATTGTTTA CTTTGAAGCC CTTTTGCCTC CATATATCTT CTCCTGACAG GGTGAAGTCA CCTATAGCAT TTCCTAGTGT TAATTTCTTT CTTTACTGGA AGAGCTACTA GCTTTTCTTC ATACAGTTTC GTTTCATAAG TTTCTTTTTG GCTTGTATCT GTTTAGGATC AGGTGATATG TCATGACTGA AGCCCGGCAA CATAACACTG AAATTCGAAT GGCAGTCAGC ATAAAACCGGA TCATCTCGAG	60 120 180 240 300 330
(2) INFORMA	ATION FOR SEQ ID NO:1142:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 294 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1142:	
TTCTGGGGAT AGAGAGCTTT	AAAGAGGCCT AGAGGGGAGC CTGGCCTCTG GCATATTCAT CAAGTATGAG GAGTCACTGT AATGATGTGA GCAGGGAGCC TTCCTCCCTG GGCCACCTGC CCCACCAACT TTGTACCTTG ATTGCCTTAC AAAGTTATTT GTTTACAAAC TAAAAGCCTC CTGCCCCAAA GCTTGTGGGC ACATGGGCAC ATACAGACTC	60 120 180 240

ACATACAGAC ACACACATAT ATGTACAGAC ATGTACTCTC ACACTCCAGT CGAG

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 331 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:	
GAATTCGGCC AAAGAGGCCT AGTTTTAGTT CAGAATAACA TTAATTTTGA GAGATTGAGG TAAAGAACCT TAACTAATGC TAAGGAGTTT ATTTTGATTA ACATAGGTTA TTCTGACCAC CACCTCTTCC TTCCTTAATC TCCTTAGAAT CTGACAGTCT CAAAGCTGTC ACACAAATTA GACTAATTTT GACACTTTGA AATGAAAACT TCAAGGAAGA AGTAGCCACG GACAGTTATG TTTATAATCA GTAGGTGGCA CTCTTTCCTC AGGTAGCCCC CCATTTTCAC ATGATGTGTT TGAAGGTTAA ATGCCACCAA AAGTGCTCGA G  (2) INFORMATION FOR SEQ ID NO:1144:	60 120 180 240 300 331
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 508 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:	
GAATTCGGCC AAAGAGGCCT ACTTCAGCAT GACTACTCAG TTGCCAGCTT ACGTGGCAAT TTTGCTTTTC TATGTCTCAA GAGCCAGCTG CCAGGACACT TTCACTGCAG CTGTTTATGA GCATGCAGCG ATATTGCCCA ATGCCACCCT AACACCAGTG TCTCGTGAGG AGGCTTTGGC ATTAATGAAT CGGAATCTGG ACATTTTGGA AGGAGCGATC ACATCAGCAG CAGATCAGGG TGCGCATATT ATTGTGACTC CAGAAGATGC TATTTATGGC TGGAACTTCA ACAGGGACTC TCTCTACCCA TATTTGGAGG ACATCCCAGA CCCTGAAGTA AACTGGATCC CCTGTAATAA TCGTAACAGA TTTGGCCAGA CCCCAGTACA AGAAAGACTC AGCTGCCTGG CCAAGAACAA CTCTATCTAT GTTGTGGCAA ATATTGGGGA CAAGAAGCCA TGCGATACCA GTGATCCTCA GTGTCCCCCT GATGGCCGTT CGCTCGAG	60 120 180 240 300 360 420 480 508
(2) INFORMATION FOR SEQ ID NO:1145:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 461 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:	
GAATTCGGCC AAAGAGGCCT AAATTGCTGG CGGATTTAGA CCGGTAGAAA ACCCGGGATG GTTTATTTTG ATTGAGCCCC CTCTGGGTGG CAGAGAGGAG GCTTGGGCTC TGGGCCCTTT ACGTTTGGAG AAATGGCTTT ATCAGCTCAG TTGAAAGGTT TTTCCCTCTA GCTAGTGAAA GATAAACTTG GAAATGCAGG TTTCTCCAGC GGTTGGTGGT GGGGACAGGG GTCGCCTAGG	60 120 180 240
472	•

AGCACAGGAG AGCCCCGCAA AGCGCCTGGG AGGCCCTCGA G

(2) INFORMATION FOR SEQ ID NO:1146:

GAACTTGCAG GGGCCGCGC CTCTGTTGTG CTCTTCTGGA GAGTGCACTG TTTGTGGAAC

TTTTCTAGAG TGGCAAAAAC GATCTCCACT GTCGGTGAAA GGGCAGTTCC TGAAGTCAGC

TCATGGTCCT GGCTCCCCTT CTCCCCAGCA GTGAACTGGG GGTGACTTCC TGATCTGCCC

300

360

420

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 291 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
() CECULANCE DECONTRACTOR CEO TO NO 1116	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:	
GAATTCGGCC TTCATGGCCT ACCATTTTGG ATTGATTTTT GTGTATAGTG TAAGATGAAC	60
CCAATTTCCT TCTTTAGCAT GTGGGAATTC TGTTTTTCTG TCACCCTTTT TTTTTGAGAT	120
GGGGTCTCAC TATGTTGCCC AGGTTGGCCA TGAACTCCTG AGGTCATGTG ATCCTCCTTC	180
CTCAGCCTCC TGAGTAGCTA GGACTACAGG CATGTGCCAC TGTGCCTGGC TCCAGCAACA	240
GTTGTTGAAG AGACTGTTCT TTATTTACTT ATTGTATCCT CTGTGCTCGA G	291
(A) THEODINATION FOR ADD TO NO 1110	
(2) INFORMATION FOR SEQ ID NO:1147:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 338 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(22) NOT FORTH BURNEY TOWN	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:	
GAATTCGGCC TTCATGGCCT ACCCACCTGC CCACGCCGAC TTGGGAGGAT GGTGGCCTGC	60
AGCGGCCAAG AAGCCAAAAA AAAAAATTTT TTTTTTTTCA GATACTGTGC TTGATTTTTG	120
GAGAGGGGAG AGGTGGAAAT TCCTAAATGG CTAATGCACT GTTCCCTCCA GCCCGAATGC	180
CTCCTGCCAA ACCCCTTTTC CCTGCTGCCT CTGTCCCCGC ATCCTTGTTC TCCCCTGGGT CCGAAACATT TTTTCCGAGG ATGAACAGGG GACATCTTTA GGTTTCTCAA CTCTTGCTTT	240
GGTGTTTGCC GCAGCATGGA AAACAGGCAC CCCTCGAG	300 338
	330
(2) INFORMATION FOR SEQ ID NO:1148:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 385 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
· .	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:	
SCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGAG CATGAGCAAG	60
GCAGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA	120
CACAGGATG GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACAGCAG GATTATGTCT	180
STTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG	240
IGAATGCTTC CAGCTCTTTT CCTCCAGCCC TTGGAAGAGG TGGTCCTATA ATTGTTAAGC	300
473	

ATCTAGCTAG GGTGATGAGT AGGAATAGCA ATAAGTGACA GGGAAGTTGA AGGCTGCAGG GCTCTTTGCA GGCGGCTTAC TCGAG	385
(2) INFORMATION FOR SEQ ID NO:1149:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 303 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:	
GAATTCGGCC TTCATGGCCT AGTCACATGA ATGAGAGAAT TCTAAATGCA AGAAATGTGC AAAGGCACAG AAACACAGAA GAGCATGTTG TACAACCTGG CTATAGTTTA GATTTTGTGT GTGTGCTATG AGAGTGTGCG TGTGCTGTGA GTGTGTGTTG GGGCGCACGC ACGCATTTGT AGGAGGTAGG GAGAAGAGTG CCGGCATAAC ATGAAATGAT ATTGGACCTC AAATGGTATG CTAAGATGTT TGACAATTTT ATTCTAAGCA GTGAGTTTTT AAATTTAGAC ATGCAATCTC GAG	60 120 180 240 300 303
(2) INFORMATION FOR SEQ ID NO:1150:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 419 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:	
GAATTCGGCC AAAGAGGCCT AATTGAATTG TATTGGTCTT TTTCTCTTTA ATATTTTAGG TGCTTTATTA TATATTAGGA TTATTAGTCC TTAGTTTGTG AAATAAGCTG CAAATATTT TTCCCCCAATT TTTCTTTTGT CTCTTTGCTT TATTTCTGGT GTTTATTTTT CCCCAGGTGT ACTGTTTTCT ATAGCCAAAT TATTGATCTT TTCTTTAATT GCTTTTTTGT TCACTCAAAG GAAGGTTTTC ACCACTGAGA GGTTATAAAA TAATTCACTC ATATTTTTAC TCTTTTTTT TGCTTATGTT AATTTTTTGT TTGGAACAAT CTCAAATTCA CAGAAGTGTT GTGAGTACGT TGCAAATAAC TTGTTTTTC CTTATGCATT TCAGAGTAAG TTACCAGTCC GCGCTCGAG	60 120 180 240 300 360 419
(2) INFORMATION FOR SEQ ID NO:1151:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 394 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:	
GAATTCGGCC AAAGAGGCCT AGCGGATGGA GTCTTTGACA GTGTTTTTGA TCTCCTGCAG ACGGCTGCTC AGGAAGCTGT TGACCCGATC CAGTTCCCGG TCGGGCCACT CCAAGAGCCT CTCCCTGGCA GGCCTTGGCT CCCGGCTTCC AGAAACACGA TTTGCCTGCT TTAGAGCTTC TGCTGCCAAC TGGGCCTTCT CCTTTTCCTT CTTTTTCAGC TTGTGCCGGG CCCGCTTGGC GGCCCTGGCG CTGTTGGGGA CTTTGGGCTC CGTGCTGTTG ATGAATTCCA GCAGCTCATC	60 120 180 240 300

PCT/US98/06956 WO 98/45437

CACATCTCGG TGGTCCACGG CGGGCTCCCC AGGGATCCCG CCCAGGGTGC CCCCCTTCAT GGGCAGCTCC TCTTTCCGCC TGGTCAGCCT CGAG	360 394
(2) INFORMATION FOR SEQ ID NO:1152:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 426 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:	
GAATTCGGCC AAAGAGCCTA CTGTGAATCA CGAACTGGCT GAGGGCGGCT GACCGCTTGT AGCTGTTCCG GCCATGCACC ATAAGAACCG GCCAAGATGC TTAAATTGAG TGATGGAGAA GTCTGCAGCC AACGAAGCCT GTTTCCTTC CTTTCCTTCC ACTCCCACGC CGCAGTCAGA TTCCTGAATC ATGCTGACGT CATTGCCTCC GTCCCCTACT GCACAGGTGA GCTTGCCCGT GCGCTCCTGA AGCAGGCGCA CGATCTGGC CTTCTGGGTG GGGCACATC NGCAGCAGAC TACGGCCGGG CACTGGCAGG CCAGCTCCAT GAACTCGTAC TCATAGTACT TGAGGCAAAC CTCCAGGGAG TCTCCCGAGA TGACCAGGGC ACAATCATGC TTCCTGCGGA AGGCGTTCAG CTCGAG	60 120 180 240 300 360 420 426
(2) INFORMATION FOR SEQ ID NO:1153:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 270 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:	
GAATTCGGCC AAAGAGGCCT AAGCTGATAT TTATTGGACA TTTGCACCAT GCCAAGCATT CGGCTTGGAT TATCCCATTT GTTTCTCACA GCCGGTATTT ATTGTCTGCT CCTCTGGCC AGGTGCTGTG CTCTGGGCAG GGGCACTGCA TGGGCTGCCT GCCCTGGTGG AGCTTGTGGT CTGATGGGTG AGGCTGACCC AAGCCCACCC CATTGCCAAC AGGGCCAGGG CAAGAGTACA CACAGGGGCC TCATACCATA TGTCCTCGAG	60 120 180 240 270
(2) INFORMATION FOR SEQ ID NO:1154:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 582 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:	
GAATTCGGCC AAAGAGGCCT AGCTGAAATC ATTCTGAAAA CTCAAACAGT AGACTTCAGC ACACAAGGAA AGCCAAAGGC ATTTGAGGGG GAATAAAGCC AAAAGCCTTT CACCTTATTC GTTCCAAGAA TCTCACCGCC CCCTCCTTAT CCCCCTCCAA AAATAAGCCA TTGCACACAG ACAGGCAGCA TGGCTAGCAA ACGAAAATCT ACAACTCCAT GCATGGTTCG GACATCACAA GTAGTAGAAC AAGATGTGCC CGAGGAAGTA GACAGGGCCA AAGAGAAAGG AATCGGCACA	60 120 180 240 300
475	

CCACAGCCTG	ACGIGGCCAA GGACAGIIGG GCAGCAGAAC TIGAAAACTC TICCAAAGAA	360
AACGAAGTGA	TAGAGGTGAA ATCTATGGGG GAAAGCCAGT CCAAAAAACT CCAAGGTGGT	420
TATGAGTGCA	AATACTGCCC CTACTCCACG CAAAACCTGA ACGAGTTCAC GGAGCATGTC	480
GACATGCAGC	ATCCCAACGT GATTCTCAAC CCCCTCTACG TGTGTGCAGA ATGTAACTTC	540
	AGTACGACTC CCTATCCGAC CACAGACTCG AG	582
	· · · · · · · · · · · · · · · · · · ·	
(2) INFORM	ATION FOR SEQ ID NO:1155:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 279 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	_
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1155:	•
CAATTCCCCC	TTCATGGCCT AGGATCCGTG AGGGAGACCG CATCATCCAG ATTAACGGTG	60
	GAACCGGGAA GAGGCGGTGG CCATCCTGAG CCAGGAAGAG AACACCAACA	
	GGTGGCCCGA CCTGAGAGTC AGCTGGCGAA AAGGTGGAAG GACACCAACA	120
	CCTGGATGAC TTTGGCTCTG AGAATGAGGG GGAGCTGCGT GCTCGTAAAC	180
		240
TGAAATCACC	CCCTGCCCAG CAGCCCGGAA ACACTCGAG	279
(2) INFORM	ATION FOR SEQ ID NO:1156:	
(i)	SEQUENCE CHARACTERISTICS:	
, - •	(A) LENGTH: 353 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
1221	MOVEGUE TUDE - DVA	
(11)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1156:	
GAATTCGGCC	AAAGAGGCCT ACATTGTTAA TATAATTTAA CAGAAGTTGT GAAACTAAAA	60
	TTAACTGGTA GTTCATTGTA AATGAACATA ATGAACAGAA TTTATGACTC	120
	AATGCTATCA AATAACTAAG GAATATATAT GGAATAAGTG TACATATGTA	180
ΔΑΔΤΑΤΤΩΤΤ	ACTAGAGTTA GATATGTGCC AAAGTCCATT TATCCCAAAT CCTGTCTGAA	240
	ACATTGGTAA ACATTTTGGA GTGCTTAAAA ATGCCAAAAA CAAAATGGTA	
	TGATAAAGTA AAAAAGTTAA ATGTGTGTAA AAAAGTGCTC GAG	353
	ATION FOR SEQ ID NO:1157:	
(2) INFORM	ATION FOR SEQ ID NO:II57:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 331 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
	SEQUENCE DESCRIPTION: SEQ ID NO:1157:	
(X1)	andonuce procutition: SEG ID MO:III):	
GAATTCGGCC	TTCATGGCCT ACGGTGGCCT TTGGGGCCGA AGTGGGCGTG CGGCTCGCGC	60
	CTTCCTGGTG ACGGAGCTGC TCCCCCCGTT CCAGAGACTC ATCCAGCCGG	120
	GCTCTACCGG AACCCCTACG TGGAGGCGGA GTATTTCCCC ACCAAGCCGA	180
	TGGAGAAGA TCCTCTTTCC TCCCTCCCA TCACCCCCT TCCCCCCCC	240

ACCTGTGCGT TTTCCACCCC GAGACGGCCT TTGTAGGGAC CCACTGCCCA CTCCGCTGCT

GIGCOCIOGG TICCGCCICC TAGGGCTCGA G	331
(2) INFORMATION FOR SEQ ID NO:1158:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 178 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:	
GAATTCGGCC TTCATGGCCT AAAAACTTAG ACTGACATCT AGCTTTGACA ATCATAGTAT GTTTTATTTT CCTGAGGGGG AATAACTTAT AATGCTGTTT AGTTTTGTAC TATTGGTGTG TTGGTGAATT TTTAAACTGT GTGCTAACTG CACGATTGAA TTCTAGACCT GCCTCGAG	60 120 178
(2) INFORMATION FOR SEQ ID NO:1159:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 401 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:	
GAATTCGGCC TTCATGGCCT AAGCACTTTG GGATGTTGAA GTGAGGGGAT TGCTTGAGCC CTGGAGTTCA AGACCAGGCT GGGCAATATC GCCAGACCCC ATCTCTTAAA AAAAGTAGTT CTTTACTGTT GCCTCTATTG ACTCTTGAAT GCAAGAAAGA ACATTTGCCC TTTGACTTCT AATATTATCT TATATTCTCT CTTCTCAAA AGATCAGAAG CACATGCTGT AAACATCAAT CATGATCATC TTTGTCTCC TTATCAGATT GTCAAAATTA TATCTTTTCC TATTTTCCTG CATACCTTAT CTTTTTCCTA AATTCTCAGT TCTCCAAGTT CTCAGAAATC ATAACTTCAG ACCTTGAAAT GATGACTCTG TTCCACCCCC ATCGTCTCGA G	60 120 180 240 300 360 401
(2) INFORMATION FOR SEQ ID NO:1160:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 350 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:	
GGGGGGCCAG ACACGCNTGG GGTAAGAAGG GCCTGGTGGG AGGAGTTCAC AGAGCAGACG GTGCACTGGG ACCAGGAGAG CAGAACACAG GCCATAACTA TAGGGCAGGT GGGGCAGGAA CGGGTTAAAA ACGAGATCCA AGCCAGCCAG ATCGCAGGAG GTGCGGGGGC GTCGTCCCC TTCTGTTCTC CCCCCAAGGT CACAGTGCAT GCAATAAAAT ATATATACAG GAGCTAGATC CGTCCTCTGC AGGGGCCTG AGGGTCCAGA GCTCCCTTCG GGTGGCGGA AGCCAGTGGC GCTCCCTGGC GGCCAGGCCG GGCTGGAGCC ACATGCGTCG GGGTCTCGAG  (2) INFORMATION FOR SEQ ID NO:1161:	60 120 180 240 300 350

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 597 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

GCCCCGGAGC	ATCTTAAGAG	CTGAGCGCAG	CTGACAACTA	GGGGCCGGAC	CGTCGCAGGA	60
GGCGTCCGCT	GGATACCTTC	CCCCTTCCCT	GACCTAGAGC	TCTACAGCTG	CTGCCTCGGT	120
ACTGACCGAG	GGTTCCCAGA	GCTGTCTCAC	CATTGCAAAA	ACGTTATAGC	AACAGCCTCT	180
GATTACGACA	TGGCTGAGAT	CACCAATATC	CGACCTAGCT	TTGATGTGTC	ACCGGTGGTG	240
GCCGGCCTCA	TCGGGGCCTC	TGTGCTGGTG	GTGTGTGTCT	CGGTGACCGT	CTTTGTCTGG	300
TCATGCTGCC	ACCAGCAGGC	AGAGAAGAAG	CACAAGAACC	CACCATACAA	GTTTATTCAC	360
ATGCTCAAAG	GCATCAGCAT	ATACCCAGAG	ACCCTCAGCA	ACAAGAAGAA	AATCATCAAA	420
GTGCGGAGAG	ACAAAGATGG	TCCTGGGAGG	GAAGGTGGAC	GTAGGAACCT	GTTGGTGGAC	480
		AAGCCGAGAC				540
TGTATAGACC	AATTACCCAT	CAAAATGGAC	TATGGGGAAG	AACTAAGGAA	CCTCGAG	597

- (2) INFORMATION FOR SEQ ID NO:1162:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 476 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

GAATTCGGCC	TTCATGGCCT	AGAAATAACT	TAAAATCCTG	AATCAGATGT	TTCTCCGTAC	60
ATGGCCTATC	CAGATCACCG	TAGGGTGAAG	CTCAAAGTCA	GCAAGCCTCA	CCCACATACT	120
CAGAGCTTCC	TTTCAGTGTT	GAGACCTTCT	TCCCTCTGAG	CAGATGACAA	AGGAGTTTGA	180
AACCAGCCTG	GCCAACATGG	TGAAGCCCCG	TCTCTACTAA	AAACACAAAA	ATTAGCTGAA	240
ATGGTGACTG	TAATCCCAGC	TACTCAGGAG	GCTGAGGCAG	GAGAATCGCT	TGAATCCGGG	300
AGGCGGAGGT	TGCAGTGAGC	TGAGATCGTG	CCATTTCATT	CCAGCCTGGG	CAACAGAGCA	360
AGCCATCACA	GATTTGGGAG	CAACCAAGAA	AGCCAGGGAC	AGGGTATGCT	TGGTAACCTG	420
GCAAGAGCTG	ACAAAGGGGA	AAAATAAAAC	CCCACAGAAA	GAGCAGGGAA	CTCGAG	476

- (2) INFORMATION FOR SEQ ID NO:1163:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

GAATTCGGCC	AAAGAGGCCT	AGATGAACAT	GAACCTGCGG	GAGCTGTACC	TGGCGGACAA	60
CAAGCTCAAC	GGCCTGCAGG	ACTCGGCCCA	GCTGGGTAAC	CTGCTCAAGT	TCAACTGCTC	120
CCTGCAGATC	CTGGACCTCC	GGAACAACCA	CGTGCTAGAC	TCGGGTCTGG	CCTACATCTG	180
CGAGGGCCTC	AAGGAGCAGA	GGAAGGGGCT	GGTGACCCTG	GTGCTGTGGA	ACAACCAGCT	240
CACGCACACA	GGCATGGCCT	TCCTGGGCAT	GACACTGCCG	CACACTCAGA	CCCTCCACAC	300

GCTGAACCTG GGCCACAA CATCAGCAAC CGCAGCGT CGCGGTGGCG GTGGCGGA AG	GC TGCGCCTCGG	GCTGGCCTCC	ACCAAGCTCA	CGTGCGAGGG	360 420 480 482
(2) INFORMATION FOR	SEQ ID NO:116	64:			
(A) LE (B) TY (C) ST	CHARACTERISTI ENGTH: 494 bas PPE: nucleic a PRANDEDNESS: d OPOLOGY: linea	e pairs cid ouble			
(ii) MOLECUL	E TYPE: cDNA				
(xi) SEQUENC	E DESCRIPTION:	SEQ ID NO:	1164:		
(A) LE (B) TY (C) ST	TT TGAGCAAACA CT CTTCTGGAAT CG CTGGACTTCC TT TTACATTGGC AA TACAGTCAGA CA GGCAAGTAAA CA GGGCACAGTG	AAGCTCTCAA TATCTTCTAA ACATTTGGGA TGTTTTCCTC TGGGAAGTAG CCAAAGACTTC  65: CCS: e pairs cid ouble	GTTGGTGATC GTCAACTGTG CCAGTTGGCT ACATTCCTCA CCCCTGCTGT CACAGTGCAG	CTCAGGAGTC GGTTGGGTAG GTNATCAGCT AGCAGGTACT CAAGGAGCTT TATGGTAAGT	60 120 180 240 300 360 420 480 494
(ii) MOLECUL	E TYPE: cDNA		٠		
(xi) SEQUENC	E DESCRIPTION:	SEQ ID NO:	1165:		
GAATTCGGCC TTCATGGC CAAGCAACTG CGCAGTCA GAAAAGACAA CAGCATTT CATTTTTGT TTTCTGAA TTGGGATCTT GCCTAATT	CA GTTGGGGCTG TT GCAATCACTG GA CGGCCTTTTT CT TTAGTACAAA	CTAATTTGGA GTGTATCCTT TTCTTTTTTA GCCTGGCCCT	AATCCAGTTT TACGAGAGAG TTATTATTAT	AGGCTGATTT CTAGTCATGC TTTTTTAAAT	60 120 180 240 298

- (2) INFORMATION FOR SEQ ID NO:1166:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 266 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

GAATTCGGCC TTCATGGCCT AGATAGAAAA GAATATTCCA AGTGTATGAA GTATAGAGGT 60 GGGGAAGTTC AGGGTAGAGA AGTANTAGCA GGAATAGAAT ATAGGGGGAC AGAAAAATAG

AGTGGAGCCA	GATTCAGAGA	ACTTTNAGAA	GCAGGTAAAG	AAGTTTAGGA	TTAATGGACA	180
AGTCATTGGG	TCTCCAGGTT	TCTTTGAGGG	AGAGTGATAT	CTGAGCTCTG	TTTTAGAAAG	240
ATTAATCTGA	AAGGAGGTAA	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:1167:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 499 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

TTCATGGCCT	AGGTAAATAA	TGCCAAGTTA	CTGGGGTCTA	GAAAGAAAGT	60
ATCAAGAGAG	TGTGAGTTTC	CTAAGTTTCT	TCAGCAGGGA	TGTTGGTCCT	120
GGTTTAAAAT	CACCAGGAAG	TAAGGGTGAG	GAAGAAAGTC	TGGGTCCATG	180
TGACTGATGG	TGGTGGAAGT	CCTTCCTGTG	ATGAGTTAAT	GATGCGTATT	240
ATGGGAAGTT	ATTTACATCG	ACATTAACCA	AATCTACCCT	TCATGCAGAA	300
CTTGGGCCAT	TCTCTATTAA	TGAAACCATA	CCAGGGTCAA	TATTACAGTG	360
ACACTGAAAA	TACTTCCCTG	GCTCAGGTGG	TGGCCCATGC	TACCTCCAGG	420
TGATTAATGA	TGCAATGGAG	ATAATCCTAT	TGCATCCACC	ATCAAGGAGA	480
CAACTCGAG					499
	ATCAAGAGAG GGTTTAAAAT TGACTGATGG ATGGGAAGTT CTTGGGCCAT ACACTGAAAA	ATCAAGAGAG TGTGAGTTTC GGTTTAAAAT CACCAGGAAG TGACTGATGG TGGTGGAAGT ATGGGAAGTT ATTTACATCG CTTGGGCCAT TCTCTATTAA ACACTGAAAA TACTTCCCTG TGATTAATGA TGCAATGGAG	ATCAAGAGAG TGTGAGTTTC CTAAGTTTCT GGTTTAAAAT CACCAGGAAG TAAGGGTGAG TGACTGATGG TGGTGGAAGT CCTTCCTGTG ATGGGAAGTT ATTTACATCG ACATTAACCA CTTGGGCCAT TCTCTATTAA TGAAACCATA ACACTGAAAA TACTTCCCTG GCTCAGGTGG TGATTAATGA TGCAATGAG ATAATCCTAT	ATCAAGAGAG TGTGAGTTTC CTAAGTTTCT TCAGCAGGGA GGTTTAAAAT CACCAGGAAG TAAGGGTGAG GAAGAAAGTC TGACTGATGG TGGTGGAAGT CCTTCCTGTG ATGAGTTAAT ATGGGAAGTT ATTTACATCG ACATTAACCA AATCTACCCT CTTGGGCCAT TCTCTATTAA TGAAACCATA CCAGGGTCAA ACACTGAAAA TACTTCCCTG GCTCAGGTGG TGGCCCATGC TGATTAATGA TGCAATGGAG ATAATCCTAT TGCATCCACC	TTCATGGCCT AGGTAAATAA TGCCAAGTTA CTGGGGTCTA GAAAGAAAGT ATCAAGAGAG TGTGAGTTC CTAAGTTTCT TCAGCAGGGA TGTTGGTCCT GGTTTAAAAT CACCAGGAAG TAAGGGTGAG GAAGAAAGTC TGGGTCCATG TGACTGATGG TGGGAAGT CCTTCCTGTG ATGAGTTAAT GATGCGTATT ATTGAGGCCAT TCTCTATTAA TGAAACCATA CCAGGGTCAA TATTACAGTG ACACTGAAAA TACTTCCCTG GCTCAGGTGG TGGCCCATGC TACCTCCAGG TGATTAATGA TGCAATGGAG ATAATCCTAT TGCATCCACC ATCAAGGAGA CAACTCGAG

- (2) INFORMATION FOR SEQ ID NO:1168:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 425 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

GAATTCGGCC	TTCATGGCCT	ACACAAACAA	ACCCAGAATA	CTCTATTACT	GTATTTGTGG	60
GGTACAATCC	ACTCAACTCT	ATTATGAAGC	CCAAAAAATA	AATCTGTTAA	AAACAATAAT	120
AGCTAÇACCA	ACCTGTTAAG	AGATAGGTAA	TATAAAAATA	TATAGTTTGA	GACAACTAAA	180
TCAAAATGGA	GGAGGGGATA	GAGTTCAAGA	AGTAGAATTT	TTTTGCGTGT	GCTTTTCTTG	240
GCCTTTGTTT	GCTTCTATTC	TTTTATTTGG	AATCAAAGAT	AAGTTATCAA	CTCTTTAAAA	300
TAACTTGTTA	TATGTATAAG	ATGTTTTCTG	TAAGCCTCAT	GGTAACCACA	GTACAAAAAC	360
CTATAGTACA	ATTCCTAAAA	ATAAAATACA	AAAAAATTAA	AATATACTAC	CAGAGAGCTC	420
TCGAG				•		425

- (2) INFORMATION FOR SEQ ID NO:1169:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 318 base pairs
    - (B) ·TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

TGGCCAGCCA AACACCTGTC CTAGAAGCTT	TTCATGGCCT AAAAGGTTTG ATCTTGTA GCCTTCAGAA TAGCTAAAGG CCTTCCTTT CCCTAAGCAC CTGGTGTCTC CATTGGAG CAGCCCGGAA GACAGGCTGC TCTCTCATC TTCCTGATTT TGCCACCAGC CCTACCGA CTCTCGAG	CC TTCCAGTCAG GC AGACTGCTCT GC TGGTGGCCCA	CCTGAGAGAG CAGGAGACTA AATTGAGAAA	60 120 180 240 300 318
	TION FOR SEQ ID NO:1170:  SEQUENCE CHARACTERISTICS:  (A) LENGTH: 346 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
,,	MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID N	0:1170:		
GTTTATCGAT TATTAAGGAT TAACAACATT AAAAGTTACT CAAAGATGAA (2) INFORMA	TTCATGGCCT ACATTGGTCG TTTTATTGACTGGACTTCT CTTTACCATT CTACAAGCCTTGGAATCTA TTGATACTGA ATTTTATACGAGACTGGAATGTGG GCTTAGAAAT GTACTTTTTCACATGACC TGAAGTTGGG AGGTTCCACTTATATTGGTT TAATGACAGA ACGGCGTTGATATTGGTT TAATGACAGA ACGGCGTTGATATATGGTT TAATGACAGA ACGGCGTTGAGACTGAGACGAGAC	ET ATGTTAAGTA AC TCCCTTATCT CT GTTGACATGG AT ATTCTGGTGA	AAAAACTTAC GGATAAGAGA AGATTTTGGG	60 120 180 240 300 346
	MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID N	0:1171:		
TGGACGTTTT GTATGCACTG ATAATAGGAN	TTCATGGCCT ACACTTTATT CCCTTTTA GTTTCATGCA GATTTAGTTA GCAACTCG, AAGCCAAATT CTCAGTAACT CAGCTTTT TCCAGAGCAG TTAACAAATT GATACAAG	AT TATCAAATGG GN TAGTCATATG	TAGAATATCT AGGATGATGA	60 120 180 240
	TION FOR SEQ ID NO:1172:  SEQUENCE CHARACTERISTICS:  (A) LENGTH: 277 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
	MOLECULE TYPE: cDNA			
GAATTCGGCC NTACTCTCCT AAAAATGCTC	SEQUENCE DESCRIPTION: SEQ ID I TTCATGGCCT AGTTTCNTTT TTGTATCT TCTAGCTTTC TGCTTACCGC ACACTGGA ATGAACCCAA TCCGGAGAAG GTTCCAGC CTCCTCTTGA CAGCGAGGAC AGGAGGGG	CT ACTGATATCA TA ACACACACAT AG GTCCCCCACC	ACACACCCAC CTCCCCTCCT	120 180

CCCGCCGGCT CTCCCCCCAC CCCACCCCCA TCTCGAG

(2) INFORMATION FOR SEQ ID NO:1173:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 258 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:	
GAATTCGGCC TTCATGGCCT AGAAAAGTCT AGAAAATAGC TTAAATAACA AACACGTGTG GATTTGTTAG ACCAAGAGCA AGGGAGACCA TTTAATGCAG TTATTTAACA ATATTTAGTA CTTTCCTTTA CCTTGTCTGC TGTGCCATCA TTCATGCCTG TCAGTGTTAA AAATCCCCAA ATTTCCCAAA CAGATTTCA TTTCACTTCC GTCAACTTTT AAATTAAAGT TTTTAAATTC CTGTCCCCAC TCCTCGAG	60 120 180 240 258
(2) INFORMATION FOR SEQ ID NO:1174:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 334 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:	
GAÀAGTTGCT TTTGATGTCA AAATGGAAAA TGAAAAGTTA GTTTTAGCAT GTGAAGATGT GAGGCATCAG TTAGAAGAAT GTCTTGCTGG TAACAATCAG CTTTCTCTGG AAAAAAACAC TATTGTGGAG ACTCTAAAAA TGGAAAAAGG AGAGATAGAG GCAGAATTGT GTTGGGCTAA AAAGAGGCTG TTGGAAGAAG CAAACAAGTA TGAGAAAAACC ATTGAAGAAT GTCTTGCTGG TAACAATCAG CTTTCTCTGG AAAAAAACAC TATTGTGGAG ACTCTAAAAA TGGAAAAAGG AGAGATAGAG GCAGAATTGT GTCGGCCACT CGAG	60 120 180 240 300 334
(2) INFORMATION FOR SEQ ID NO:1175:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 403 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:	
GAATTCGGCC TTCATGGCCT AGTGCTTGAA CTCACGCATC TGTTTTACCT GCATCTGCAG GCGATGGGGC AGGGGCCACG GAAAGAGTCT GAGGGCTGCT TGGTGTAGTC AGGTTGTGTC CAGGCATGCG GAGCTGTAG TGCCTGCAGG AGAGACACCC AGGAGGAGTT TTTACATTTT GGTCTAAAAA GCTCTTGGAT TCATCTCATC TCATGGAATG ATCCTGTCGG ATGACGCTGA CGTGATTGCT TCAGACTTAG AGGTGAATAA ATTGAGGTCC AGAGAGGTCA CAGTCACGAA GCTCATGGTA GACTGAGGCC ACTAAACACC CGTCTCCTGA TTTTCAGTGG CGTCCTCATT TGCATACACC TGGGCCATCT TGGTTTTTGC AAGAAAACTC GAG	60 120 180 240 300 360 403

- (2) INFORMATION FOR SEQ ID NO:1176:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 590 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

GAATTCGGCC	TTCATGGCCT	AGGTACCTTG	AACATGGCTG	TAAATTAATC	TTTAACTGCC	60
TTGGTGGAGT	CTTCCTGATT	TATTGAAGAG	AATAATCACG	AAAATAATTT	TTGTTTGTTT	120
TTTGAGACGG	AGTCTCGCTC	TGTCAACCAG	GCTGGAGTGC	AGTGCCACGA	TCTCGGCTCA	180
CTGCAGCCTC	TGCCTCCCAG	GTTCAAGTGA	TTCTCCTGAT	TGAGCCTCCT	GAATAGCTGG	240
GATTATAGGT	GTGCACTACC	ATGACCAGCT	AATTTTTGTA	TTTTTAGTAG	AGATGGTGTT	300
TCACCATGTT	GGACCGGGCT	GGTCTCGAAC	TCCTGACCTC	AGGTGATCTG	CCCTCCTCAG	360
CTTCCCAAAG	TGTTGGGATT	ACAGGCATGA	GCCACCGCAC	CTGACATAAA	TATTTAATGT	420
AATACCGTGT	AAGACTTTTC	CATTGGGTTT	TGAGAAACAC	GTTAATGAGA	GAAATTGCTT	480
AACATTGGAG	AGGATTGCAG	AGAATATTGA	CTAATATGGT	GGGGTGAGGA	GGAACAACAT	540
CAATTAAGAT	TCAGATTTAT	TATTTAAAAA	AACTAAAAGG	CGGCCTCGAG		590

- (2) INFORMATION FOR SEQ ID NO:1177:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 562 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

CTCGAGGTAG	CCACAGTCCT	GATCCTAGTG	ACAAATGGGG	GCATGTGTCT	ACATCCGGGT	60
CGGCGGAGGG	CTCATTTCAT	CTGGCCTGGG T	GGGAAATGAG	TATTAATTTG	TTTACACAGA	120
CGTAAACACA	GCCCAAAACG	CATCAGCACG	TTGACTCAAA	CGCCCGCAAC	GCCAGGGCAA	180
AGGCAATTTG	GTTAACAGGG	GGAAGCGAAC	AGACGGAGAC	GCCTGGAGAC	CCAGGTGCCA	240
CAACCCGGTT	AATCGCGGTG	CAAATAAGGG	CAAGTCCCCT	CCCCTTGTCC	GTGTGGTCTT	300
GACAACGACA	CTAGTTCATT	CTACTAACAA	GGCGGGCGGG	GGGTCAGATG	GGCCACACAC	360
				TGCTGTGCTA		420
AGACGCGTTC	CCCATTCGGA	AGCCGCAGGA	AAGCGCGGCG	AGAGCGGGTT	AGCCCTCGGA	480
GCGGCTAAGA	GCCTCGGAAT	AGCGCAGAGG	AAGTCCCCAC	CCCTCTCGGG	GCTGGGAGCC	540
CTAGGCCATG	AAGGCCGAAT	TC				562

- (2) INFORMATION FOR SEQ ID NO:1178:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 339 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

TTCTCCACAC TTCCTTCCCA AGATCCCGGC TAACTCGAG

(2) INFORMATION FOR SEQ ID NO:1179:

TGGAAGCAGG GAGCAGAGTG GGGAAAACAG CAGTCTTATG GGACTGAGTC CTCAATCTGT

GTGATCTGAC TCTATCTGCA AGGTAGTGTT GGAAGTGAAC AGGGTTGGAG AATGCCCAGC

TGGTGTCCAC CGCAGAATTG ATTTCATGTT TGGTATGCAG GGACCCCCCA CTCCACACTT

AGTCACAGAA ATCTGTGTTG ATTGTTGTGG CATGAAAGCA GGGAAAAATA GTTTGTTTTT

120

180

240

300

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 353 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:	
GAATTCGGCC TTCATGGCCT ACTCACCGGA GAAAAGAAGT TTCNGAAGAA AACCACAACC ATGCCAATGA ACGAATGCTA TTTCATGGGT CTCCTTTTGT GAATGCAATT ATCCACAAAG GCTTTGATGA AAGGCATGCG TACATAGGTG GTATGTTTGG AGCTGGCATT TATTTTGCTG AAAACTCTTC CAAAAGCAAT CAATATGTAT ATGGAATTG AGGAGGTACT GGGTGTCCAG TTCACAAAGA CAGATCTTGT TACATTTGCC ACAGGCAGCT GCTCTTTTGC CGGGTAACCT 1GGGGAAAGTC TTTCCTGCAG TTCAGTGCAA TGAAAATGGC ACATCTCCTC GAG 353	)
(2) INFORMATION FOR SEQ ID NO:1180:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 296 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:	
GAATTCGGCC AAAGAGGCCT ACAGAGTGCT GTGCTTAAGT TTTACTTCTT TCCACCTTTA  AATCTCTGAT AAGTTTCTTT TTATCTAAAG GTTCCACTTT GTTCATTACT TTTTGTTTCC  TTATTATTGA TTTGTTCGAG AACCTGAGTT TCTTGACCTG TGTGATTTTG TACCACCTGG  ACTTTCTGAC TGTGTTTGCC CAGGCTGGAG AGCAGTGGTG GGATCATAGC TTACTGGACT  CAAGCCATCC TCCCGCCTCA GCCTCCCAAG TAACTGGGAC TATGGGCCACA CTCGAG  296	)
(2) INFORMATION FOR SEQ ID NO:1181:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 277 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:	
GAATTCGGCC TTCATGGCCT ACTTGAGTTG TACATTAGAT CTTTAAACTT GTTAGTCCTA CATATCTGCT ATTTTTATC CTTTGACCTA CATTTTCCCA TTTCCTCCCA GTGTTCTCTC CCCAGGTAAT CATTGTTTTA TTCCCTTTCT CTGTAAATTT GACTTTTTT TTTGGATTCC ACATATAAGT GAGATCATGA TCATGCGGTA TTTTTCTTTC TGTGTCTGGC TTATTTCACA  240	0
484	

277

TAGTATTATG TCCTCCAAGT CTACCCACGA ACTCGAG

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 192 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:	
SAATTCGGCC TTCATGGCCT AGAGATACTG GCTGGCAATT CTTGGCGTTC CTTGGCTTGT AGCTGTAAGA TGCGCTCTAA TATCAGTCTC TGTTGTCATT TGCCTTTTCT CTGTGTCTGT GTTCAAATGT CCTTTTTTT TTTTTTTTA GGGAGTCTTG CTCTGTTGCC CACTCAAACT GCTGGGCTCG AG	60 120 180 192
(2) INFORMATION FOR SEQ ID NO:1183:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 296 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	`
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:	
GAATTCNGCC AAAGAGGCCT AGTAAATAGT TGTTCTGTTA CATTGTTTAG AGAATAATGA CAAGAACAAA AATCTGTGTG TTCAGTATAG ACACAACCAT CCTTTTCTTT TTTTTTTTT TGAGACAGAG TCTCGCTCTT GTTGCCCAGG CTGGAGTGCA AGGGTGCGAT CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCAAT TCTCCTGCCT CAGCCCCCCG AGTAGCTGGG ATCACAGGCA TGTGCCACCA CGCCCGGCTC TTTTTGTATT TTTAGTAGAA CTCGAG	60 120 180 240 296
(2) INFORMATION FOR SEQ ID NO:1184:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 234 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:	
GAATTCGGAC TACTACAGGT GATACTACAG TGACTACTAC AGTAATTCGG ACTACTACAG GTGGCTAATT CGGATTACTA CAGGTGGACA TAATTCGGAC TACTACAGGT AATTCGGACT ACTACAGGTG AGCTAATTCG GACTACTACA GGTGGACATA ATTCGGACTA CTACAGGTGC ACCTGTAGTG GAGAACATTT AGCAATGATA AAGCCGCTGC TGATCCTTCT CGAG	60 120 180 234
(2) INFORMATION FOR SEQ ID NO:1185:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 300 base pairs  (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

GAATTCGGCC	AAAGAGGCCT	AGAACAGTTT	AGAAACAATT	TCCCTGCCTT	TGCTTTGGGT	. 60
TCCCTGTGAT	TGTTCTCCAC	ACTGTTTTCC	TGGCTCTATC	TGTCTCCCTT	GCCACGGCCA	120
CTCAAGCCTA	GCTGCCCAAC	AGCTCCTTCC	CTGAAGAACC	CCGGCCTTCA	GGCTTGACAG	180
GTGATCTCAT	CCCTCTTCTT	TTCCTCCAGG	TTGTTGTAGA	CTTCCACCTT	CCCTTCTTCT	240
CCTGGTCCTT	TCCCCTTTCT	AGTGCCAATG	TGGGCCACGC	TTTCATCCCA	CCTACTCGAG	300

PCT/US98/06956

- (2) INFORMATION FOR SEQ ID NO:1186:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 324 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

GAATTCGGCC	TTCATGGCCT	AGTGATGAGC	CCTCCTCTTC	AGCTAGGAAA	ATGACGGTGT	60
TCAGAAAGTT	AAAACTTCTT	CGCTGGAAGG	ATTTCATCTT	AAAGTTGGGA	GACTGGAAGA	120
AATTAAAGTG	TTCTAAATGG	AAGAGCATTC	ACCACATGTG	TTCTGTTTTG	GGTTGACATT	180
TAGCTTTTGT	TTTTATTTTA	GAAACGGAAG	ACTCTGGTAG	CAGTCCTTGA	AATCTTGATG	240
CCATTGCTAT	TTTCTGCATT	GTATTGTATC	TTCGTTTTAG	TAGTGCTCCA	ATAAAAAGAC	300
CTGCTACTAG	CTGCAAAACT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:1187:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

GAATTCGGCC	TTCATGGCCT	AGTACGTTGC	TGAAAAGAAG	TTTATTGCTA	TTTTCTTATT	60
TTATTATACA	AAACTAGATT	TGCTTAAAAC	ATTTCCCAGT	CTCTTTAAAG	GAATGCTAGT	120
TAGTGGGAGG	CCACAGCTAG	TAAATTACCC	TCAGTAGTGG	TTTCAAGTAG	TCCATAACTA	180
TAAAAATCGT	TACGGCCAGG	ATATGCCGGA	ACAGAACACT	CCCCACTGGG	GTCCTCAGCC	240
TTGGATGTCA	GCTCGGCCCC	TCAAGGGGTC	CCTACACCTG	GAAGCTGATT	CCACTCATCA	300
GTCTCGAG					•	308

- (2) INFORMATION FOR SEQ ID NO:1188:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 251 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

GAATTCGGCC	TTCATGGCCT	AGAATGAAGA	AGGTTCCCAA	GAAGTTAGAG	GAGATTCCCC	60
CAGCCTCTCC	GGAGATGGCA	CAGATGAGGA	AGCAGTGCCT	GGACTATCAT	TACCAGGAGA	120
TGCAGGCTCT	GAAGGAGGTC	TTCAAGGAGT	ATTTGATTGA	ACTGTTTTTC	TTGCAACACT	180
TTCAAGGGAA	CATGATGGAT	TTCTTAGCTT	TCAAGAAGAA	ACATTATGCC	CCATTACAAG	240
CACCACTCGA	G					251

- (2) INFORMATION FOR SEQ ID NO:1189:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 359 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

GAATTCGGCC	TTCATGGCCT	AAGGAGTTGG	AAATTGTGCA	CAAAGAAAGG	TGGTGAATAA	60
GTAAAGTCGT	AAATTCAAGA	CCACAACAGA	AAGCTTCACT	GCAGACACTG	GACTTGAACC	120
ACCATTGAAA	ACAGTCAGGA	TTTGGAGATG	ATAATTAGGA	GGATGTGTAT	TCTAGCTGTG	180
GAATTTATTG	TGGGCAAGCA	TAGGAATGAG	AAAGTACAAT	GAAAAAATGT	AAGTAGACCC	240
ACCAAGTTAG	AGAAGAAGGT	CCTGGTTAAG	AAAAATGAAA	GATTTTTTTG	AACAACAGAT	300
TAATGTGATG	AAATAGATGT	TCAAGAGTGA	AGATAAGTTG	AAGATAGGGA	CCCCTCGAG	359

- (2) INFORMATION FOR SEQ ID NO:1190:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 245 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

GTTGTTAGGC	TGGTGTTGTT	ATGTTGCTGT	TGTTATGCTG	GTCGTGCTGC	TCCATGTTCT	60
CCAGGTGTTC	TTCCCTTTTA	TCGTCACAGT	TACCCCGTAC	ACCTGACAAC	TGGACATCTG	120
CGCCTGGGGT	CTTCAGCCTA	AACACACCTA	AACCCTCCAC	CAAACCCCTC	TGCTTCCGCC	180
TCCCCGTGTC	TGTGAGCGCC	TCCACTGCCC	ATCCCTCTGC	TCAGGCCCCA	TTTCCAGGGC	240
TCGAG						245

- (2) INFORMATION FOR SEQ ID NO:1191:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 257 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

GAATTCGGCC TTCATGGCCT AGTCTCAAAA AAAAAAAAA AAAATAGTGT TCAGCAAGGT	60
TGAAGCATAA AAGGTTAATA GCCAGAATCA TTTATCAATT GTATTTCTAT ACATCTACAA	120
GACACAATCT GAAAATGAAA TTAGAGAAAC AATTTCACTG GGCAACAAGA GCAAAACTTC	180
ATCTCAAAAT AATCATCATC ATCATCATCA TCATCATCAT CATCATCTAC AATGTCATTT	240
CCCATCCAAC GCTCGAG	257
(2) INFORMATION FOR SEQ ID NO:1192:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 748 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(11) MOLECOLE 11PE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:	
·	
GAATTCGGCC TTCATGGCCT AAGGACATGG CAGAGTTCCT GCTAAAAGAG AAGACAGTTA	60
TTTAAGGAGG TTTGAGATTC AAGGGCTTTT TTAATTTTAA AATTAACCAT GGTAGAAACC	120
TGTGTGTTAA TATGCTGAGG GAAGTTGCCA ATAGTGAGAT GAAAGATCTA GGCAAGGGGA	180
TAGCAAGGTG ACTGCACCAG ATACCTGGAT CTGGGCAGGA ATAAACCTCA ACAGTGATCA	240
TGTTGACCTT GAGTGACAGG GTATAATGTT TGGGAAGGTG CTTTGTAAAC TATAAGGGGC	300
AATACAAACA TGTAGTACAC CTTCTCTGAG ATCCGGGAAA GGACAACCTG AGCATAGGTT	360
GGGGCTGGTC ATAGGCCACT CTCCCCTACT GTTTCTCTAG AGTGTGTGTA GTCCCTAGCA	420
AGTCTCAGAT GCCTCGACCT TCATGGCCTA GAGAGTTCTC ATCAGAACAG GAAGGCAGTG	480
ATGATCCATT GCATGGGCAG GATTGTTCTA CGAAGACGAA GATCTCCGGA AAGTGAAGAA	540
GACCCGGAGG AAACTAACCT CAACCTCTGC CATCACAAGG CAACCTAACA TCAAACAGAA	600
GTTTGTGGCC CTCCTGAAGC GGTTTAAAGT TTCAGATGAG GTGGGCTTTG GGCTGGAGCA	660
TGTGTCCCGC GAGCAGATCC GGGAAGTGGA AGAGGACTTG GATGAATTGT ATGACAGTCT	720
GGAGATGTAC AACCCCAGTC GACTCGAG	748
(2) INFORMATION FOR SEQ ID NO:1193:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 227 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
• •	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:	
•	
GAATTGCGAA CATGGCAGCG CGTTGGCGGT TTTGGTGTGT CTCTGTGACC ATGGTGGTGG	60
CGCTGCTCAT CGTTTGCGAC GTTCCCTCAG CCTCTGCCCA AAGAAAGAAG GAGATGGTGT	120
TATCTGAAAA GGTTAGTCAG CTGATGGAAT GGACTAACAA AAGACCTGTA ATAAGAATGA	180
ATGGAGACAA GTTCCGTCGC CTTGTGAAAG CCCCACCTAA TCTCGAG	227
(2) INFORMATION FOR SEQ ID NO:1194:	
12) INFORMATION FOR DEQ ID NO.1134;	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 258 base pairs
    (B) TYPE: nucleic acid

  - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

GAATTCGGCC	TTCATGGCCT	AGTATATATA	TAAAATACTG	AGGATTTAGG	GCTGATGTAT	60
AAAATAAAA	TACTGATAAC	TTTTTTCCTT	TCTTTTTCTT	TTTTTTTGA	GATAGTGTCA	120
TGCTCTGTTG	CCCAGGCTGG	AGTACAGTGG	CACCAAACCG	CTAACTGCAG	CCTTGCCCTC	180
CCAGGCTCAA	GCAATCCTCC	TGCCTCAGCA	CCCTCAATAA	CTGGGACCAC	AATTGCATGC	240
CACCAAACGC	ACCTCGAG					258
(2) INFORM	ATION FOR SE	EQ ID NO:119	95:			
(i)	(i) SEQUENCE CHARACTERISTICS:					
•	-					

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

CARPPOCECC	THEOREGICA	יייייייייייייייייייייייייייייייייייייי	CATTTCCTGG	ACCCTCAACA	TCTCTCCACC	60
TGTCTGTGGC	CAATGTTAAG	CCTACGACTT	TAGATGAGCT	GGCATAAATC	TTGGGAGAGT	. 120
TTTCTTGTCT	GTGTTCCCTC	TGAATTTCTC	TGTGCTGTTA	GAGGCAGGGA	CAGAAGAGAA	180
CCAGCATGGC	AGTGCTGGGC	TCAGGGTGAT	GCCTGCCTGC	CAGCACAGCG	GTTCTTGTCC	240
CTGTCCCACA	TTGCTTCTTG	GAAGCCTTTT	TACAGCCTCA	ATCATCTTGC	TTTTTCTACC	300
GCAGCTATCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:1196:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 385 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

GAATTCGGCC	TTCATGCGGG	GACTTCCACT	CTTTCTCGTT	TTCTCGGAGC	TCCGCCTCCA	60
GCTCCTCTAT	CTTCCTCTTC	AGCTGCGTGT	TCTTCTCCTC	TCTGTGGATC	TCACGGCCTC	120
TTCCTCTGCT	CCACGCTGGC	CACCGACTCC	TGCAGCGCCG	TGGGCAGCCG	GGCGTCGCTC	180
TCCCGCCGGG	TCTGCAGCTC	CATCTCCCAC	CTCTTCCCGT	GGGCAGCTCT	CTGCGTCGAG	240
GCCGCCTTCA	GCTTGTGGTT	CCCAGACTGC	AGGTGCGTGT	CAGCTGCAGC	GGCCTGAGAG	300
GCCTTTCATC	GTCCGTCCCG	TTGACACTGG	ATGCCGGAGT	AGAAGATGGG	GCTCCATGCC	360
CGGATTCTCG	GGATTATTAC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:1197:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 256 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

GAATTTGCAG TGAACCGAGA TTGTGCCATT GCACTCCAGC CTGGGCAAAA GAGCAAGACT

CCATTTCAAA	AAAAAATCTT	AAAAATACGA	AGTTTTTCAT	TTTTCTTAAA	TTTTCATTGT	120
GACTACTTTA	GTAGACTTGC	CAGTAATAAG	CCAGTTACCG	CTTGAATCTC	AGTTTCTTTA	180
TCTGGAAAGT	GGTCATTATT	TATCTGCTGT	CCCCTTACCT	AGAGGGAATC	AAATGCGTTT	240
GATACAGGTT	CTCGAG				-	256

- (2) INFORMATION FOR SEQ ID NO:1198:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 446 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

GAATTCGGCC TTCATGGCCT	AGAGAGCCCA	TCTCCATCTG	CCAGCCTGGA	AGCAGCCATG	60
GCAAATGGGA TGTGTCCCAC	TGCCCCCGTT	TGGTGCCACA	GTTGGGTTTA	TTCTCACAGC	120
TGCAAACCCA CGTGCTGGGC	TGCACAGCTG	CCTGAACGAA	GCTGGAGCGT	GCAGAACAAA	180
CTGCATGGAA TGTCACGTGG	GGTTTTCCAC	TCTCGCCCAC	AGTGAGTTGG	CAATGCCTGG	240
CCACGTGTGC TCTGTGGTCT	TTGAACTTGA	TCTGGGAGGA	CAGAANTTCA	AAAGGAAGAT	300
GAAGGCCCCA GCAAGGGAGG	TATTCCTGTC	TTGAGCAGAA	GGTAAAGGTA	GAAGGTGCAG	360
ATTAGGTACT GGGAATAGTC	ATGGTTTGGT	TTGAATGGAG	TAGAAGATTC	CAGAGGAAGA	420
GCAGTGGGGC ACAGTGGCTC	CTCGAG				446

- . (2) INFORMATION FOR SEQ ID NO:1199:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 369 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

GAATTCGCCT	TCATGGCCTA	AATTGTAGCT	AGGAAAATAA	TATATGTCTT	AGTTTAAGAA	60
CTCATACTCT	GGAATCAACT	CATTGCACTT	TCCTATATGT	TTGGCCATGG	GCAAAGCACA	120
TAACCTCTTA	ATCAATTGGC	TCGTCTCCAA	GGTGAGGATA	GTTATACTTA	ATCCTCTTTA	180
GGAGTGAGAA	TAAAAATTAA	ATATGTGTGT	AGCATAGTGT	CTACAATGTT	AGAGGTATTT	240
GAAAAGTGAT	AGTTTATTTT	TTGGAATTAT	TTAGCATTAT	TAAAAACAAG	GGGGAGCACA	300 .
CGGTGGCACG	TTTCTGGTCC	CAGCTACTTG	GGAAGCTGAG	GTAGTAGGAT	CGCTTGAGAT	360
CCGCTCGAG						369

- (2) INFORMATION FOR SEQ ID NO:1200:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 483 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

AGGACCACGG AGGGAGGCTC GTCATTGGAG GAGTAAGTTA AGACTATCCT	GGAGCAACTA GTGCAAAGCC CCTGAGACAC AACTGCACCT ATCCAGATTA AGGAAGCCAC TGTAGGAGCA CAAAAAAAGT AGGAGATGAA CAGAGAGGTG CGTAGGTCCT AGTATGCACT TTGGCATTTA TTTACTGATT GAGATGGCAG GATTCGGAGC AGAGGAAGGA TATAATCTGA CATTTTAGCA GGATCCCTTT GCTGCGTAGA CCTAAGATGA ACAAGGACAG CCACAGCAAG ACCTGTAAGG TGTAATCCAG GCAACAGATG ATGGCAGCTT GGACCAGGGT AGTAGCAGTG GAAGTGGTTG AAATCTGGAT ATATTTTGAA GATGGAGCCC ATGGGGTCTC	120 180 240 300 360 420 480
(2) INFORMA	ATION FOR SEQ ID NO:1201:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 192 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1201:	
TATATTCATT	TTGCCACTTG AAGTGTACAA ATTCAGTGAC TTTTAGTAAA TTCACAGTTA AGGATATTCA GAGTTATATA TTCATCACCA CAGTCACTCT TAGAACATTT AAAAAGAAAC CATGCACTCC TTAGCCATCA CTCCTAACCC AACTCTCCCT AG	60 120 180 192
(2) INFORMA	ATION FOR SEQ ID NO:1202:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 281 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	٠
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1202:	
ACTCTTAATT TTAAGGGTAA TCAGAAGAAA TGNGTGCAGT	TTCATGGCCT ACTTTAAACA TGTGGTCTTA CTGCCTGCAA ACACATACAG TTTATTTACA TAGATGTAAA TATACACATA TATTACTCTA AAGATAAACC GAAAATTATA AAGTATGTGT GTTTNTGTGA ATATGAATTT GTACCTATAT AGAGCAATAT TGGCACAAAA CAAATCATCT TAATAAGGTA ACTAATTGGN GGCTCACGCC TGTAATCGCA TCACACTCGA G	60 120 180 240 281
(2) INFORMA	ATION FOR SEQ ID NO:1203:	
(i) <sub>.</sub>	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 328 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA -	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1203:	
	TTCATGGCCT AGTGATCTAC TTAGGTAGCT CCTGGAAAGC AAAGGAGAGA TGTACAGACT TTGTTTATGA GGAAAGCTAT ATAAGGATTA TAAGAACTGA	60 120

TAACTAGCCT	GGGACGTTTT AGCCATGTAG TTTCTTTTTA TTCCTCTTTG ATACCCTG TAGAAACACA AGTAAAGCTC CCAAAATTTC ATTTTCTACA TATTTTAT TTCTAGACCT GCCTCGAG	
(2) INFORMA	ATION FOR SEQ ID NO:1204:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 307 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1204:	
TTCNAAACAA TAATGATTAT CACTTGACAT	TTCATGGCNT AGGTCCTAAA AAGAGTAAAA GGTGAAAACA CTAAGTGA AAGAAAAAGA TGAAAAATAA GAACCTTGGT TAAAGAGCAG TCGAAATA AGCTATGATT TATATAGCAC TTNTTACAAG AAGCCAGGCG CTGTTTTA ACTTATTTGC TCATTTCATA ATTGTAACAA CCCTATCAGA TAGGTACT CTTTACAGAG GAGAAACTGA GGCACAGAAT TTTAAGTGAT TTGGCCGG	AG 120 AA 180 'AT 240
(2) INFORMA	ATION FOR SEQ ID NO:1205:	
, (i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 425 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1205:	
CTGCTGACTT CTTTGTATCT AGGCTATTTC AAAAAAAAAG ATATCTGTGG	TTCATGGCCT AAAAAAAAT GTAGTCTAGA AAGAGACTAG GAATAGAA GTTCTTATAC CAAGAGCTGG AGGCATAAAC AGTTTTAATA AAAAAGAA TTTGATGTAA CTTCCCTTTA GAGATTCTGT TTCCCCTGTC TTAAATTG TGATTGCTGT TTAAATAATT GGTAGTTACT ATTTGAGTCA NGCTTCTT ATATAAAAAT TCGCCAGCTC AGCTTTCATT TAATTAGTAT CAAAGAAA CAGTGAACAT TAGTAGCTTG TTCCAGGGTT TATTGTAGGT TTGTTCAA CATCTTGGCA CTTAGGTTCT TGGAATACAG AGGTGGATAA GGTTTGCC	TA 120 TC 180 TAA 240 TG 300 GT 360
(2) INFORM	ATION FOR SEQ ID NO:1206:	
(i)·	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 504 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1206:	
TTCCAAAATG	TTCATGGCCT AAGACCAGCA CCATCGTGAG CAAGATTCCT GCTGCGCTGAAAAGCATC ACAACTAAAT ACCTAATATC CTACCAAACA AACCACACCCTACTTCAG TCCCAGGAGA AGGAATCCAT GAATGGGCTG AGGTTCCC	TC 120

GGTAGGTTGT GGATGTCTTT CTCTAGAGGG GTCCCACACC TGGAAAAGAG GACACCCAGC	240
CCGNGGGATG AGGGAAGCTG GGCAAGGGAG AAAGTTGTTG AGTCACACTG GGGACCCCAG	300
ATGTAGTGAG CTCAGCAAGA AAAGCCAGGT CCAGAGAGAG TCGCACAGAA TTCCTGACTC	360
ACAGCGCCCC TCGGTCCACA GTGGAGAGGA GGAGGAGGAG GAGCAGAAGG AGGGGGGAGGA	420
GCTGCAGGAG GAGGAGGATT TGAAAGCGCT TTGGCCTTGT GTTATGTTTT GCTTCTTTTC TGTGCCCCCC TCTAGGCCAT GAAG	480
IGIGCCCCC ICIAGGCCAI GAAG	504
(2) INFORMATION FOR SEQ ID NO:1207:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 242 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:	
GAAATTTTTC AGTAACTCAG TGTCTTTAAC TAATAATTTA ATCATTCTAG TAAGAAAACA	60
TGCTTTGTAT GATTTTAGTC TTTACATTTA TTAATTTATG TAAATTAATA TGTGGGTTTT	120
ATGATCACCC ACGACATTGT CCTAACTTGT CGACTGTTCT GTGTGCTCTT TTAAAGAAGG	180
TAGTCTGTTG GCCGGGTGCG GTGGCTTACG CCTATAATCC CAGCACTTCG GACAGGCTCG	240
AG	242
(2) INFORMATION FOR SEQ ID NO:1208:	
•	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 152 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
this grounded broadstand and the second	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:	
GTAGAATTGT ACAGTGCTTA TGAGTTATGC ATGTGTTCCT GGTCTTTGTT CTAGGATTTT	60
TTTTTTTTTT TGATTGCTGC TCCAGTTGCC TTACTTACTT TGACATTGGA GTTGACCACA	120
TGATGGTGTT CCACACTTCC CCTAGGCTCG AG	152
(2) INFORMATION FOR SEQ ID NO:1209:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 317 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:	
GAATTCGGCC TTCATGGCCT ACTACCCCTT TATCATTCAC TAACGTGAAT GTGGTGCTAA	
TTTTTCCAGT CCATATCTTT GAACTTTTTG TAATATATGC ACATCAATAA GCAATCGAGT	120
TTTATCTATT CTAATTGTTT TAATGTACAA CTTTATGGGT ACATGTGCAA TTTTGTTTCT	180
TGCATGGTGG CCAAATCAGG GCTTTTAGAA CATCCAACAT GCGAATAATG TACATTGTAC	240
CCATTAACTA ATTTCTCAAT ACTTCTGAGT CTTCCTTGTC TATGATTCCA CTCTCTACAT	300
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- (2) INFORMATION FOR SEO ID NO:1210:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 282 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

GACAGAT	TTC	ATTACCTTGA	AGTTCACTGC	ACTGAACAAT	TCTCACTCTG	GATGTATTCC	60
TGCTCTA	GGA	TGTGAATTTA	GACTTTTGTA	ATAGAGTGGG	CTTTGAGAAA	TAGCTTTTCT	120
GCTCATT	TTA	GTTTCATGAT	GACTGCATGG	AATGTTTTGC	TTCACGCTTA	TGCATTGAGT	180
TTTATCA	AGC	ATTAAGCAGT	TGGCCGAAAC	AGGTAATACT	TGAACATTCA	GTCCAAGAAA	240
AACAAAA	TGG	ATTTGAACAT	ACGTAGAATC	AGTAAACTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:1211:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

GAATTCGGCC TTCATGGCCT	AGTCAAACCC	TAGAGCAATG	CAGGCCTTGT	TACAGATTCA	60
GCAGGGTTTA CAGACATTAG	CAACGGAAGC	CCCGGGCCTC	ATCCCAGGGT	TTACTCCTGG	120
CTTGGGGGCA TTAGGAAGCA	CTGGAGGCTC	TTCGGGAACT	AATGGATCTA	ACGCCACACC	180
TAGTGAAAAC ACAAGTCCCA	CAGCAGGAAC	CACTGAACCT	GGACATCAGC	AGTTTATTCA	240
GCAGATGCTT CAGGCTCTTG	CTGGAGTAAA	TCCTCAGCTA	CAGAATCCAG	AAGTCAGATT	300
TCAGCAACAA CTGGAACAAC	TCAGTGCAAT	GGGATTTTTG	AACCGTGAAG	CAAACTTGCA	360
AGCTCTAATA GCAACAGGAG	GTGATATCAA	TGCAGCTATT	GAAAGGTTAC	TGGGCTCCCA	420
GCCATCATAG CAGCATTTCT	GTATCTTGAA	AAAATGTAAT	TTATTTTTGA	TAACGGCTCG	480
AG					482

- (2) INFORMATION FOR SEQ ID NO:1212:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 343 base pairs

    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

1	GAATTCGGCC	TTCATGGCCT	AGGGTGATAT	TTAACTCGTT	GCCAATGGCT	AAGCTCCAGA	60
	CTTTGCCTCT	CACACTTGGA	GGGATTCCCT	GCCACCATAA	ATCTCGAACT	TTTCTAGAGC	120
	ACCACATTGT	TTCCCAGTTA	GGTAAGATCT	CATTATTCCA	GGTGAGCACA	GCGTTTCCAA	180
	TGCTTTCCTC	GACTCTGCAT	CTTTCTTCCA	GCTGCTTCTT	CCTTCGCTGG	GCTTCTTTCA	240
	GCTCTCGCTT	TTTGGCCTGA	ACCACCATTT	CTTCATACTG	CTGTCTGTGC	TTCTGAGCTT	300
	CTTCAGCTGG	TTTTGCTGGG	AGATTTGCTG	GTCTGTCCTC	GAG .		343

- (2) INFORMATION FOR SEQ ID NO:1213:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 285 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

GAATTCGGCC	TTCATGGCCT	AGAGAAACTA	AAACTCAGAG	<b>AAGTTAATTA</b>	CTGAACTCAA	60
GATCCCAAAG	TGCTGGGATT	GCAGGCGTGA	GCCACCGCGC	CTGGCTGAAA	GAGCTTTTTT	120
AATGTATTAT	TTATTTGTGT	CAGGATAGAC	TCATTGATGC	GTGTTTTATT	CAGTGGGTTA	180
TAATTCTTTA	TTATGTATTC	TGATGTTGGT	GTTTTCCCAG	TTTTAGCCAA	TGGCATCCCC	240
TTCCATCTGG	ATCCTGTGTT	CTTTTGACAT	GGCTCCAATC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:1214:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

GAATTCGGCC	TTCATGGCCT	AGAACCAGGC	CTTCCAGTAC	GAGTTTGGAG	CCATGTATGC	60
ATGGATGCTG	TGTGTCTTCA	CTGTCATCGT	GGCCTACAGC	ATCACTTGTC	CCATCATCGC	120
GCCATTTGGC	CTCATCTACA	TCCTGCTCAA	GCACATGGTG	GACCGGCACA	ACCTCTACTT	180
CGTCTACCTC	CCAGCCAAGC	TGGAGAAGGG	GATCCACTTT	GCCGCTGTGA	ACCAGGCCTT	240
GGCAGCCCCC	ATCCTGTGCC	TCTTCTGGCT	CTACTTCTTT	TCCTTCCTGC	GCCTGGGTAT	300
GAAGGCCCCC	GTCACTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:1215:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 446 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

GAATTCGGCC TTCAT	TTTTGA AAGATATTTT	TGTAAAAATC	TGTTTGTTTT	CTTTTAATAC	60
TTTCCAGTGT TATC	IGGGTT TCTTAATTTC	TGACTTAAGG	TCTGTAATAA	TTTCTGCTTT	120
CATTCCTCTT AATA	TATTGT GTCTTTCTTT	GTCTACATTT	AAGATTTTAT	CTTTATCACG	180
TGTTTTGAAA AGTT	TTATTT TGATGTGCTC	TTTATGTTTT	TCTTTATTTG	TAGTGCTTGG	240
ACCTTGTGGT GCTT	TTCTTA TTTATAATTT	TCATCAAATT	TGGGGGGTTT	GACCATTATT	300
GCTTCAAAAA TAATO	CTCTGT TCTCTTTCTT	CACTTTCTCC	AGTTACATAC	TGTAGAGTAA	360
ATGATAGCTA CCGA	AGACAG AGTGATCCGT	GATAAATATC	ATTAATGCCT	CTGAAGAGGA	420
GAATGACTCC AGTG	GAACCA CTCGAG				446

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 263 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:	
GGACTTTTTG GAGAAGCAGT ACTATTCATT AATTAAGTAT AGAGTGTCTT GTTAATCCTA AAAGAAAGAG AGCCTTAATG AGGATCATGA ATTTTTTTT TTTTTTTT TTTTGGGATG GAGTTTCGCT CTTGTCGCCT AGGCTGGAGT GGGGTGCTAT CTCTGCTCAC CACAACCTCA GCTTCCTGGG TTCAAGCGAT TCTCCTGCCT CTGTCTCCCG AGTAGCTGGG ATTACAGACA TACGCCGCCA TGCCCAACTC GAG	60 120 180 240 263
(2) INFORMATION FOR SEQ ID NO:1217:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:	
GAATTCGGCC TTCATGGCCT AAACAACAAC AATAACAACA ACAAAAACAT GTATAACTGG GAAAAAACTG AAAGAGAATG CAGGATCATA AAAATATAGC AAACAAAGTG AGTGGGATTT AAAATTAGTG GAATAAGAAA TAATGGGTAA CAATGAAGAA CATAATTTAG GTAATAGTAT AGTATCTTGG GAGCCCTCCT GGAAGTATCT AGTTATGGAC AGTGAGCAGC AGAAACAGGA TGTAACTCAA TTCAGCATAC TTGATGGTTG TGGTAACCCT AGAAAATGAC TCCAGGAAAT AGGTGAGAAT CCAATCTATC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:1218:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 293 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:	
GAATTCGGCC TTCATGGCCT ACAGAGATAG GGTCCCATCC AGGTTCCTAA CTGGGTGGCA CATGCATGGG CTAGATCCAA ATAGCATTGC AAAGGCCTGG AAAACAGAAC TAGAATTGAA ACCACCGCGG AAGACTCATT CGAACTCGTG GGCTGAACTC AACCAGGTCA ATGCTTCAGA AAAATACCAG CATTCTCCAC AGGACATAAA CAAGATTGTC TCATAACATA CCATTCAAAA TATTAGGATA CAATCCAAAA TTGCTCATCA TAAGAAGACA GGAAAAACTC GAG	60 120 180 240 293
(2) INFORMATION FOR SEQ ID NO:1219:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 265 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

GAATTCGGCC	TTCATGGCCT	ACGAGGATTG	GGGTAGGTAT	GNGCTTTNGG	CTCATGTTTG	60
TGATGATAAC	TGAAGTCTNT	TGTGGGTCCG	ACCTGTTGTA	GGGTGTGGGG	GAAAGTGAAG	120
GAAGAGAATG	AAGGTGAGTC	CCCGCCGTTG	CAAACCTTCA	CCAAACCACG	CGGCCCAGTT	180
TTCGTGAGTA	CCCCTGTGTC	CCAGAGAGGA	GGACCCAGCG	TCCTCGGCTC	TGCCGCAGGC	240
CTTCTTGGTC	TGGTGGGTAC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:1220:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 266 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

GAATTCGGCC	TTCATGGCCT	AAGGAATTGA	AACCCAGTAC	TTTGCAGAAC	TTCTTATGAC	60
TTCTGGAGTG	GTCCTCTGTG	AAGGGGTCAA	ATGGTTGTCA	TTTCATAGCG	GTTACGACTT	120
TGGCTACTTA	ATCAAAATCC	TAACCAACTC	TAACTTGCCT	GAAGAAGAAC	TTGACTTCTT	180
TGAGATCCTT	CGATTGTTTT	TTCCTGTCAT	TTATGATGTG	AAGTACCTCA	TGAAGAGCTG	240
CAAAAATCTC	AAAGGGGGAT	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:1221:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 312 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

GAATTCGGCC TTCATGG	CCT AGCTCATTCT	GCTGGGGGTA	GAGATGAGGG	GAGGGAGTAA	60
GTTAAACCTT GGACTAG	CAA GTAGAAGCCT	GGGGGGATGC	GTGTGCCTCA	GTTTCCTCCT	120
CCACAACTGA ATATAGTO	GGC TGAAAACTGG	GGAGATACTT	GATGGCGCGA	ATGTCCGTTT	180
TCTCTCCCTT CCCACCT	CCT GCAGGAAGCA	GGACGGGGCA	GGCAGCACCT	GGTAGGCACA	240
GTGCTTTGCC CCTCCTC	CCC TTCCCTTCTG	GAAGTCTTGG	GGCCTCAGTG	CTTGCAACAG	300
CCACTCCTCG AG			•		312

- (2) INFORMATION FOR SEQ ID NO:1222:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 512 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

GCGATTGAAT	TCTAGACCTG	CTGGCCTCAA	GTGAACCTCC	CGCCTCGGCC	TCCCAACGTG	60
CTGGTATTAC	GGGCATGAGT	CATTGTGCCC	AGTCACAGAA	TTCATTTTAT	TTGTGAAAAT	120
ACAGTGGTAC	AAGTAGGCCT	TTGTTAAATG	ACTAACCTGA	AACCTCTTGT	GAATGACAAA	180
CTCCTCTCTA	CTCCAAATAC	TGGCCCATCC	CTGCTTAAAT	ACTGCTCAAT	GAAGTTACTC	240
ATGCTAGTTC	TTGAGGGAGT	AACTCTAGAA	TGATTCCATC	TAGGAAGACA	TAAGATAAAA	300
TGGTAAGTAT	TCTAAGTTCT	ATAGGTAGTT	TAGTCATGCC	ATATTATAAA	CCTCCACTCC	360
AAAAATAGTG	TGAGGTCATT	TCTGGCCAGA	GTGAAATAAA	AAATGTATAA	TGCCTGAACA	420
GTCTATTATT	CTGACAATGA	AAAAGATTAA	TGCAGTTCCC	TTTATCACTT	GCATGAGTAA	480
AAAAATATAT	ATATATATTG	GCTGGGCTCG	AG			512

## (2) INFORMATION FOR SEQ ID NO:1223:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

GGGTGTTTCA	TACAAAGAAT	ACAAGTAACT	GATGAATGAA	GGGGGCATCT	TGTGTCCCCA	60
CAATCCTGCT	GTGCGCACAC	CACAGGTGAG	CCGTTCTGCC	TAAGGGAACA	GCCCCGGCCC	120
CTCCCTCCGG	CTCCTCCCCA	GCACCGTCTC	CTCCACCCAG	TGGCCTGGCC	GTGGATGCTG	180
CCTGTGGCCC	AGCTTTGAGA	CACCGCCCTG	ACACGTGTCC	AGCCTTACGT	GGAAGGATTT	240
GTCTGTTTTG	TGGCATCCTA	GTAGATGCCA	CGTTAGTAGA	TGCCATGTTA	GTAGAAGGGA	300
TGTGGGCATT	TCTTTGTAAG	TTCCCAAAAG	CCTATGAGGG	TTTTTTCCAC	GATTCCGTTC	360
CCAGTTTGGC	TTTTGTTGTT	GTTGTGGCTG	TTCTTGGCCC	CCCTGGGCCC	TGCAGTGGAG	420
TGGGGGGCTG	CACCTGGGAG	CCTCGAG				447

- (2) INFORMATION FOR SEQ ID NO:1224:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 235 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

GAATTCGGCC	TTCATGGCCT	ACTTTGTTTT	ATATAATAAA	GTATGCCTGT	TAAATTAAAT	60
AATAAGAATA	TGGCAATTAG	CGATATAGCA	TACCCAAACA	AAGATGTTCT	CGATACAGTC	120
TGGCAAAGAC	TATCCCAAGG	TTATTTTAAT	GAATTCAGAC	ATTTTTTCCT	GTGGATATTT	180
CTCCATCCTA	AAAAAAGTGG	CAACCAAGGA	AAATATTTAG	ATGCAAATAC	TCGAG	235

- (2) INFORMATION FOR SEQ ID NO:1225:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 134 base pairs
    - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

GCGATTGAAT TCTAGACCTG CCTCGAGACT GACGCCGCAC CATGACCCTC CTGCTGCTGC 60
CCCTTCTGCT GGCCTCTCTG CTCGCGTCCT GCTCCTGTAA CAAAGCCAAC AAGCACAAGC 120
CACCGCATCT CGAG 134

- (2) INFORMATION FOR SEQ ID NO:1226:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 556 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

GAATTCGGCC	TTCATGGCCT	ACACACATCT	GGTAAGCAGA	AGCACGGAAG	GCCTTTGTTT	60
CAGACAATCT	TTTAAATGAT	GTTTGTATAG	GGAACAGCTT	TGGAAGATAA	AGAATGTCTC	120
TCTCTCTTAT	GGTTTGAATG	TGTCTCCAAC	ACTTTATGTG	TTGAGACTTC	ATCCCCAGTG	180
TAACAGTATT	GGGAAGTGGA	GCCTTTAAGA	GCTAATTAGG	TCATGAGGAC	AGCTCGCTCA	240
TGAGTTGACT	AAAGCTGATA	ATGTGGGAAC	GTGTTGGTTA	TCACAGGAGT	GAGTTCCTGA	300
TAAAAAGAAT	GAGTTTGGCC	AGATTGTCTC	TGTCTGTCTC	ATCTGCCTGC	TTCCACCTTC	360
TGTACTTCCA	CCTGGAATGA	CCCTCACCGG	ATGCTGGTGC	CATGCTCTTG	GACTTCCCAG	420
CATCCAGAAC	TTCTGTTTTT	ATAAATTACC	CAGTCTATGG	CATTCTGTTA	TAGCAGCAGA	480
AAATGGACAG	AGACACCCTC	AAATTAAAGG	ACAGTCTTGC	TGACTATGAA	TTAGAAAATA	540
TCTGGGTTAG	CTCGAG					556

- (2) INFORMATION FOR SEQ ID NO:1227:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 175 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GAATTCGGCC	TTCATGGCCT	ACCTGCCTCG	AAATACTACC	GTATGGCCCA	CCATAATTAC	60
CCCCATACTC	CTTACACTAT	TCCTCATCAC	CCAACTAAAA	ATATTAAACA	CAAACTACCA	120
CCTACTTCCC	TCACCAAAGC	CCATAAAAAT	AAAAAATTAT	AACAAACCAC	TCGAG	175

- (2) INFORMATION FOR SEQ ID NO:1228:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 220 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

GAATTCGGCC TTCATGGCCT ACTGTTTCCT TGCCCTTTTC ACCGTCTGGT GGTTCCCTGC

TGTCATCACA	TTGTGGCCCT CTCATCCATC TT TCGCCTTCTC TTGAGAAAGA TC GCCTGTCTTC CCCTACCCCC AC	CCCAGGCTG (			120 180 220
(2) INFORMA	ATION FOR SEQ ID NO:1229	:		-	
(i)	SEQUENCE CHARACTERISTICS  (A) LENGTH: 526 base  (B) TYPE: nucleic aci  (C) STRANDEDNESS: dou  (D) TOPOLOGY: linear	pairs d			
(ii)	MOLECULE TYPE: cDNA				
(xi)	SEQUENCE DESCRIPTION: S	SEQ ID NO:1	.229:		
TTAATTATTC CAAGCACTTG AGGCTTCGCC GTCGAAGTCC ACCAACTCCA GGGTGGAGCA CCCTCTGCCC	TTCATGGCCT AAGTCTCTTG ACCCTGAGGAGG GCAACTTCGG TACTTCTAAT GTTTGCTGTG CTGAGGTCCC TGACCCCTCT TCGAGGTCCCG GCAGGAGAAT CACTTCTGGGCAGAGAGAT TAGGGAAGAAG GAACCAGGG CAGGACCCCAGG CAGGAGAGAGA	ATGGCGGTT ( PTTCGCTCC ( CTACAATGG T CCTCTCTAT / ATCCTCTTG T AGGATCAAA / TATTATAAC /	GGAGGTGGAC GCTGAGTCAC ICAGACCCAC AACGATTGGA IGGGGCGGAG ATCTCTGAAG ATTTAGCTCA	AGGCTCCTAA CCAACCCCTG AGGCAAAAAA AACTGTCCAA AGTGGGGGGTA ATGCAGAGCT	60 120 180 240 300 360 420 480 526
(2) INFORMA	TION FOR SEQ ID NO:1230	:			
(i)	SEQUENCE CHARACTERISTICS  (A) LENGTH: 312 base  (B) TYPE: nucleic aci  (C) STRANDEDNESS: dou  (D) TOPOLOGY: linear	pairs d			
(ii)	MOLECULE TYPE: cDNA				
(xi)	SEQUENCE DESCRIPTION: S	SEQ ID NO: 3	1230:		
TCAGGCCTCG AGCATGATTC CATAACTGGA	TTCATGGCCT ACCATTGGGC TO TGGACATCGT GGATATAAGG ACCAATAGAGAA GGCCCAGGGG CGAAGTGAGTT GTATGCCCAA ACCCCAGATCAT CTGTTACCCT GGAG	ATGCTCTCG CCATCCTGC CAGTCTCTG	TAGGAGGGTA TCATNGTTGG AACGGTTACA	CAAGAACCCC TCAGGATGAC GGCCCATGGA	60, 120 180 240 300 312
(2) INFORM	ATION FOR SEQ ID NO:1231	:			
(i)	SEQUENCE CHARACTERISTICS (A) LENGTH: 297 base (B) TYPE: nucleic aci (C) STRANDEDNESS: dou (D) TOPOLOGY: linear	pairs ld			
(ii)	MOLECULE TYPE: cDNA				
(xi)	SEQUENCE DESCRIPTION:	SEQ ID NO:	1231:		
	TTCATGGCCT AGCTTTATCC A				60

ACAGATCTTG TAAACCAACA ACAAACCCTG GAGGAGAAGA TGCGGGAAGA CCGGGATAGC CTGGTGGAGA GACTACACCG TCAGACTGCT GAGTATTCCG CATTCAAGCT GGAGAATGAG AGGCTGAAGG CCAGCTTTGC TCCAATGGAG GACAAACTCA ACCAGGCACA CCTCGAG	180 240 297
(2) INFORMATION FOR SEQ ID NO:1232:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 360 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:	
GAATTCGGCC TTCATGGCCT ACGCAGCTCT ACCTGCTCCA GGGGCACCTG GACCTGTGTG AGCAGCACTG TGCCATCCTC CTGCAGACTG AGCAGAACCA TGAGACCGCT TCTGTGAAGT GGAAAACTTG AAGACATTCC TGCCTTCTTT GAATTGGCCA AGAAGGTGTC TAGCCGGGTG CCTTTGGAAC CAGGGTTCAA TTACTGCAGA GGTATCTACT GCTGGCACAT AGGGCAGCCC AACGAAGCCT TAAAGTTCCT GAACAAGGCA CGCAAGGACA GCACTTGGGG CCAGAGCGCC ATCTACCACA TGGTGCAGAT CTGTCTGAAT CCAGACAACG AGGTTATGGT GCGGCTCGAG	60 120 180 240 300 360
(2) INFORMATION FOR SEQ ID NO:1233:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 423 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:	
GAATTCGGCC TTCATGGCCT AGAAGGACTG AAATGATGTT ATACTAAGGG CTACTGAACT TTTTGCCTGT TCTTCCAGG TGTGACAGCC TTTTTTCTTTC TTTCCAGGTG GTTCGCTTTG AGGTGGTCTG AAGCCAAGGC CTCGCGGAGC TTCTTTGTGT GTCACCTTGC TTCCACGTTT CAGTTCTTGT TTTGTTTCTA CTGCTTTAGT TTTTTTTAAA GTTCTCCAGT GTCCCCAAGA GGGAGGGAG TGATAGCTTA ACTGCTGAAG CCAGGCGGGG GTCTGCTGGA GGATTCCAAC AGAGAGTATT TCCTCCACTG TACAATGTCA CAGACTATCT CTATCATCAT TGCTTTGTGG CAT	60 120 180 240 300 360 420 423
(2) INFORMATION FOR SEQ ID NO:1234:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 475 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:	
GAATTCGGCC TTCATGGCCT AGCATGTAAA ACTTCAGTCC TGAACATTTA TAGGGTTTTA TAGAAGGGCA TCCTCCAGGG CTGGTCCATT CAGAGAAATG CTGCATGCTG CCGTCATGGA	60 120

GCTGAGCAAA CCCTCCAAAG CCCTCCTCAC GCAGTTACTA ACAATAGCAT GGGCTTACAG CACAAGCACG TGTTCTCACC TTTTTCCTAT GCCCTGGACT AAGGTTTGGC CAGTGTAATC ATATAAGGCC ATCCTGACAT TGTTTCTGTG TTTCAAAATT TGGATTTTA TTTACATTAG AACTACATTG CTCCTAGTAG AACATTACCT TTAGGGGACT AATTTTCCAT GGAGAACTAT TTCAGCATAT TGCATGCTGC TCAGACCCCA AGTCAGATAT GCCCACAAGC TCGAG	240 300 360 420 475
(2) INFORMATION FOR SEQ ID NO:1235:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 301 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:	
GTTTTGAGCC TAGTAGCACT ACCTTCCAAG TGAGTCACAA CAAATTTGAT CCTATTTGGT ATGTTTTTGT CCACTGTTAT GATTNATCAT GTATCTTACA AGAGCCACTC AAGCAAGACT CTGCTTCTAT GTATGGTGAG GCCTNGTTGT TCTAGGCTAG AATAAACTCT TTGTATGCCT CATTGAATAT GCCAGGTAAA ATTTATGCAG TCAAGAATGA ATTATTTTC TGACTAAAGT GTGTAGCAGT AGTTCAAAAAT TGTGCCCTTG TTTTAACAGT TTCTGTCNAC ACCTTCTCGA	60 120 180 240 300 301
(2) INFORMATION FOR SEQ ID NO:1236:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 346 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:	
GAATTCGGCC TTCATGGCCT AAGAGAAGAT AACATTTACA AGTAAACAGT AAGTGCAATT GTATTTTAAT TTCTTGGTCT CCGAAAACTC AGCTGTGACT GCTTTCCATT AACAGTTCCA GCTCTATGTG TTTCCTCTAA CGCTAAAGGC ACAGCCCCCG GGAATCTACT GCTTCCTAAG AGTCTCCATG GAGTCTATTT TACAACCTCC TTTCCCTCCA TGCTTCCGCG GAGGAGTCTA TACTATCTCT ATATACACAT TTTAAACATT ATTCTTCATT TGAAATTCCT TCAATAAAAA CACAGTCACC ATTCTTCATC TCCTGGGAA ATGGCCTGCT CTCGAG	60 120 180 240 300 346
(2) INFORMATION FOR SEQ ID NO:1237:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 355 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:	
GAATTCGGCC TTCATGGCCT ACTCACTATG TTGCTCAGGC GGATGTGGAA CTCCTGGGCT CAAGCGATTC TCCTGCCTTG GCCCCCAAAG TGCTGGGATT ACAGGTGTGA GTCATGGCAG	60 120

PCT/US98/06956 WO 98/45437

ATGAGCCCCT	CACAATTGGA	CACAGTTTTG	CAAAGGGGTA	AAAGGACAAG	AATCGGTAGC	240
TGTGACTGTG	GATGAGCCTC	TGAGCTTCAC	TTTCCCTCCC	TGAAAGGGGG	TGACAGTGGC	300
ACCTCCCTGG	AGGTTTTCGT	GGAGGGGAGG	AAACACATGT	AAAATACTTC	ACCCC	355

- (2) INFORMATION FOR SEQ ID NO:1238:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 560 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

GAATTCGGCC AAAGAGGCCT	ACTAGACCTG	ATCACCACGT	TCAAAAGTTG	GCTTTCTCCA	60
TTTTAAGTTC TTCCTTAAAG	CCTCTTTAAG	CAAAGTCCCT	GAAATGATAC	AGTAGAAAAA	120
TCACACAGAC TTATTTAAAA	TGAATTCTAT	CACTATTCCT	GAGATCTCGC	CTGCCCCACT	180
GAGGACATTT TGTTTTCGCA	AAGTGCTTTG	AAATGTGATA	AAGGATCTTA	AAGAATATTT	240
GTAAAATTAT GCCCAAAGAA	GACATTCTTT	GAGGTTAACT	TGCAGTGTCT	AAAAGTCAAG	300
AATGAGGAAG GAAAGGAAAA	TAACAGATTC	ACTTTAAAAT	GGACCACGCT	AATTGGGCAG	360
TGAAACATCC TTGTGTCACA	CCATTTACCG	TAGCAGACCA	GAAGAGGGAA	AAGGCTTGAT	420
TTTTCTCTCA TAGATACCAC	AGTTCACTCT	CAAAAACATT	CCTAAAATGG	ATTGATATTT	480
CTCTGATAGA GCACCTGTTT	TGCTACTGAC	AGTGTTAAGT	TCCATACTAA	TCAGCTCATC	540
TAGCCTAACG ACAACTCGAG					560

- (2) INFORMATION FOR SEQ ID NO:1239:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 569 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

GAATTCGGNC AAAGAGGCCT	AAGGAGAANG	AGGCTCAGAA	GGAGACGATT	AAGGATCTTC	60
CCAAGATGAA CCAGGAGCAG	TTCATTGAGC	TGTGCAAGAC	GCTTTACAAC	ATGTTCAGTG	120
ANGACCCCAT GGAGCAGGAC	CTGTACCACG	CCATCGCCAC	CGTGGCCAGC	CTCCTGCTCC	180
GCATCGGAGA GGTGGGGAAG	AAGTTCTCAG	CCCGCACAGG	CAGGAAGCCC	AGGGACTGTG	240
CCACTGAGGA GGACGAGCCA	CCAGCACCCG	AACTGCATCA	GGACGCAGCC	AGGGAGCTTC	300
AGCCCCCAGC TGCAGGAGAC	CCCCAAGCCA	AAGCAGGCGG	AGACACACAC	CTCGGAACAG	360
CCCCACAGGA GAGCCAGGTG	${\tt GTGGTGGAGG}$	GGGGCAGCGG	CGAGGGACAG	GGCTCACCCT	420
CCCAGCTGCT GTCTGACGAT	GAAACCAAAG	ACGACATGTC.	CATGTCCTCC	TACTCGGTGG	480
TCAGCACGGG CTCCCTGCAA	TGTGAAGACC	TTGCAGACGA	CACGGTGCTG	GTGGGCGGGG	540
AGGCCTGCAG CCCCACAGCG	CGACTCGAG				569

- (2) INFORMATION FOR SEQ ID NO:1240:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 405 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

GAATTCGGCC	AAAGAGGCCT	AGAGACCAGC	CTGGCCAATA	CGGTGAAACC	CTGTCGCTAC	60
TAAAAATACA	AAAATTAGCC	AGGCATGGTG	GCTCACACCT	GCAGTCCTAG	CTACTTGGGA	120
GGGTGAGGCA	GGAGAATCAC	TGAAGCTTGG	GAGGCAGAGG	TTGCAGTGAG	CCAAGATTCC	180
ACCGCTTCCC	TCCAGCCTGG	ATGACAGAGT	GAGACTCCGT	CTCAAAAAAA	CAAAAAAAAA	240
GTTACTTCAA	TAATGTACTT	TTTTTTTCA	AATTACAGAT	AATCTATAAG	GAATTAATCT	300
TGAAATTAAT	TCCAGGTTTA	ATTGTTAATG	AAATTTCACA	AGCCTAATTT	AACACTTGTC	360
TGGATAACTC	ATTTTGATAC	TGAGTAAATA	GTCACCGGTC	TCGAG		405

- (2) INFORMATION FOR SEQ ID NO:1241:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 542 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

GAATTCGGCC AAAGAGGCCT	AGGGCTTTTG	TGAATAAATT	TTAAAAGAGA	CTACTGCCTG	60
TCCTTAAATT CCTTTTTCTT	TTTATAAAAA	AAGAACTATT	AAAAATGATT	GACAAATTTT	120
GAGTTAAAAA ATTGTTAAAA	CATTCTCTAT	ATTTAATTTC	AATTTTATAA	TAGATTACAG	180
GAAGATGCTT ATGAAACAAA	TACATTTGTT	TCAGTACATG	TCTTTAAATG	ATAGACTTAT	240
AAGTATGTAA ACAACTATAT	AATAAAAGGT	TTCCAAACGC	TGCCTGTAAG	AAATCAGGCA	300
AATTTTACCA TAAGCAATAA	ACCATTCCAA	GCCTTCCAGA	CAGTCTCCAT	AGCCGCACCA	360
GCATGGCAAT AAGCTTTAAC	CAAACGAAAA	CAAACAAACA	AAAGCACTTC	GCAATTTGTT	420
GCTGCAAAAC AGGGAGAGAA	AAGAGTGTAC	AAACTTGATG	GAATCACAAC	AGTCAATATA	480
ATTTAAGGGA CAATAAAGTC	AATAAGGTTG	ATGGTGTTTA	TTGTTTAAAA	AGTTAGGCCT	540
CT					542

- (2) INFORMATION FOR SEQ ID NO:1242:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

GAATTCGGCC	AAAGAGGCCT	ACTGATACAA	TTGTTGACTT	TTCTTTTACT	ATGTGTAAGA	60
AATACCCCAA	ACATGAAAAG	ATTGTTTTGA	TCATATGCAT	GTATGTAGAA	TATTTTTGCA	120
GAGCAGAAAG	ATTATGTTAG	AAGTGTGATT	TTTATTTTCA	GAAGTCATAT	ACATGTAAGC	180
TACAATTTTG	AGTGCTTTAT	AAACACTTAA	GATATATATA	TAAATTTTAA	TTTCATAGCA	240
ACTTGTAAAA	AATAAAATAC	TTGTTGAAAA	GCCTTTTTCA	ACATATCCCT	AAGCTAAGGG	300
AAGAGGAAGG	AATAACAACT	CAGTGAAAAG	ATGGTCTCCA	GTTTCTGAAT	GAAAAAGCTA	360
CAACCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:1243:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 374 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

GAATTCGGCC	AAAGAGGCCT	AGCCTCATCA	CGGGCAGGGC	TCTGGCCCAT	AGTGGCTGGA	60
CAGACACTGG	CACAGTCTTG	CTGGTCTGCT	GGGAGCACAC	AGACATTGGC	ACAGACTTGC	120
TGGTCTCTTG	GAAGAGGGCA	AGACCCCAAA	CCAGAGCAAA	ATACACTTCC	AGCTCTTAAC	180
CAGGCTCCTT	CCAGTCACAA	GTGTGCAGAA	TCAGAACAGA	AGTAGTACCA	ATCAATGTCA	240
CATGAACAAA	CAAGCTGCCC	CCAGGGTACC	ATTTGGGGAG	GGGAAATCTT	TTCTTTCTTT	300
CCCCCTTAAA	AAAAAACACA	TCTGCCCCGA	ACACTTTCCC	ACTGTTATTC	TTTCCTCATA	360
CCCCAACGCT	CGAG					374

- (2) INFORMATION FOR SEQ ID NO:1244:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 468 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

GAATTCGGCC	AAAGAGGCCT	ACACACCAAA	CTGATTATCC	ACCAGACACT	CAGCGTCTTA	60
GAAGATATTG	TGGAGAATAT	CTCGGGGGAG	TCCACCAAGT	CTCGACAGAT	TTGCTACCAG	120
TCGCTGCAGG	AATCTGTTCA	GGTCTCCCTG	GCCCTCTTTC	CAGCTTTTAT	CCATCAGTCA	180
GATGTGACTG	ATGAGATGCT	GAGCTTCTTC	CTCACTCTGT	TTCGAGGCCT	TAGAGTACAG	240
ATGGGTGTGC	CTTTCACTGA	GCAAATCATA	CAGACTTTCC	TCAACATGTT	TACCAGAGAG	300
CAGTTAGCCG	AGAGCATCCT	CCACGAGGGC	AGCACAGGCT	GCCGGGTGGT	GGAGAAGTTT	360
CTGAAGATCC	TGCAGGTGGT	GGTCCAGGAG	CCAGGCCAGG	TGTTCAAGCC	CTTCCTCCCC	420
AGCATCATCG	CCCTGTGCAT	GGAGCAAGTG	TATCCCATTT	CGCTCGAG		468

- (2) INFORMATION FOR SEQ ID NO:1245:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

GAATTCGGCC	AAAGAGGCCT	AAGCTTATGG	GGAGGACACA	TATTTACTCA	AACATCCTGG	60
CAATTCATAT	CTAGGGCACT	CCCTCTGTGT	GTCAGACGCC	CTTGCATGTG	TCAAATGTCA	120
TCTGATAACA	TTGATGAAAA	ATATCATTCA	CTTCTTCTTG	GTGCAGAAGG	CATAGACCGG	180
ATTATGCAAT	CACTGAGAAG	TAGCTTCTGG	ATGTGTTTTC	TGGTGGCGTC	TTAACAATTT	240
CAGCCGACTG	AAGGCTCTTG	GACACTTGGA	ACATTTGTAG	GGTTTCTCTC	CGGAGTGGAT	300
GCGCTGGTGC	TCCTTCAGGC	TCCCCCTGTA	GGTGAAAACT	TTCTTGCAGT	CTTTACATTC	360
GAAGGGCTTC	TCCCCCTGTG	TGGCTTCTCT	TGTGACACTT	CAAGTAGGAC	TTCTGGGTGA	420
ACTGCTTAGG	CCTCTTTGGC	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:1246:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

GAATTCGGCC	AAAGAGGCCT	AGTATTTTGT	ACTAGTTTTT	TAATAATTAT	AAGTCTTACA	60
CGTTCTCTAA	TTCTTCTTGA	ATCTGTTTAA	TTTTTCTCCC	TTGGGAATTG	TTAAGTGTAC	120
ATGTATTGTG	ATAACTGCTA	TAATTTTGCT	TTTATTGATT	TTTTTTGCTT	TATATCTGCT	180
ACAATTTGGT	TCCTCCAAAT	CCCATGTTGA	AATCTGATCC	CCAGTGTTGC	TGGGGGATCT	240
AATAGCAGGT	GTTTGGGTCA	TGGGAACAGG	TCCCTCATGA	ATGAATTAAT	GCCCTCACTG	300
GGAGGAGGGG	ATAAGTAAGC	TCTCACTCAT	TTAGTTCCCA	AGACAGCTGG	TTGTTTAAAA	360
GAGCCTAGTG	CCACTTCTCT	CTTGCTTCCT	TTCTTGCCGT	GTGATCTCTG	CACATGCCAG	420
CTCCCCTCGA	G					431

- (2) INFORMATION FOR SEQ ID NO:1247:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 389 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

GAATTCGGCC AAAGAGGCCT ATTTTTTTT TTTT	TTTTTTT TTTTTTTT TCNGGGTGTA 60
GAACATTTAT TTATTTTTCC CACAAATCAC TGAA	AGTTTA GGTCAGTGGG AAATAATTTT 120
AATCAAATAA TTGTACATAT TCTTCCCACA TATC	CCTGCCT TGTATTAGGA AATGACATTG 180
TGATCCATTT CATTACAAGT AAAATATTAC AAAA	TATTTA CAGGAAAATA TTAAAAATAA 240
CTCAAACACA AAAGGCAAGA TGAAATAAAC TGTT	TTTTTTT TCTCCAGAAA TCTCTACTCC 300
AGTGCCCACA GCACACAAGA GTCAAAACAA ATAA	AGCAACT AAGATCCCCC GATCACAAAT 360
TTCCAAAGAA CTAGGCCTCT TTGGCCGAA	389

- (2) INFORMATION FOR SEQ ID NO:1248:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 380 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

GAATTCGGCC AAA	GAGGCCT AAAGGAAGGC	CACTTCTCAA	CTGGCAGAAC	TTCTGAAGTT	60
TAGAATTGGA ATT	ACTTCCT TACTAGTGTC	TTTTGGCTTA	AATTTTGTCT	TTTGAAGTTG	120
AATGCTTAAT CCC	GGGAAAG AGGAACAGGA	GTGCCAGACT	CCTGGTCTTT	CCAGTTTAGA	180
AAAGGCTCTG TGC	CAAGGAG GGACCACAGG	AGCTGGGACC	TGCCTGCCCC	TGTCTTTTCC	240
CCTTGGTTTT GTG	TTACAAG AGTTGTTGGA	GACAGTTTCA	GATGATTATT	TAATTTGTAA	300
ATATTGTACA AAT	TTTAATA GCTTAAATTG	TATATACAGC	CAAATAAAAA	CTTGCATTAA	360
CTTAGGCCTC TTT	CGGCCGAA				380

(2) INFORMATION FOR SEQ ID NO:1249:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 386 base pairs(B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

GAATTCGGCC	AAAGAGGCCT	GTTTGGTTTG	TGACTAGACT	TAAAAATACT	AAAATAAGCC	60
AAATAGATGC	TAACAATACT	AATTTGCACA	CAAGATTTGA	AAAAAGTACT	TCAAGTTTTA	120
TCTCTTATCC	CTAGAGAAAG	TAAATAAAA	GTGGCTCTTG	CAAAAATAAA	TGAAAACAAA	180
ACCACCAACA	AAAACTAATC	ATATAAGATA	CTGTTTTTCT	TTTTGAATAC	TTCAATTGGT	240
CCTATATTAG	GATAAGGTTT	TGATAGCAAG	GACTTCCTAG	CTTCTTCCTT	TATCTTCCAT	300
TCTCTAGTCA	CTTCCGTGTT	TTTATCAAAC	AAGGCTACGT	GTAGGCTTTC	CTACAAAGTC	360
AGATTGAATT	CTACCACCCT	CTCGAG				386

- (2) INFORMATION FOR SEQ ID NO:1250:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 428 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

GAATTCGGCC	AAAGAGGCCT	AACCATGTCT	GACCAGATCA	TTGGGAGAAT	TGATGATATG	60
AGTAGTCGCA	TTGATGATCT	GGAAAAGAAT	ATCGCGGACC	TCATGACACA	GGCTGGGGTG	120
GAAGAACTGG	AAAGTGAAAA	CAAGATACCT	GCCACGCAAA	AGAGTTGAAG	GTTGCTAATA	180
ATTTATACTG	GAATCTGGCA	TTTTTCCAAG	CCAAGAGAAG	ATCGAATGGC	TTTTTGCAGC	240
TAACTACTAT	GTGTAGACAG	GTTTTATATT	ATAAAGTATG	CATTCTTATC	ACCTAGTATA	300
TAGTTAGTTT	GTAGAGTGAT	TTCCCCCCAG	TTTCTTGAAC	ATGGTATCTT	CACATCTTGG	360
ACCTTGGTCA	GTTGTGCTAT	TCATTATTAA	ACACTAAAAC	TTTGGCGGTT	TAGGCCTCTT	420
TGGCCGAA						428

- (2) INFORMATION FOR SEQ ID NO:1251:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 264 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

GAATTCGGCC	AAAGAGGCCT	AAGAAAAGTA	GTATGAATGA	GTTTTTCTAC	ATATTAACTA	60
CAATTTATGG	TAATTTGTGA	AATGTTTTTC	CATTTTTAAA	TGTAAGAGTC	TCTATCTCCA	120
CTCACAAAGC	AACAGGCACT	GCTAGGGGTC	TTAGGCTAAC	ATCTGCCACC	CCACCAGTCT	180
GCATGGCCCA	TAAACAGGTG	CAGAGGACCA	GAGTTCACCT	GTCAGCAGCA	CCGCAGAATC	240
CAACTCTAGG	CCTCTTTGGC	CGAA				264

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
,-,	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:	
GAATTCGGCC AAAGAGGCCT ACTTTTTTT TAATTTTCCA CTTTCTTCTT AACTTTACTT	60
CTCTTTTTGT CCCCCCCAT CTTACAGAAG TTGAGGCCAA GGGAGAATGG TAGGCACAGA	120
AGAAACATGG CAAACTGCTC TGTGCTTTCA AACCAAAGTG TTCCCCCCAA CCCCAAATTT GTCTAAGCAC TGGCCAGTCT GTTGTGGGCA TTGTTTTCTA CAACCAAATC TGGGTTTTTT	180 240
TCTTCTTTCT TTAAACATAG AGGTACCACC ACAAGGGATG CCCTACTCTC TCGCAGCTCT	300
TGAAAGCATC TGTTTGAGGG AAAGGTCTCT GGGCAAGCAA GTGGTTATTT GGATTGCTTG	360
CTTCCCTTTT TCCACCTGGG ACATTGCAAT CATAAAATAA CAGTAAATTC CAAACCTCTA GGCCTCTTTG GCCGAA	420 436
(2) INFORMATION FOR SEQ ID NO:1253:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 399 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:	
GAATTCGGCC AAAGAGGCCT AGGGTAGATC ACTTGATATC AGGAGTCGAG GCGGGAAGAT	60
CACTTGACGT CAGGAGTTCG AGACTGGCCC GGCCAACATG GTGAAACCGC ATCTCCACTA	120
AAAATACAAA AATTAGCCTG GTGTGGTGGT GGGCACCTGT AATCCCAGTG ACTTGGGAGG	180 240
CTAAGGCAGG AGAATTTCTT GAACCCAGGA GGCAGAGGTT GCAGTGACCA GCAAGGTTGC GCCATTGCAC CCCAGCCTGG GCGATAAGAG TGAAAACTCC ATCTCAAAAA AAAAAAAAAA	300
AAATTCCTTT GGGAAGGCCT TCTACATAAA AATCTTCAAC ATGAGACTGG AAAAAAGGGT	360
ATGGGATCAT CACCGGACCT TTGGCTTTTA CAGCTCGAG	399
(2) INFORMATION FOR SEQ ID NO:1254:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 444 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:	
GAATTCGGCC AAAGAGGCCT ACCCGGTACT TACTTCTCAA TCCTAAAGAG AGAAAACAGG	60
TGTTTGATCA GTATGTAAAG ACCAGGGCAG AGGAAGAACG CAGGGAAAAG AAAAATAAAA	120
ATGCAAGCCA AGGAAGATTT CAAAAAAATG ATGGAAGAAG CAAAATTTAA TCCAAGAGCA	180
ACTITIAGIG AATITIGCAGC CAAGCAIGCI AAAGAITCAA GAITCAAAGC AAITGAAAAG AIGAAAGACC GAGAAGCCII GIITAAIGAG IITGIGGCCG CIGCIAGGAA GAAAGAGAAA	240 300
GAAGATTCGA AGACCAGAGG TGAGAAGGTA AGATGGTTTT AGTTCCAGTG GTGTGATTGA	360
TGGGAGTGTG AATGGGAAAG GTCTATGCTG GTGTTATGTT TCTAACCTTA TTCATTGGCA	420
TAAATAATAG GACGTACACT CGAG	444
508	

- (2) INFORMATION FOR SEQ ID NO:1255:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 284 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

GAATTCGGCC	TTCATGGCCT	AAGAAGGACT	ACCCTGCACT	GCTTTCCTTG	GATGAGAATG	60
AACTCGAAGA	GCAGTTTGTG	AAAGGACACG	GTCCAGGGGG	CCAGGCAACC	AACAAAACCA	120
GCAACTGCGT	GGTGNTGAAG	CACATCCCCT	CAGGCATCGT	TGTAAAGTGC	CATCAGACAA	180
GATCAGTTGA	TCAGAACAGA	AAGCTAGCTC	GGAAAATCCT	ACAAGAGAAA	GTAGATGTTT	240
TCTACAATGG	TGAAAACAGT	CCTGTTCACA	AAGACAAACT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:1256:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 691 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

GAATTCGGCC	TTCATGGCCT	AGTGGGAGTT	TGCTAATGTG	AAACCTAATG	ATGTCTGAAA	60
ATGGTCCTGA	TGGGTATTAA	TAGCCATCTG	GAAAAATTTT	ACATCTTCAC	AAATAATCCC	120
AATAATTTAT	ATTGTGAAGA	TATTATCCTG	ATAGTCCTTC	TTTTCCTATA	TTCTTGTCGG	180
CTGTAGGATG	AGAGCAGTAT	GAAGCAAACA	GAAGACATTT	TGAAATTAAT	CACAAAATTC	240
CCATTGCTTT	GAAGCCTGCT	ATTATTATAC	TAAGCCTTCT	TATAGCTTTA	AAAATCAAAC	300
AATGCCAAAC	AGTATATCTA	ACATTTTTAA	TTTCCTTTGA	GCCAAACCAA	TTTGGTTTAA	360
ATTTCTCTGC	CTCCGTGAAG	ACAAGCTGGG	CTGGGGAGGA	CGGTGTCTAG	GAGGGATGAC	420
CCCACTCAGC	TCCAGGCAGT	GTTCTGCCGA	GACCCCAAGA	ACTCGGGGTG	TCAGAGGGCA	480
AAGGAACTAC	CTGCCTTTCA	CGGCTGCTGA	CTTCTCAGGG	CTGCAAGCAG	CACAGAATGT	540
TATCCTTACG	TCCTGAGCCG	GTTTAAGTCT	GTGGAAAAGG	AAGCACGGGA	GAAATCCACG	600
TAACCTTTGC	TTTCTTTTTA	AGGGAAGCGG	TTCCGCCGTG	AACTTGGAAC	CCTCAGCTCC	660
GGGTGTTCTC	GGCAGAAGGG	CAGCTCTCGA	G			691

- (2) INFORMATION FOR SEQ ID NO:1257:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 383 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

GAATTCGGCC	TTCATGGCCT	AAGCTGATCC	ACGATCAGAG	TGCTCCCAGC	TGCCCCAGCA	60
GCTCCCCGTC	CCCAGGGGAG	GAGCCTGAGG	GGGAAGGGGA	GACAGATCCG	GAGAAGGTGC	120
ATCTCACCTG	GACCAAGGAC	AAGTCGGTGG	CAGAGAAGAA	TAAGGGCCCC	AGTCCTGTCT	180
CCTCTGAGGG	CATCAAGGAC	TTCTTCAGCA	TGAAGCCGGA	GTGGGAGAAC	TTGAACCAGT	240

CCAACGTGCG GCGCATGCAC ACGGCCGTGC GGCTGAACGA GGTCATCGTG AAGAAATCCC GGGACGCCAA GCTTGTTTTG CTCAACATGC CTGGGCCTCC CCGCAACCGC AATGGTGATG AAAACTACAT GGAGTTTCTC GAG	300 360 383
(2) INFORMATION FOR SEQ ID NO:1258:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 418 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:	
GAATTCTGAG GGACTAACTA CGACCATGAG ATTGGCAGTG ATTTGCTTTT GCCTATTTGG CATTGCCTCC TCCCTCCCGG TGAAAGTGAC TGATTCTGGC AGCTCAGAGG AGAAGAAGCT TTACAGCCTG CACCCAGATC CTATAGCCAC ATGGCTGGTG CCTGACCCAT CTCAGAAGCA GAATCTCCTT GCGCCACAGA ATGCTGTGTC CTCTGAAGAA AAGGATGACT TTAAAGCAAGA AACTCTCTCCA AGCAATTCCA ATGAAAGCCA TGACCACATG GACGACGATG ATGACGATGA TGATGACGAT GGAGACCATG CAGAGAACGA GGATTCTGTG GACTCGGATG AATCTGACGA ATCTCACCAT TCCGATGAGT CTGATGAGAC CTTCACTGCT AGTACACAAG CAGTCGAG	60 120 180 240 300 360 418
(2) INFORMATION FOR SEQ ID NO:1259:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 189 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:	
AAAAATTAAA TAATGCTTGA CTTTTTTTT TTTTTTCTC TTTTTGAGGC AGGTTCTTGC TCTGTCACCC AGGCTGGACT GCAACAGCAT GATCTTGGCT CACCTCCGCC TCCCAGGCTC TGGCAATCCT CCCACCTCAG CCTTCAGAGT GGCAGAGACT ACAGGCTCAT ACCACCGCAC CCACTCGAG	60 120 180 189
(2) INFORMATION FOR SEQ ID NO:1260:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 278 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:	
GCGATTGAAT TCTAGCCTTT CCTCCGTTCA AGTAAATTTA GAAATTTCCT AAGTTTCTT TATAACAGGT AGCCTAAATC TATATCATAC TTTTAAAATA AAAATCTAGG TGCAAATTTG TTCTTATGGT TAAGGTTAAC ATGTACACTT CACAAACATT GAGACTTTTG TTTTGTTTTC TGGGACAAGG TCTTGTTCTG TCTCCCAGCT GGAGTGGATA CAAGCATGGC TTGCTTCAGC CTCAACCTCC CGGACTCAAG CGATCCCCCC CCCTCGAG	60 120 180 240 278

- (2) INFORMATION FOR SEQ ID NO:1261:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 265 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

GAATTCGGCC	TTCATGGCCT	ACTCACTGGA	TGCTGGGGGA	GGGCCCCTCA	GGTGAGCAGC	60
CCACCACTGA	CTTCAGCGTT	GCTGGCTCGG	TTATCAGACT	CTCATCCAAC	ACAAGCTCAC	120
AGGGAAAGCC	GTTCCTTGCT	CCTTGTGGAG	GGAGCTACCG	TCATTGCCCT	GAGACCACCA	180
GCCAAGAAAG	TAGGTATGTC	CAGGTAGGGA	ATTCAGAGGG	ACCCAGTGCA	TCCAATTATA	240
CAATTATACC	CAGAAAGTCC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:1262:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 426 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

GGTCAGTATT	GAAGGTTGTT	TTCTGAGCCA	TTGTATGAAG	CTGCTGTTTT	GGCGTCCCTA	60
ATGCAGGGTG	AGATGGTAGT	${\tt GTGATTCTTG}$	TTGTGACATC	TCGTGACTGG	GCAGGACGCT	120
GAATACTGAT	TGCTGCAGAT	GGAGGATGCT	GGATAGACAA	GGTTGGCCTA	CTAAGTGCTG	180
AATCAGTAGC	ATGCGCCGCT	GTCGTAGTGA	TGACTGGAGA	CTGAGCTCTG	GTGGCTGAGA	240
CAGTTGCTAC	CACAGCAGGA	GGGATGGCAT	TGGAGGTGGT	CACAGGTGGC	CGAGACTGGA	300
TTGGTTGGTG	AATGATGTGC	TGTACTGCTG	GCTGAGCAGT	AGCAGCATTT	GGCAGCTGTG	360
AGGTCGGCCT	CAGGACTGTG	GTTACTTTAG	AACTGGACAT	CACAGCAGCA	GCAGCTGCAC	420
CTCGAG						426

- (2) INFORMATION FOR SEQ ID NO:1263:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 398 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

GAATTCGGCC	TTCATGGCCT	AGGCCGGTGT	TTATGCACGA	TGGCGTTGAA	AGCTAGTCCA	60
TCTCTCCAGC	TGGTGGTGAA	GTTGTGTACA	TTGACGTTGG	GATAACCTGC	AGTCTTCATC	120
TGGCACCACA	GAAGCAGGGC	ATCCTTGGCT	GACTTCTTCT	CCTTGTTGTC	TTCTGTCTCC	180
ACACTGATGT	CTTGGATCTG	GAATCGAAGG	ATGATGGTCC	AGACCAGCCC	AAGGGTCAGT	240
CGGTGGTTTC	CGTCCACAAT	GTCATGGGAG	CCCATGTTTT	CCAAGTGCAC	TTTCTGCTCC	300
TTGAGGAACT	GCAGTGCCTT	GTCCACGTTC	TCCAGGCAGT	GGATCCGCAT	GCGGCCCTTT	360
GTAGGCTTTG	GCAGTATCTC	TCCCGAGAGC	ACCTCGAG		*	398

(2) INFORMATION FOR SEQ ID NO:1264:

(1) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 256 base pairs	
(B) TYPE: nucleic acid	
(C) ·STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:	
GAATTCGGCC TTCATGGCCT AAAAAAAGCT GTTAAGAAAA TATGTTTTAA AAATTTGCCC	60
AACAGGAAGG AGAAAATTAG AATCTAATAG CAAACTTGTG TCAAAGCAGG GGAGACCACA	120
TGATCTTCCT CTTTGAAAAT CTGTCCTGGG TGATGACCAT ATGCTCTCTA AACAGGTTTT	180
CTGTGTTTTA GGGAAAGAAG CTCAGAAAGG ACCCCTGCTC TTTGATGACC TCCCTCCGGC	240
CAGCAGTAAC CTCGAG	256
(2) INFORMATION FOR SEQ ID NO:1265:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 249 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:	
GAATTCGGCC TTCATGGCCT ACAGAGTCTA ATTAGCCATA TTTATATGAT AATAATAAAC	60
ATTTTGGCTA CAGTCCTACC TAGATTTTTT TTTTTTAGAT GGAGTCTTGC TCTGTCGCCC	120
AGGCTAGAGT GCAGTGGTGC GATCTTGGCT CACTGCAACT TCTGCCTCCC AGGTTCAAGC	180
AACTCTGTTG CCTCAGCCTC CCAAGTAGCT GGGATTACAA GCGCACATGA CCACGCCTGG	240
CAGCTCGAG	249
•	
(2) INFORMATION FOR SEQ ID NO:1266:	
taran da araba da ar	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 265 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:	
GAATTCGGCC TTCATGGCCT AGGTTATATA GCAGTGATGC TTTCATAGTA TTTTTCTTGA	60
ATAAGGTCCC CAAAACCTTA TTAAGTTCCT GGTAGGCATG GAGCATTGAA GATGGCAGAC	120
ATGGTGCAGT CTCTCAAGGA GTTTACGCTC TAGTGGAGAA AACAATCAGA CAGCCTTAAA	180
ATACATGTAT GGCTACTATA ATAAATACTG TGAAGCAGGA GTGCACCACG AAACCTGGAG	240
TCCTCTCCAT CCTCCCCTTC TCGAG	265
·	
(2) INFORMATION FOR SEQ ID NO:1267:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 293 base pairs	
(B) TYPE: nucleic acid	
·	
512	

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

GAATTCGGCC TTCATGGCCT ACTAG	ACCTG CCTCGAGATT	AGGGGGGTTA	GACTCAGAAT	. 60
TCTGTCCAAA CTCCTGGACG ACCTC	TTGAA ATTAAGTCAG	GGATTTTATG	TACTGGGTTA	120
ATTTCGTAAC CTCTGGGTAT AATAT	TAGGT TTGCATGTAG	AAAGGGTCTC	CAGTATAGGA	180
CTTCAAAGAA ACTAAGCCAT AGACG	TAATT TAAGGGCTGT	TCTGATCTGA	AGAAGTGCCA	240
TGGGTAGAAG TTTTAGCCAT GGTAA	AGAGG CTTCCTGGCA	TCATTTGCTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:1268:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

GAATTCGGCC	TCATGGCCTA	CTGGTCCAAG	CTGATTACCC	TCATAGTGTC	CATCATTGAG	60
GAAGACAAGA	ATTCCTACAC	TCCCTGCCTC	AACCAGTTTC	CCCAGGAGCT	GAATGTGGGT	120
AAAATCAGCG	CTGAAGTGAT	GTGGAATCTG	TTTGCCCAAG	ACATGAAGTA	CGCCATGGAG	180
GAGCACGACA	AGCATCGTCT	ATGCAAGAGT	GCCGACTACA	TGAACCTCCA	CTTCAAGGTG	240
AAATGGCTCT	ACAATGAGTA	TGTGACGGAA	CTTCCCGCCT	TCAAGGACCG	CGTGCCTGAG	300
TACCCTGCAT	GGTTTGAACC	CTTCGTCATC	CAGTGGCTGG	ATGAGAATGA	GGAGGTGTCC	360
CGGGATTTCC	TGCACGGTGC	CCTGGAGCGA	GACAAGAAGG	ATGGGTTCCA	GCAGACCTCA	420
GAGCATGCCC	TATTCTCCTG	CTCCGTGGTG	GATGTCTTCT	CCCAACTCAA	CCAGAGCTTT	480
GAAATCATCA	AGAAACTCGA	G				501

- (2) INFORMATION FOR SEQ ID NO:1269:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 330 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

GAATTCGGCC	TTCATGGCCT	AGGCCCCTGC	TCCACCTGGG	GGGACTGGGA	GTGTGAGTGT	60
GCATGGCATG	TGTGTGGCAC	AGATGGCTGG	GACGGGTGAC	AGTGTGAGTG	CATGTGTGCA	120
TGCATGTGTG	TATGTGTGTG	TGTGTGTGGC	ATGCGCTGAC	AAATGTGTCC	TTGATCCACA	180
CTGCTCCTGG	CAGAGTGAGT	AACCCAAAGG	CCCCTTCGGC	CTCCTTGTAG	CTGTTTTCTT	240
TCCTTTTGTT	GTTGGTTTTA	AAATACATTC	ACACACAAAT	ACAAATTGAC	AGGTCAAAAT	300
CCATGAAATG	AGATCCCCCA	GCGGCTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:1270:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 502 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

GAATTCGGCC	TTCATGGCCT	ААААААААА	TACTGATTCA	CTTTTGCAAT	TTTTCAGATA	60
CTACTTGATG	TGACACCTCC	CCTAGGCTTG	CTGTGGGTCT	CTTGGAAGAT	AGAGCTATAT	120
TAACTCCTTG	ACTTAAAGGG	CAGCAGACTA	TATAAGGTCT	CTTTACAGAC	AGAGTAGGGA	180
GAATAATGAA	AAACTTTTTG	ATTTCTAGAG	AGAAGAGAGA	AGACATAGCA	ATGGAACTGT	240
TCTTAGCTTT	GTTTGCTACA	ACTCTTCAAA	GTTTAATTTT	AGATTCAGTG	CATTTATTCA	300
TAGAGCATGA	AACATATAAT	CATGCCTTTT	ACTAATTGCG	GATACTTAAA	ATTATATATT	360
TTTGACCTAC	TGTGTTATGG	TCAATTTGAA	AAAGAATGGT	TTGATTATAT	ATTATTGTCT	420
GTAGATTCCC	TGTACTATTC	TAGGATCATA	TGACATATTA	TCATTACTAA	ATATAGCACT	480
AATTATTGAT	GCTCCGCTCG	AG				502

- (2) INFORMATION FOR SEQ ID NO:1271:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 285 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

GAATTCGGCC	TTCATGGCCT	ACCCCTGACT	ATTCAGTAGG	AGAAGAAATC	AAAAATCCAT	60
TCTTTTCTCC	TTCTCTCCCT	CCAACAGTGG	CCAGGGGAAG	GGGAAGTGAG	GGCAGGGGCA	120
AAAAGATTTG	GGAATTTTTA	TTTATTTATT	TATTGTGACT	TTTCATTTTT	TTGGTATTTG	180
GCTTTACTGG	AATAGGAGGG	CCCCTGCCCA	CTGTGCCCCG	TTTATCCCTT	ATTCCCCAAA	240
CCCTGCTCTC	CCCAACACCT	ACTCACTTAA	GCACTTGTCC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:1272:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 405 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

GAATTCTAGA	CCTGCCTCCA	ATTTGAAGAT	TTATTTCTCT	CTTTGGATAT	AGAACAAAAT	60
AACTTTATGT	ACATTTTATT	TCACTTTATT	TTACTATTGG	GTTGGTGCAA	AACAAATTGC	120
AGTTTTCCCA	TGAAAAGTAA	TGGCAAAAAC	TGCAATTACT	TTCGCACCAG	CCCAATATTT	180
TATTTTGAGA	CAGAGTCGCA	CTCTGTCACC	AAGGCTGGAG	TGCAGTGGTG	TCATCCCAAC	240
TCACTACAGC	CTCTGCCTCC	TGGGTTGGAG	AGATTCTTGT	GCGTCAGCTT	CATGTGTAAC	300
TGGAATTACA	GGTGCACGCC	ACCACGCCCA	GCTAATTTTT	GTATTTTTTG	TAGAGATGGG	360
GTTTCGCCAT	GTTGCCCTGG	CTGTTCTCAA	ACTCCTGACC	TCGAG		405

- (2) INFORMATION FOR SEQ ID NO:1273:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 412 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

GCGATTGAAT	TCTAGACCTG	GCTCGAGGCA	GGTCTAGAAT	TCAATCGGCT	TCCTGGCAGT	60
GCCCTCTCCC	AGATGAGACC	TGATCTCTTT	TTTGTTTTTT	GTTTTTTGTT	TTGAGACAGA	120
${\tt GTTTTGCTCT}$	TCTTGCCCAG	GCTGCAGTGA	GTTGAGATCG	CACCACTGCA	CTCCAGCCTG	180
GGTGACAGAG	TGAGACCCCA	TCTCAAAAAA	AAAAAAAAA	ATCTGGCCTT	ATGGACTGTG	240
TACTACACTC	TAGTGGGGGT	AAGAGGCAAT	GGGTAAATAG	GTAAGTAGAT	TATTGGATGT	300
ATTAGAAGGG	GCATGGGGAA	TGTGGGGTCA	AGGTTATAGT	TTTAAATAGG	GTGGTCAGGG	360
AAAGCTTTCT	GAGAAGGTGA	CATTTGAAAC	AAATACTTGA	AGGAGTCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:1274:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 285 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

GAATTCGGCC	TTCATGGCCT	AGCTATTTTT	AAACAATATC	TGAGATTATT	CATTCAACTA	60
AAACTTATTA	AGCATTTAAT	ATCTGTCTGG	CATTCTTCAG	GCACCAAGGA	TATTTCGTTG	120
AACAAAACAA	AATCTTTGTC	ACTATGGAGT	TTACGTTTTG	TGGTGGCATT	GGAGTGAAGA	180
GCTAGGGAAT	AAAAAAACAA	GTCAATATGT	AGTATGCCAC	TTGGTGGTAA	GTCATTTGGA	240
GAATGATGTA	GTAGGGAAAG	AGGAAAAGGG	TGTAGGCATC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:1275:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

GAATTCGGCC	TTCATGGCCT	ACTCCACACA	TTCATCTCCC	AAAGGACTCC	TTGAATATTT	60
GCCCCAAAAC	ATCAGCTCCC	AGAAAACACC	CCTCCCAGTC	ACACACACAC	CCAAATTCTC	120
CGATGTATTT	TCATTTTTT	TCTCCTCTTC	TCTTCTCTTT	TTCCTTCCTT	CCTTCTCTCT	180
TTTCTCTCTT	TCCATCCCTC	CCTTCCTTCC	TCCCTCCCTT	CCTTCCTCCC	TCCCTTCCTT	240
CCTCCCTCCC	TCCTTTCCTT	CCTCCCCCCA	CCCACTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:1276:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 220 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

GAATTCGGCC	TTCATGGCCT	ACGAGTGGTG	CGATTTTTTT	TTCTTAGCTT	ATCAGCTATG	60
GTTAGTGTTA	GCGTATTTTA	TGTGCGGCCC	AAGACAATTC	TTCCTCTTCC	AGTGTGGCCC	120
AGGAAAGCCA	AAAGATTGGA	CACCCCTGGT	AGAGGCAGAA	ACTCACTGGG	TTAGTTCCAC	180
AGCATCTGAT	CAAAGATATG	AGGCCAAAGA	GCCTCTCGAG			220

- (2) INFORMATION FOR SEQ ID NO:1277:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 246 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

GAATTCGGCC	TTCATGGCCT	ACGAGCTGAG	ATTGCGCCAC	TGCACTCCAG	CCTAGGCAAT	60
AGAGTAAGAC	TCCATTTCAA	ааааааааа	AAATGTTGAT	CAAAAGAAGC	CAGATGACAG	120
AGTACTCACT	GTGTGAGTCC	ATTTATTTGA	AATTCTAGAA	CAAAAAATAA	ATATCCATTG	180
ATAGAAATGG	GAACAGTGTT	GGCCTATGAA	GAATGGAAAT	TGACTGGAAG	GAGGCCTCTG	240
CTCGAG	•					246

- (2) INFORMATION FOR SEQ ID NO:1278:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 499 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

GAATTCGGCC T	TCATGGCCT	AGCTGGGCGT	GATGGCGGGC	GCCTGTAGTC	CCAGCCACTC	60
GGGAGGCTGA GG	GCAGGAGAA	TGGCGTGAAC	CCGGGAGGCG	GAGCTTGCAG	TGAGCCAAGA	120
TTGCGCCACT G	CACTCCCGC	CTGGGCCACA	GAGAGAGACT	CCATCTCNAA	АААААААА	180
GAAAGAAAAA AA	AGAAAATAA	ACAAAGAAAA	AATTAAGATT	TTTGAAATAA	AAACAAATAT	240
TAAAAATTAT TO	GAAATATAT	TGAAAGTTTT	TTCACCATAT	ATATTTACCT	TTTAAAAGGA	300
TATGAATTCA A	TATTTTAT	TTGCTTATGG	AAAATAGATC	CACTGCTCTA	AGATGCTACT	360
AATCATGCTC AG	GAGGATTCA	CAACAAACAG	ACTGATAAGG	TATTACTTAA	AGCGCTCTAC	420
ATTAAATAGA G	CATTCCAGT	TTTCTAGGGC	ACACTACTTG	CTGTATTTCC	AAGGTCAAGC	480
AAAATAGCTT TO	CGTTCGAG					499

- (2) INFORMATION FOR SEQ ID NO:1279:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 317 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

GAATTCGGCC	TTCATGGCCT	AATGAGCTAA	AAGCAGTGTC	ATCTCCGCAT	GTTGGAGCAG	60
CCAAGAAATA	GTTTGGTACT	ACCGACATTG	TCTAATCCAT	GTCACATCCT	CATACAATTT	120
AATTGCTCAA	CCATGCATTT	AAAACTCCTC	AAGAAAGGAT	TGGTACTGCA	ACTGTAGGTA	180
AACTGAAAAA	AAATAAGAAA	GAAAGAGTTG	GATGAAAATG	TGAAAGCCCA	AGTTTAGATG	240
TGCATTAAGT	ATTAAATAGC	ACAGTATCTT	CTTCATGGAG	CCTTTTTTCC	TCCCCCATCC	300
CCTGCAGCTA	CCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:1280:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

GAATTCGGCC	TTCATGGCCT	ACTTCCTTTC	ATTTTGAAGC	AACAGTTTAT	AAACAGGAAA	60
GTCTACTGGT	TTCATAGAAT	CTGTCAGATT	TGCTTATTTG	CTACTGGTTT	CACGCGCGTG	120
GACTATATTC	CAGTGTTTCT	AGTCAAAGAC	CTTTATCCTC	AAATCATGAG	ATTAGAGTAA	180
AACAACTGCT	GTAAGGTTGA	GCATTTCATG	ACCAATGACT	ATGAAGGCAC	ATTCACCAAA	240
CACAGGCACT	TTAAGGGCAT	CCTTGATTAA	TTTGCTAATT	GCTATTTTTT	GTTGGTATGT	300
GAATTCCTGC	TAGGAGGCCG	AGGCTAGTAG	GCAATGAAAA	AGACAGAACA	ATGGTAAAAT	360
GCAGCCCCGG	TCCTCTACAA	ATTGACAGTA	TAATTTAGGG	GCTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:1281:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 281 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

GAATTCGGCC	TTCATGGCCT	AAGATTGACA	AAGAAATAGA	GCTTCACAGA	ATTCTTCATC	60
ATAAGCATGT	AGTGCAGTTT	TACCACTACT	TCGAGGACAA	AGAAAACATT	TACATTCTCT	120
TGGAATACTG	CAGTAGAAGG	TCAATGGCTC	ATATTTTGAA	AGCAAGAAAG	GTGTTGACAG	180
AGCCAGAAGT	TCGATACTAC	CTCAGGCAGA	TTGTGTCTGG	ACTGAAATAC	CTTCATGAAC	240
AAGAAATCTT	GCACAGAGAT	CTCAAACTAG	GGAACCTCGA	G		281

- (2) INFGRMATION FOR SEQ ID NO:1282:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 250 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

GAATTCGGCC TTCATGGCCT AGTAGTTTAT TATATAGAAA TTATTTGTCC TTGTCTTAGT TGTGCCCTTT GACTCAGCAA TTCCCCTTCT ATAAAATTTT CCCAAGCAGA TGATTATGGA TATATGCACC AATTTGGAAA CAGGGATGTT TATTGTTTAT AGTÁGCACTC AACTGAAAAC AACATAGTTG TCTTCAGGAG CGGGGACTGA TTAAATTATG ACATGAAGCA GAATAATGCA AAATCTCGAG	60 120 180 240 250
(2) INFORMATION FOR SEQ ID NO:1283:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 257 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:	
GAATTCGGCC TTCATGGCCT AGCTGAAGAA GGCCTTCACA GAGCTTCAAG CCAAAGTTAT TGACACTCAA CAGAAGGTGA AGCTCGAGA CATACAGATT GAACAGCTAA ACAGAACGAA AAAGCATGCA CATCTTACAG ATACAGAGAT CATGACTTTG GTAGATGAGA CTAACATGTA TGAAGGTGTA GGAAGAATGT TTATTCTTCA GTCCAAGGAA GCAATTCACA GTCAGCTGTT AGAGAAGCAG TCTCGAG	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:1284:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 434 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:	
GAATTCGGCC TTCATGGCCT AAAGACTAGC ATATTTATCT TTGACTTGAT TAATCAGACC TAATTTGCAT TCGCAAATGA GACTGATAAA AATGGATTTA CCTTTTAACC TTTAGAGGAG GAAAGGTATT TCTCTGCAAG ATTTCTGGGG CTATCGTTTC TTAACCGATA AGAAGCCACT CCTTTATCAA TAAAGATGAA AATCCGCAAT TTGCATTAGT GAATGGACT GATTATTATA TAGTTAATTA GCATCTGGAA ATGAGGATTA TCTTAATTAC AAAGCACAAT TTCCCTAATA GCTACAAAAC TGTAAGTTTG ATCCATGTGG AAATTGGTAA CATTATTATG TAATTAGTGA TAACATTAAT AGTGTAGAAT ATTTAGATGT AATTTGCATA TGCAAATGTG ATTTACCTGA GCCAAAAACT CGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1285:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 302 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:	
AGCAATATTT ATTTTAGACA GACTTCTGCG TTATGACCCG GCTGCTGGGC TACGTGGACC CCCTGGATCC CAGCTTTGTG GCTGCCGTCA TCACCATCAC CTTCAATCCG CTCTACTGGA	60 120

ACCTGGCCTG CT	CATGGGAA CACAAGACCC GCAAGCTGAG CAGGGCCTTC GGATCCCCCT FACTCTCTA AGCATCACCA TCCTGCTCCT GAACTTCCTG CGCTCGCACT GCCATGCTG AGCCAGCCCA GGATGGAGAG CCTGGACACC CCCGCACTCG	240 300 302
(2) INFORMATI	ON FOR SEQ ID NO:1286:	
(i) SE	QUENCE CHARACTERISTICS:  (A) LENGTH: 245 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) M	OLECULE TYPE: cDNA	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:1286:	
GCAGAGGTCT TO TGTTTTTTGA GA	CATGGCCT AATCTTTCT AATTTGTCTT AATGCTTTAT AATTTTCTAT STAGATCTC TTTCCAAGAT ATTTGATGTT TGTTTGTTTG TTTGTTTGTT ACGGAGTCT CACTCTGTTG CCCAGGCTGG AGTGCAGTGG CGTGATCTTG CCTCCGCCT CCTGGGTTCA AGCAATTCTC CTGCCTCAGC CTCCCAAGTC	60 120 180 240 245
(2) INFORMATI	ION FOR SEQ ID NO:1287:	
(i) SE	QUENCE CHARACTERISTICS:  (A) LENGTH: 232 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) M	OLECULE TYPE: cDNA	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:1287:	
TATAACATAA TI GGATAGAACT TI	CATGGCCT AATTTTTTT CTCCTCTTTC TTCTAGTACA TATTGATAGG PAAGGTTTA AAAAAAATTA GACATAGTTA TTCAGATTTA GGACCAGTAA PCTCTTATT TATGAAAAAA AATGCTAATA ATTTTGGGGC AGTTTTTTCC PTTTCAATT TCAAGTTTAA TTTTATTTTA GCTGATCTCG AG	60 120 180 232
(2) INFORMATI	ON FOR SEQ ID NO:1288:	
(i) SE	QUENCE CHARACTERISTICS:  (A) LENGTH: 298 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) M	OLECULE TYPE: cDNA	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:1288:	
TTGAATCTGA GA GCAACAGAGT GA GTGTAGGGTT TT	CATGGCCT ATAGGCCATG AAGGCCGCCT TCATGGCCTA AGAAGATCAC AGGTAGAGG CTGCAGTGAG CGAAGATCAC ACCACTGGAC TCCAGCCTGG AGACCCTGT CTCAAAAACA AAGAAGAGCA CTAGCTTCTC TATCAAGTAA CAAAAAACA CAAATGGACT TTGGTAGACC AAAACAAAAG CCCACGAGTA CTTGAAGTT GGAAATTCAA TTTCCCCCTT ACCCCCCCAA CCCTCGAG	60 120 180 240 298

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 227 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:	
GCGATTGAAT TCTAGACCTG CCTCGAGCCA TACCCATGGT CAGCCTCTTC CTCGTGTTCA CGGCCTTCGT CATCAGCAAC ATCGGCCACA TCCGCCCGCA GAGGACCATT CTGGCTTTTG TCTCTGGCAT CTTCTTCATA CTATCGGGCC TCTCCTTGGT GGTGGGCTTG GTTCTTTACA TCTCCCAGCAT CAACGACGAG GTCATGAACA GGCCCAAACA GCTCGAG	120
(2) INFORMATION FOR SEQ ID NO:1290:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:	
GAATTCGGCC TTCATGGCCT AGACAACTCT TAGCTAAATG TGGTTTGGTT	120 180
(2) INFORMATION FOR SEQ ID NO:1291:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 323 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:	
GAATTCGGCC TTCATGGCCT AGGTGCTCTC AAGGATCAGT ACTGGGTAAC AATAATCAAA CTTTGAATTT AAACATGCAT CTATTATTTG TGTTTTTTGT TTTTGTTTTT GAGGCAAAGT CTCACTCTGT CACCCAGGCT GGAGTGAAGC AGCCCAATCT TGGCTTACTG CAACCTCCAC CCCCTGGGTT CAAGCAATTC TCCTGCCTCA GTCTACCTAG TGGCTGGGAT TACAGGCGCC CGCCACCACG CCCAGGTAAT TTTTGTGTTT TAGTAGAGAT GGGGTTTCAC CATGTTGGCC AGGCTGGTCT AGAATTCAAT CGG	60 120 180 240 300 323
(2) INFORMATION FOR SEQ ID NO:1292:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 289 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

GCTCGAGAAA	CTTCTGCTGC	ACGTGCGTCT	TCCCCTCCAC	CTTCACCCCT	TGTGGCTCAC	60
TCACGCACCC	ACTCTCCAGT	CCACCCCTCC	TCAGAGACCC	TGTCCACTCA	TCCATCTCTC	120
TCCCATTGCG	CTTCCTCTTC	ACTCCGTTCC	TTCTGCCTCC	CACCATATGC	AAATCTTCTC	180
CATCCTTAAA	AGCCTGATTG	CCTCCTCTGG	ATTTTTCCAC	ACTCTTGGGG	AACTTCCTGT	240
GACTCCCTGC	CCTTCACCAC	CAGCCTTTCC	CAAAGAGAAA	TCCCTCTCA		289

- (2) INFORMATION FOR SEQ ID NO:1293:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 421 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

GAATTCGGCC	TTCATGGCCT	AGTTGAAATC	TTTAGGAATG	AACTTCTGAG	GGCCAAAAAA	60
TGTGACTGAC	GGGAACAATT	CTTAAACTGA	TTAACTAGCT	GTAATATAGT	TTTGTGAATT	120
TATTGCACTG	ATGTTGTACC	TTGTGGTATA	TCTGTCCCTA	TTAAATAAGT	GTTGTTTTCT	180
CCTCTTTAAT	ATTGCTGTGA	ACAGTGGTGC	CCATTGTAGC	<b>ATATGTTTGA</b>	TTTTTTTTTA	240
TTATTTCATA	AGAAAACTAC	GTTAATTTTA	CCTTACTTTC	ATTGTAAATA	AGCCTGTCTT	300
CCTATCTGGA	TTTTTTGTGT	GCATACATAT	TCTACTGATT	AACTACTTTT	GCAGTTTTAA	360
TCCTGTATTA	TTTCTTCTAC	TTTGTTTTGT	GTAAAAGGGG	AAAAAATAAA	AAAAGCTCGA	420
G						421

- (2) INFORMATION FOR SEQ ID NO:1294:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 408 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

GAATTCGGCC	TTCATGGCCT	ACAGGTGTAT	GTCACCATGC	CTGGCTAATT	TTGTTTTTCT	60
TTTCTTTTTT	TTTTTTTCCT	AGAGACAGGG	TCTCACTATG	TTGTCTGTCC	TGGCTGGTCT	120
CAAACTCCTG	GGCTCCATCT	TCCCGCTTCG	GCTTCCTGAA	GTGCTGGGAT	TACAATAGGC	180
ATGAGCCACT	ATGCCCATCC	TAAAGTTTTA	CAGCCCAATA	ATAGTAATAT	TCCATCACTA	240
CAGCTATCAT	TGAGTTTCAG	AAGTTAGACT	GTTAAAAGTT	TCAGTAAAGA	GCTTTAACCA	300
GTTTATTGTG	GCAATACTGT	GTACACAATT	ATTTTTTGTA	AAAGGAAGGA	GATTTCTGTC	360
TTAAATAGCT	TTAATAAAGT	TTCAGTTTCA	TATACAGGAA	ACCTCGAG		408

- (2) INFORMATION FOR SEQ ID NO:1295:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 259 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

GAATTCGGCC	TTCATGGCCT	ACAGGCACTC	CAGTTATAAT	TATGTGCCTT	TCTTCCATTT	60
CTACCACTTT	CTCTGATACT	TCTCACTTCT	TTCTCTGGTA	CTTCTCACTT	CTTTCTCTGG	120
TATCATTTTC	ATTCTTCATC	ATTGTTTTAG	TGCCTTTACT	TCAATTCCTT	CATTATTTGA	180
ATTTTTCTTT	TTATCATCTT	GTGATTCAGT	TTTTATTTAT	TTTTTGATAG	TATTCTCCTT	240
TTCTTCCATT	CCACTCGAG					259

- (2) INFORMATION FOR SEQ ID NO:1296:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 257 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

GAATTCGCCC	TTCATGGCCT	AGTGGAGAGT	GCTATCATTA	ACACCTGAAC	TCTGGGCCAG	60
CTTAAGTGTA	TATTCTGTAA	AAAATTTGAA	ATCCCCCAAA	TGTCACATGC	TATGACAGTC	120
ACTTTCTTTA	GTACTTTGTA	ATCATACAAA	ATGGTGTATG	GGCTAAATAT	TGCAGCACCT	180
ATGTCGTCAT	CCTCCATGTT	GCTTATTGAT	CATGGAATGT	TAATTTAGCA	ATAATTTTCT	240
CTGTGTGTGC	GCTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:1297:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

GAATTCGGCC TTCATGC	AG TAGGGTATGT	AGGCTTCAGT	TGGTTCTACT	TTCAGAGAGT	60
TAAGATGGAA TGAGGCAG	CT CATGGCACTA	CAGGTCAGTT	GCCTTCTCTC	CAAAATGTTC	120
ACTCATGCAT GTGGGCAG	TC ATTGTATTTG	AATAACAGCA	ACAGTGCCTC	CCTCAGTTTG	180
GAACCTCTAG TCCACTTC	CT CACTCATGGT	CCCTGCCTTA	ACCCCAGTCA	AGTTCAAAGC	240
CATAGGCATC ATTTGTCO	GA CTGACATATT	AGGGCATCTA	CCAGTCAAAG	GGTGATTGTT	300
GTAGATGACC TTTGGCCC	CGT TCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:1298:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

GAATTCGGCC TTCATGGCCT ACACTCTCAT GTTTGTTGCA GCATTATTCA CAATAGCCAA GGTATGGAGT CAACCTGAAT GTCGAACACA TGAATGGATA AAGAAAATGT TCACACACAC AATGAAATGT GATTTAGCCT TTAAAAAGAA GGAAATCCTG CCATTTGGAA CAACATGGAT GAACCTGGAG GGCATTGTGC TAAGTGAAAT AAACCAGACA CAGAAAGACA AACACTGCAT GACCTCACTT ACTGTGGAAC CCCTCGAATT CTGGATCTCC CTCGAG	60 120 180 240 286
(2) INFORMATION FOR SEQ ID NO:1299:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 285 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:	
GAATTCGGCC TTCATGGCCT AATGAATTTA GTATTATTTC TATCATTTCA ATTGCAAATT GTCAGTATCC CCTGCTACGT TTCTACTAAT TTACCATCGC TTCTTCAAAA AATTGTGTTC AGAGTGCTAC AATTTCAGAC TTTGAAATGA ATCACTATAA CTTTTAAAAAA TTAGAGATTT TAAAAACTGG AGATTGAATA TATATAAAAA ATACAAAATT TGACATTTAA AACCTCATTG AACTTTTAAA AAAGCCAGAC TCATATTAAG GCACACACCC TCGAG	60 120 180 240 285
(2) INFORMATION FOR SEQ ID NO:1300:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:	
GAATTCGGCC TTCATGGCCT AGGGCCAATG GCCAGGATCT CTGGGGACTA GAAGGGTGGA TTCCTGAACC TGGGTAACAA CGAGACAAAC TCTAGCAATC TGAGCAAGGG AAGGGTCATC AAAGTCCCAA AATCTAGCCC ACTAGCTGCC TAGCCAGGTA AACCAAGGCT TAGGGAGTTT AGACCCTTTC ACATAAAGAA GCTTAATAAA AAGTGTTGGG TGAAGAGATA AACACATGAA GGGGTTGGCT AAAGTCAAAA GAAGATCCGA GGCAGGTCTA GAATTCAATC GG  (2) INFORMATION FOR SEQ ID NO:1301:	60 120 180 240 292
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 548 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:	
GAATTCGGCC TTCATGGCCT ACTCCTCATT TGCCACCACC AGGCCAGTTT GTCCCTTTCC AAACACAGCA ATCACGATCG CCTCTGCAAA GGATAGAAAA TGAAGTGGAA CTCTTAGGAG	60 120

180 240 300

AACATCTTCC AGTAGGAGGT TTTACTTACC CTCCATCAGC CCACCCCCCA ACATTACCTC CATCAGCTCC CTTGCAGTTC TTAACACATG ATCCTTTGCA TCAGGAGGTG TCCTTTGGAG

TACCTTATCC TCCATTTATG CCTCGGAGGC TTACAGGATA GTAGATACCG ATCCCAGCAG

CCAATACCAC CTCCCCCTTA TCATCCCAGC TTACTGCCAT ATGTGTTATC AATGCTTCCA GTGCCACCTG CAGTGGGCCC AACTTTCAGC TTTGAATTAG ATGTAGAAGA TGGAGAAGTA

360 420

GAAAATTACG AGGCCCTGTT AAACCTGGCA GAGCGACTGG GAGAGGCAAA GCCTCGTGGA CTGACTAAAG CAGATATTGA ACAACTTCCT TCTTATCGGT TCAATCCTAA CAACCACCAA TCCTCGAG	480 540 548
(2) INFORMATION FOR SEQ ID NO:1302: .	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 384 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:	
GAATTCGGCC TTCATGGCCT AGTATCTATC TAGTGCCTGT TTGTGCGTTT TTTTCTTTCT TCCGCTGCTT CCCCATTTTC CTTCTGTCCT TTTTCTCTG CTCCTTGTTT TCCCAGCAGC ACATGGGGTT CCTCGAGGA GCAGAGGTG CCGCCGTGG GGGCGTTTG GGCTGCGTG CTGCGTCATT TTTCCTTTGC TTTCTCTTTA CTTTAGACAC TGGCCCAACT CCAGGCGTTT CCTTTCATTC CCTCAGTGCT TCTCTTCTGA CCTGCATGTT GAGTTCTGTA TTGCTGGGGC TTCCAACAAA AACCAGAGTC ACTGACAGAG GGAACAGCAG AGACCTTGTT GGTATTCAGC TGTGATGGAT ATAGCGATCT CGAG	60 120 180 240 300 360 384
(2) INFORMATION FOR SEQ ID NO:1303:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 140 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:	
GAATTCGGCC AAAGAGGCCT AGGGTACGTG AATCTATTTT TTCAGCTGGA AATTTTATGA AATCTGGTGT GTATTTTATA CTTATAGCAT ATCTCGAGGC AGGTCTAAAT TCAATTCTAG ACCTGCCTCA AGAGCTCGAG  (2) INFORMATION FOR SEQ ID NO:1304:	60 120 140
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 620 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:	
GAATTCGGCC AAAGAGGCCT AAATAAGTTT ACTTTTATTT TTGGTAACAC TTTACTGCAT TGTCTGAATA TTGACAATCA GTATGCATTA TGAAGCTACC TGGCTAACAT TGTGTACTCA CTGTGTGTGC CAGGCCCTGG GTTCAATGCT CTACATGCAC TTATATTTCA TTTAATTCTC TCTGCAACCT GAGATGGTAT AGCCACCTCA TTTTACAGAG TTGAAACTGA GGCTCAGAGA CTGAAAGTTA AGCCTGAGGT TGCAGTCAAT AAGAGGCAGA GCTGGAACTG AAACCTACCT	60 120 180 240 300
524	

GTGTCTGACC	ACCAGTTCGT	GTTCTGACGG	CAGGCTAGTC	TGCATCACAG	AGTGTGGAGT	360
AGATGGTGCA	TGCCTGCTAG	GATGGGCTAG	GTATCACTGT	AGGTAAGAAA	CAGCCCCAAA	420
CTATGGAAAT	GTACACCACC	GAAGGCTCTT	TTCCTGCCCA	TGCTGCACAT	CCTCCATGGC	480
TCTCCTGTGC	CCTGTGCCCC	ACATGCCCTC	ATCCTGCCAC	GAGAATAAAG	GAGCAGCCTC	540
CATATGGGAG	CTGTCAGCTG	CTCTAAGAGA	TGAAGGAGAG	AGTGGCCCGT	CTCAATGGCT	600
CCCAACTCTT	CTGCCTCGAG					620

- (2) INFORMATION FOR SEQ ID NO:1305:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 736 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

GAATTCGGCC	AAAGAGGCCT	ACTTTTGGCT	CAATGTTTTC	CAAACTTATT	TGACCCCAAA	60
ACCTTTTTCA	TATACCCAAT	AATAAGCTAC	AGAACTAATA	TTCTGCAAAT	GTCTCTTGGA	120
ACACACTGCC	TTAAACAGAT	ATTTCTATAG	CTGTCAGTAT	AGTTATGTTG	CTCCCAAGCC	180
TAGTTATCTC	CAGTTGTTTT	${\tt AAGGGTGTTA}$	TGAAAAATTC	TTAAAATATA	TATGAATTTG	240
TGTAACACAC	ACAGAGACAC	ACACACATAC	TACTTTAAGG	GGGTGAGGAT	CATTAATTCA	300
GATAATTTTT	AAGTTTCCTA	GTGATTCTCA	ATCTCTTTGA	ATTTTACTTA	CATTTACACA	360
CACACGCACA	CACATATGTA	TATACACATA	TCATTTTAAG	AAGCTGAGGA	TCACTAATTC	420
AGATAATGTA	TAAGTTTCCC	AGTGATTCTC	AACCTCTTTG	AATTTTACTT	ATAATTACAT	480
AÇACACACAC	ACTGCTACTT	ATATAAATGT	TCTCATGTAA	TCATGGTAAC	AGCTCAAATT	540
CCCAAAGCAA	GGGAAGACTT	CTCATTGTCA	GTTAAACCTG	TTAAAACATG	AAAATATTCA	600
TTGAGCCTAG	TTCCTTGTTA	TAAAATACAA	GAAATAAGAC	ATTCAGGCAT	TTTCCCTTTA	660
TGAAGATGTT	CAGTCATCCT	TTCCTTGAAC	TACAATTAGG	AAAAGTATAT	GTCTTTATTC	720
CATTGAAGTT	CTCGAG					736

- (2) INFORMATION FOR SEQ ID NO:1306:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 511 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

GAATTCC	GCC	AAAGAGGCCT	ACAGCAATAT	GCATCTTGCA	CGTCTGGTCG	GCTCCTGCTC	60
CCTCCTT	CTG	CTACTGGGGG	CCCTGTCTGG	ATGGGCGGCC	AGCGATGACC	CCATTGAGAA	120
GGTCATT	rgaa	GGGATCAACC	GAGGGCTGAG	CAATGCAGAG	AGAGAGGTGG	GCAAGGCCCT	180
GGATGG	CATC	AACAGTGGAA	TCACGCATGC	CGGAAGGGAA	GTGGAGAAGG	TTTTCAACGG	240
ACTTAGO	CAAC	ATGGGGAGCC	ACACCGGCAA	GGAGTTGGAC	AAAGGCGTCC	AGGGGCTCAA	300
CCACGG	CATG	GACAAGGTTG	CCCATGAGAT	CAACCATGGT	ATTGGACAAG	CAGGAAAGGA	360
AGCAGAG	GAAG	CTTGGCCATG	GGGTCAACAA	CGCTGCTGGA	CAGGTTGGGA	AGGAGGCAGA	420
CAAACTO	GATC	CATCATGGGG	TCCATCACGG	GGCCAACCAG	GCGGGAAGTG	AGGCAGGGAA	480
GTTTGG	CCAG	GGAGTCGACA	ATGCACTCGA	G			511

- (2) INFORMATION FOR SEQ ID NO:1307:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 219 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

GAATTCGGCC	AAAGAGGCCT	AATTTTTCCC	CACACCACAC	CACTGTCCTC	TGTGCCTGTG	60
GAAACCACTC	AAATGCCTCT	CCCCAAGCCT	TCTTTCAGTA	ACAACCATCT	CATCCGGTTG	120
ATTACTGTAG	CTTTCGGCCT	GTATAACCCC	TCCTTATGTC	ATGCCTGTAC	CAGATGTTCC	180
ACTGCATCTG	TATCCCACCA	GATTGCACAT	ACTCTCGAG			219

- (2) INFORMATION FOR SEQ ID NO:1308:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

GCACTGCGCC	TGGCCCTTGT	GGATACTTTC	TAGGTGATTT	GAGGAGGAAA	GGCACAGCCA	60
TGTCTCCTAA	AGTTAACAAG	CACTAAGCTT	TCCCAAGTAG	TGAAATGTCA	AGCCTCTGCT	120
TCTGTCACTT	ATTTGTTCAT	TCAGCAGAAA	GTCACTGAGA	GCCTTCTGTA	CACCAGGCAC	180
AGTGCTGGGC	AGTGAAAGAG	ACAGACATGT	CCCTGGATCC	AGGGAGGAGA	TGACCAAGTG	240
ATGGCTGTCA	GGCCCAGACC	TTGCTGTTTG	TCTGCAGCCT	CTTCCCTCAG	GCAACTTGTT	300
CTCTATCAGG	AGAAATGAAA	TAATTATTAT	CTGGAGCTCT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:1309:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 565 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

GAATTCGGCC	TTCATGCCTA	AAAAGGGTCA	GAGGAAGGCA	GTATCCTTGG	GGTGTTGCTG	60
AAGTTGAAAA	TGGTGAACAT	TGTGATTTTA	CAATCCTAAG	AAATATGTTG	ATAAGAACAC	120
ACATGCAGGA	CTTGAAAGAT	GTTACTAATA	ATGTCCACTA	TGAGAACTAC	AGAAGCAGAA	180
AACTTGCAGC	TGTGACTTAT	AATGGAGTTG	ATAACAACAA	GAATAAAGGG	CAGCTGACTA	240
AGAGCCCTCG	AGTTGCAGGG	AGCCCAGATC	ATGCCACTGC	TCTCCAGCCT	GGGTGACAGA	300
GCAAGACTCT	GTGCCCCCC	CCCACCCCAA	AAAAAAAGAA	AACAAAAATT	AAAATCTTTA	360
GTTACTGTAT	TATTCAAAAA	TGTCTACTTT	CAAGAAAAAC	TACAGCCATG	CAAAGAAACA	420
GTAAAATGTG	ACCATACTCA	GGAAAAAAAG	CAGACAATAG	AAATGGCTTC	TCAGTAGGGC	480
TATATGTTGG	ATTTAGCAGG	CAAAGACTTC	AGAGGCCTTT	TAATAAGTAT	ATTCAAAGAA	540
TTACAGGAAA	ATATGAAAAC	TCGAG				565

- (2) INFORMATION FOR SEQ ID NO:1310:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 104 base pairs
    - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310: TGCACAGCTG TAGTACCCCA AGAAGAAAAT GTTACTTCTC TCATCTGGGC AAAACCCACA 60 GAAGACTTCC CAGCTTCTGC CACATAAAAG ACACAGAACT CGAG 104 (2) INFORMATION FOR SEO ID NO:1311: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311: GAATTITIGCG TTCTGTTTAG CATGCTATCC TGTGTGAAAG AAACTGAAAT CCAATATTAT 60 GGAGAGTATG TTAAAGCCAC CTCTGAAATG AAGACCACTC TCGAG 105 (2) INFORMATION FOR SEQ ID NO:1312: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 407 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312: GAATTCGGCC TTCATGGCCT AAAGGGAAGG GAGGTGTGAG GAGGATGGAG TAAGAGTGAG 60 AGGTCCTAAG AACATGGAGG GAGGCTGTGT GTGATCGATG GAGAAATATG GTCCTGAGAG 120 ATTTCTTGTA GTCAAGAATG GCCAATACAT GTCTACCTTT AACTGGTATT GGAAGGAAGT 180 AGTTTCCTGC TCTGTGCTCT AAATACTCTC TATTACCCTC AAGATGTCAG CAAAATGTGA 240 TACATAGCAA TCTTGTGTTA GAGATGCTTT AGGAATTGCA GAAAAACCAT GCTATCAAGT 300 GGTAGGGAAG TGAGTGGCAA GAGGATGTCT GTCACAGAAA CTAGGGATAG AGGGGCTGGC 360 AATGGCAGAG ATGCAGGTGG AGTGGACTGA TTAAGGGGAG TCTCGAG 407 (2) INFORMATION FOR SEQ ID NO:1313: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313: GAATTCGGCC TTCATGGCCT AGGTCTTGCC ACATTGGCCA GGCTGGTCTC GAACTCCTGG

PCT/US98/06956 WO 98/45437

GTTCAAGTAG TCCTCCACCT CAGCCTCTCA AAGTACTGGG ATTACAAGCG TTGAGCCACC CTCCCAGCCT TTGCCTTTTT TTTTTTTTT TTTTTTTTTA GGAGGAGAAT TAATTGATAC ATAGACCCCT TAAGAGAAGG GATGCTATGG GCAGGAAGAG ATTGAAGGTA AAGGAAAAAG GATTCAGCAC CCAAGCAAAA CAATTGGCCT GTGATAGAAG GGCGATCTCG AG	120 180 240 292
(2) INFORMATION FOR SEQ ID NO:1314:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 309 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:	
GAATTCGGCC TTCATGGCCT AGATCCAAGA AGCTCAACAG ACCTCAAGTA GGATAAACAC AAACAGATCT TCACTAAGTC CTACTGCTGA AAGACAAAGA CGAGGAGAAC ATCTTGAAAG CAGTGAGAGA AAAACAACTC ATTATGGAGA GAGCAATGAT AAAATTCTTA TCAGAACAGT GGAGGCCAGA AGGAAATAGA GTGACATATT CAAAATGCTG AAGGAAAAAT TTGCAACTAC AAGTTCTAGA TCCAGCAAAA TTATCCTTCA AGAATGAAGG TTTAGTAAAG ACATTCCCAG ACCCTCGAG	60 120 180 240 300 309
(2) INFORMATION FOR SEQ ID NO:1315:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 469 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:	
GGCCCCAGCT CCTGAGTAGC TGGGATTACA GGCATGCACC ACCACACCCA GCTAATTTTG TATTTTTAGT AGAGACAGGG TTTCACCATG TTGGTCGGGC TGGTCTCAAA CTCCTGACCT CAGTGATCCA CCCGCCTTAG CCTCCCAGAG TGTTAGAATT ACAGGCGTGA GCCACTGCAC CCGGCTGGGA AACATTTTTA AAACGGCGCA GGGTTGTCCT TGAAAGTCCC AGGTTTCCTC ATTGGCCCTG CCATTGGCGG GTGGGTGATT TCAGGCAGGA CACGCAGTGT CTGGGGACCC TGGCTTTCTC ACTGGAAGAC GATTGTTATG GTCCAGAGGG TGGTAACTCA GGTGTTCATG TCTGATTCTG GATGTTCTC GCAGCTGCTG GAGTCTCCTG ATTGGAGAGC AGCAAATGAC TGTTCAATGA CAGTTCTAGT TGTACCTCTA GCACCCCCAC TCGCTCGAG	60 - 120 180 240 300 360 420 469
(2) INFORMATION FOR SEQ ID NO:1316:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:	
GAATTCGGCC TTCATGGCCT AATCTATGTG TGTCAACTTT CATAGAACCC TACACCAAAA AAGGTGAATT TTATTTCGTG ATAAATTAAA AAGTAAAACA AAAGAGACAA AAATAGTAAC	60 120

	TTCAAAAAAT ATATGTTCTT GTTCAAGACC AGCATGGCCA ACATGGCGAA	180
	TAATAAAAAT AGAAAAATTA GCCAGGCGTG GTGGTGGGCG CATGTAGTCC GCACCGCTCG AG	240
CAGCIAICCA	GCACCGCICG AG	262
(2) INFORM	ATION FOR SEQ ID NO:1317:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 497 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1317:	
GAATTCGGCC	TTCATGGCCT AAAGGAATGG TATTTTGGCA ACGCAGACAA AGAAAGGAGT	60
	GATTTCAIGA GATGCAAGAA TTGTGGACCA AAGGAATGTT AAATGCAAAA	120
ACCAGATGCT	GGGCTCAAGG CATGGATGGA TGGCGACCAC TTCAGTCCAT ACCCCAGCTC	180
CGAGTCATAT	AAGGTAACCC AGACAACCAC CTACGAATTT AAAGCTCCTA TAAGTTGCCC	240
	CGAAGTGTGA TATTTGAAAG TTAAAAACGT TATCTTACAT ACATAGATCT	300
	CTTACACCAC AACCTACTCA CAGATGCAAA GGCAGTGGTC GTGGTCTTCC	360
	GTCCTGGGGC CGGGTTTGAG GCTGAATGTC AGGGTTTCCT TTGCCATAAC	420
	ACCACGTGCT GTCAGCCAGG CAGCCAATGT GGACTTGGAG GCTGGCATCT	480
GCTGGGCACT	GCTCGAG	497
(2) INFORM	ATION FOR SEQ ID NO:1318:	
(5)	SEQUENCE CHARACTERISTICS:	
(1)	(A) LENGTH: 451 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
,		
(X1)	SEQUENCE DESCRIPTION: SEQ ID NO:1318:	
GAATTCGGCC	TTCATGGCCT AATCTGGATG TCTGTCCAAG GCCTGACTGC TGAACTCCTA	60
CTTTTCCTAC	AAAACCCTAC CCACATGGCC CTTCCTGCGG GAAGAGATCT TGAGCCTCCC	120
TGGCTATTAA	GACTCTGCTG TGCAGCCTTC TTTTACTGGA CTCAGGGCTA TCTTCCCCAG	180
ACTAGGGCCT	TCTTGAGGAC AATCGTGGTG GCCCAGTGGT TGACGCTGTC TCCCCTGCAT	240
	TTCCTGGTTG CTTCTTGCCC CTGTGGCTCC CTTGGGAGAC TGAAACTCAG	300
	CTGGTCTGCT GTTACATGGC TCCCACAGGG AGACTGGCCC CACCTGTGCC	360
	CAGCTAGGGC CTGGGATGGG TCAGACACTG GAAGAGCCTC CCCCTAGGCC	420
ATGCATATGG	ATCGTGCCCA CACGCCTCGA G	451
(2) INFORM	ATION FOR SEQ ID NO:1319:	
(5)	SEQUENCE CHARACTERISTICS:	
127	(A) LENGTH: 477 base pairs	

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

GAATTCGGCC TTCATGGCCT ACACTACGGT ACTCCCAGCA TATCACCCTT AATGTAACTT TAAATAACAT GGCCATTTTT TAAAAAGGAC ACAGGAACTA CATAACATTT TTTTTCAGAT TTTGGAAAAT TCTAAATATG TCTAGAAAAA CTTTTCTTTC TGTTCCATTC TCCCTAT TCTCCATGAC CCCCTCCCCG CGGACTGTAT CAGGTACAGC CTGTTGGAAA TCCAGCACCG CACATTAGGC ACACCAGTGG TAAGTTTACT TGTTGAGTTA TCACCTTTTT TTTCCTTTTA ATCAGAGAGG CAGCTCTGTG TTGAAGATGC TAGGTAGTGA TGGAAAAAGAC ATTAGGAAAA TTTGTTACCG TGGTAACCGG GGATGGACAT CATGACCTTT TGTGATATGC ATGCTGTGGC CTTGGTAGTC TCTTCCCCTA ATTAACATCC TGTGAGAAAC GTGAGAGATG ACTCGAG	180 240 300 360
(2) INFORMATION FOR SEQ ID NO:1320:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 284 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:	
GAATTCGGCC TTCATGGCCT AGACGAGGC TGGAGATTCA CATGGGGCGA GGAGTTGCAG ACCAGCCTGG GCAAAGCATG GTGAGGCCCC GTCTCTGCAG AAATGAGAAA ATGAGCTGGA TGTAGTGGCA CCGACATGTG GTCCCAGCTG CTGGGAGGGC TGAGGTGGGA GGATTGCTTG AGCCTAGGAG TTCAAGGCTG CGGTGAGTAG ATCGTGCCAC TGCGCTCCAT CCCTGGCAAC AGAGCAAGAT CATTTCTCAA AAAGAAAAAA AAAGCCATCT CGAG	120 180
(2) INFORMATION FOR SEQ ID NO:1321:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 254 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:	
GAATTCGGCC TTCATGGCCT AGGGAAATGT GTGATTGGGA AAGAGGCAGC TTTTAAAAAT GTGTCTGGCC TTTGACCACG CAATTTCACT TTCCAGTATT TATTCTAGGA AAATACTCAT ACTATTGCAA AGTTTATATA TAAAGATAGT TATAACTGCA TTGTTTATCA TTTACAAAAA GAAAACATCT GAAAGCCCAA CAAGACGGAA CTGGTTATTC CACATTGGCA CATTCATACA AGGCAATGCT CGAG	60 120 180 240 254
(2) INFORMATION FOR SEQ ID NO:1322:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 352 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:	
GAATTCGGCC TTCATGGCCT AGGCACAGAA AAATTGGAAA GGATTGGTGG TCGTACATCT TGCAGCTCAC TTAGTAGCTG CATGCATGTA GACCGGGTGG TGTTGATGCA GTGTTGACTT	60 120

GAGGTTGGTG TCTGCCTGGT	GGGTGGGTGG TAGCATGGTC AAGCT CAGGGAAACT CTGTGGGTGT GTCTA CTTTGGGGGG TCAGGTGGAG ATGTC GAGGGCATGG TGCAGGCACA TGGAT	ATGCA AGGATAATGA CTTTT GGAAAGGCAG	CAATGTCCTG CCATTCTCTT	180 240 300 352
(2) INFORMA	TION FOR SEQ ID NO:1323:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 440 base pair  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:1323:		
TTATTCCAGT TAAGTAATAA TTTGCAGTTT TGTAATCCCA AATAATTGTG	TTCANGGCCT ACTGTGTGTA GAATT ACTTTGACTG CTAGTATTGC TGTTG CCCTTTTATT TGGCTGTGTT AAGCC TGTATAATGT ATTGAGGGCG TTATT CTTGGGATTC TTTGGGCTTC CTGGA GAAAATTCTT AACCATTATC TCTTT AATTAGACAT ATAGTCTATT TTTCA CATACTCGAG	AAAAG TCTTAATTGC TTTTT TTTTCCTTCC TTTTT CATTCCATCA TCTGA GGATAATAAT GAATA ATGCCTCTTA	CCTTCCTTTG CATTTAGTGT TTTTATTTTT AATGTCTTTG TTTCTCCTT TTCATCCTTT	60 120 180 240 300 360 420
(2) INFORMA	TION FOR SEQ ID NO:1324:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 280 base pair  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	rs		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:1324:		
AATTGTATAA CTTAGCACTG TTAATGAATA	TTCATGGCCT AATTGAATTC TAGAC ATTCTTGCCA AAAGTGTTTG AACTT TGCTCATCTT GAGGGGACAT AGTCC TGTGTAGACT TCATATGGTT GTGGG TATAGCTAAG TTGATCCGCG GATCC	AATAC AAACTTCCCA CAATT TTGTATTTTA TAAGA GAATACTGCA	TCTCTTACCT TATAATACTG TTCAGATAGA	60 120 180 240 280
(2) INFORMA	TION FOR SEQ ID NO:1325:			
(i).	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 281 base pair  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	rs		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:1325:		
TGAGACAAGC	CTACTTACAA AGAAAATAAA TAGAA CATTGTAAAT TGTTACTAGA CTAAC TCCACTCAAA TTTGTAAAAA GCAAT	STAGTA GTATACCAGT	CATTGACTGG	60 120 180

TGATCTAAAG AGGCTTTACA TAAGAGACAG AGTCGCTCGA G

TTTTTTAAGG TTTTTGTTGT TGTTTGGTTT TTTGGCAAAA CATGATACAT TTCTCATGCT

240

281

(2) INFORMATION FOR SEQ ID NO:1326:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 348 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:	
GAATTCGGCC TTCATGGCCT ACTATCTTGA ATGTCCAACT CCAACTCCTA ATTATTTTAA AAATCTATGC ACTTCTTCA CTTGAATTC TATGCCCTCA TAGACTTTAC AGGCACATGT TCTATCACCA ATTAAGAGAA ATTTAACTTA CACATTTTAC AACTTATACA TGCAATTTGG CTGAGCTTAT ACAGCACAGA TCAACATTAC AATCAATTTA CTGCCATGTT AAAAAAAAAA	60 120 180 240 300 348
(2) INFORMATION FOR SEQ ID NO:1327:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 680 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(11) MODECODE TIPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  GAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC TCAAACTACG AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA CTCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTAACCTCGC CTTACCCCCC ACTATTAACC TACTGGGAGA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC	60 120 180 240
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  GAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC TCAAACTACG AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA CTCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTAACCTCGC CTTACCCCCC ACTATTAACC TACTGGGAGA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC ACTCTCCTAC TTACAGGACT CAACATACTA GTCACAGCCC TATACTCCCT CTACATATTT ACCACTAACC CTCGAGACCA CTTCATATAA ATACTTATTT ATTTCCTATT TCCCCTGACT	120 180
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  GAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC TCAAACTACG AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA CTCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTAACCTCGC CTTACCCCCC ACTATTAACC TACTGGGAGA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC ACTCTCCTAC TTACAGGACT CAACATACTA GTCACAGCCC TATACTCCCT CTACATATTT ACCACTAACC CTCGAGACCA CTTCATATAA ATACTTATTT ATTTCCTATT TCCCCTGACT AGAAATATAA GCTCCATGGT AGCAGAGATT CTGATTGCTG CCTACTCTAT CCCCCAGCTCC	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  GAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC TCAAACTACG AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA CTCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTAACCTCGC CTTACCCCCC ACTATTAACC TACTGGGAGA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC ACTCTCCTAC TTACAGGACT CAACATACTA GTCACAGCCC TATACTCCCT CTACATATTT ACCACTAACC CTCGAGACCA CTTCATATAA ATACTTATTT ATTTCCTATT TCCCCTGACT	120 180 240 300 360
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  GAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC TCAAACTACA AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA CTCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTAACCTCGC CTTACCCCCC ACTATTAACC TACTGGGAGA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC ACTCTCCTAC TTACAGGACT CAACATACTA GTCACAGCCC TATACTCCCT CTACATATTT ACCACTAACC CTCGAGACCA CTTCATATAA ATACTTATTT ATTTCCTATT TCCCCTGACT AGAAATATAA GCTCCATGGT AGCAGAGATT CTGATTGCTG CCTACTCTAT CCCCAGCTCC TATACTAGGC ACCATGAGTA CATGATCAGA AAATATTCAT GGAAAAAAAT ACATAAATGT ATAACAATCT TCATTTGTGA GTAAGAAGAT GGGCTCTGGA ATCAGACTGC CTGGATTGAA ATCCTAACTT CATCACTTAC TAGTCATGGG ATATTTTACC TCAGTTTCAC TTTTTGAAAA	120 180 240 300 360 420 480 540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  GAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC TCAAACTACA AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA CTCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTAACCTCGC CTTACCCCCC ACTATATAACC TACTAGGACA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC ACCTCTCAC TTACAGGACT CAACATACTA GTCACAGCCC TATACTCCTC CTACATATTT ACCACTAACC CTCGAGACCA CTTCATATAA ATACTTATTT ATTTCCTATT TCCCCTGACT AGAAATATAA GCTCCATGGT AGCAGAGATT CTGATTGCTG CCTACTCTAT CCCCAGCTCC TATACTAGGC ACCATGACTA CATGATCAGA AAATATTCAT GGAAAAAAAT ACATAAATGT ATACTAGCT CATCACTTAC TAGTCATGG ATATTTTACC TCAGTTTCAC CTGGATTGAA ATCCTAACTT CATCACTTAC TAGTCATGGG ATATTTTACC TCAGTTTCAC TTTTTGAAAA TGCACACAAA	120 180 240 300 360 420 480 540 600
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  GAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC TCAAACTACG AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA CTCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTTACCCCCC ACTATTAACC TACTGGGAGA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC ACTCTCCTAC TTACAGGACT CAACATACTA GTCACAGCCC TATACTCCTC CTACATATTT ACCACTAACC CTCGAGACCA CTTCATATAA ATACTTATTT ATTTCCTATT TCCCCTGACT AGAAATATAA GCTCCATGGT AGCAGAGATT CTGATTGCTG CCTACTCTAT CCCCAGCTCC TATACTAGGC ACCATGAGTA CATGATCAGA AAATATTCAT GGAAAAAAAT ACATAAATGT ATACCAACT CATCACTTAC TAGTCAGG ATATTTTACC TCAGTTTCAC CTGGATTGAA ATCCTAACTT CATCACTTAC TAGTCATGG ATATTTTACC TCAGTTTCAC TTTTTGAAAA TCAAGACTAC CTGGATTCAAC ATTAGGCCAT GAAGGCCGAA	120 180 240 300 360 420 480 540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  GAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC TCAAACTACA AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA CTCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTAACCTCGC CTTACCCCCC ACTATATAACC TACTAGGACA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC ACCTCTCAC TTACAGGACT CAACATACTA GTCACAGCCC TATACTCCTC CTACATATTT ACCACTAACC CTCGAGACCA CTTCATATAA ATACTTATTT ATTTCCTATT TCCCCTGACT AGAAATATAA GCTCCATGGT AGCAGAGATT CTGATTGCTG CCTACTCTAT CCCCAGCTCC TATACTAGGC ACCATGACTA CATGATCAGA AAATATTCAT GGAAAAAAAT ACATAAATGT ATACTAGCT CATCACTTAC TAGTCATGG ATATTTTACC TCAGTTTCAC CTGGATTGAA ATCCTAACTT CATCACTTAC TAGTCATGGG ATATTTTACC TCAGTTTCAC TTTTTGAAAA TGCACACAAA	120 180 240 300 360 420 480 540 600
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:  GAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC TCAAACTACG AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA CTCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTTACCCCCC ACTATTAACC TACTGGGAGA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC ACTCTCCTAC TTACAGGACT CAACATACTA GTCACAGCCC TATACTCCTC CTACATATTT ACCACTAACC CTCGAGACCA CTTCATATAA ATACTTATTT ATTTCCTATT TCCCCTGACT AGAAATATAA GCTCCATGGT AGCAGAGATT CTGATTGCTG CCTACTCTAT CCCCAGCTCC TATACTAGGC ACCATGAGTA CATGATCAGA AAATATTCAT GGAAAAAAAT ACATAAATGT ATACCAACT CATCACTTAC TAGTCAGG ATATTTTACC TCAGTTTCAC CTGGATTGAA ATCCTAACTT CATCACTTAC TAGTCATGG ATATTTTACC TCAGTTTCAC TTTTTGAAAA TCAAGACTAC CTGGATTCAAC ATTAGGCCAT GAAGGCCGAA	120 180 240 300 360 420 480 540 600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

GAATTCGCGG	CCGCGTCGAC TGTCACTGAG CTTCTTGGCT CTCTTATATA TATTCTTTAT	60
	TTTGGTGGAC GAAGAGAAGG AGAGAGTTGG AATTGGGCCT GGGTCCTCAG	120
	GCAAGACATA TTGGATATTT GGAACTCCTC CTTAAATTGA TGTTTGTGAA TTGCCAGAGC AGACTACTAA AGCTTTACCT GTGAGGTTTT TGTTTACAGA	180 240
	CTGTCCAGTG TAGGTGGAGA AACTTCTCTG GCTGAAATGA TTGCAACCCT	300
	TGTGAAAGAG AGTTTGGCTT TTTGGCAACC AGGCTTTTTC GAGTATTCAA	360
GACTGAAGAT	ACTCAGGGTA AAAAGAAATG GAAAAAAACA TGTTGTCTCC CATCTTTTGT	420
	TTTATCATTG GCTGCATTAT ATCTGGAATT ACTCTTCTGG CTATATTTAG	480
AGTTGACCCA	AAGCTCGAG	499
(2) INFORMA	ATION FOR SEQ ID NO:1329:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 200 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1329:	
GAATTCGCGG	CCGCGTCGAC CGCTGCCAAA TGCTTCACTC CTATCTACTC TCCCGATTCC	60
	GAACCTCCTC AACAGAAATC TTGCTCTCTC CCTAAATCCT CAGTGCAACA	120
	AAAACTAAAT GATCCCTCCT CAGCCAGACA GAAAACTCTC AACATATCAA	180
CACTCCCAAG	GCGTGGACAG	200
(2) INFORMA	ATION FOR SEQ ID NO:1330:	
(i)	SEQUENCE CHARACTERISTICS:	
,-,	(A) LENGTH: 158 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1330:	-
GAATTCGGCC	AAAGAGGCCT ACAGTCTTTT TAGGCATGTT TTTTTTTTTT	60
	AATATGCATT TTATCTGTAG TGGTTTTAAA TCCTGTATTA AGCGTTGTTT	120
TCTTTTCAGA	CTGCAAAATT CAAAATGGGG CTCTCGAG	158
(2) INFORM	ATION FOR SEQ ID NO:1331:	
(1)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 552 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1331:	
GAATTCGCGG	CCGCGTCGAC GATCATGAAG CGCTCGGTAG CCGTCTGGCT CTTGGTCGGG	60
	GTGTCCCCCA GTTCGGCAAA GGTGATATTT GTGATCCCAA TCCATGTGAA	120
	TCTGTTTGCC AGGATTGGCT GATGGTTCCT TTTCCTGTGA GTGTCCAGAT	180
GGCTTCACAG	ACCCCAACTG TTCTAGTGTT GTGGAGGTTG CATCAGATGA AGAAGAACCA	240

ACTTCAGCAG	GTCCCTGCAC	TCCTAATCCA	TGCCATAATG	GAGGAACCTG	TGAAATAAGT	300
GAAGCATACC	GAGGGGATAC	ATTCATAGGC	TATGTTTGTA	AATGTCCCCG	AGGATTTAAT	360
GGGATTCACT	GTCAGCACAA	CATAAATGAA	TGCGAAGTTG	AGCCTTGCAA	AAATGGTGGA	420
ATATGTACAG	ATCTTGTTGC	TAACTATTCC	TGTGAGTGCC	CAGGCGAATT	TATGGGAAGA	480
AATTGTCAAT	ACAAATGCTC	AGGCCCACTG	GGAATTGAAG	GTGGAATTAT	ATCAAACCAG	540
CAAATCCTCG	AG					552

- (2) INFORMATION FOR SEQ ID NO:1332:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 760 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

GAATTCGCGG	CCGCGTCGAC	CTCAGAACTA	TTTAAATTTA	GTTAAATTAC	TATTATATTT	60
TATAGTAAAT	ATTGGTCCAC	TTTATAGCTC	AGAACCTAAA	AAGAGAATAT	GTACCCAAAC	120
TTCTCTATGT	TTACAACCAA	CCCAGAGTTT	AAGATTCTGA	ATTGTGCTTT	GTTTTGTTAA	180
AAATTTAACC	AAGGGTCAGG	CACAGAGGCT	CATGCCTATA	ATCCCAGCGC	TTTGGGAGGC	240
CGAGGCGGGT	GGATCACTTG	AGTTCAGGAG	TTCGGGACCA	GCCTGGCCGG	CATGGTGAAA	300
CCCCGTCTCT	ACTAAAAATA	CAAAAGTTAG	CCGGGTGTGG	TGGCATGTGC	CTGTGGTCCC	360
AGCTGCTTGG	GAGGCTGAGG	CAGGATAATC	NCTTGAACCC	AGGAGGCAGA	GGTTGCANTT	420
GCAGTGAGCC	GGGATTGTGC	CATTGTACTC	CAGCCTAGGC	AACAAGAGCG	AAACTCTGTC	480
AAAAAAATT	AAAAGAAAAA	AAAATTAACC	AAGGTTCTCC	TTTCTCTAAA	TCTAGCAATT	540
TGTTCTATTT	TTCAGAAATA	AACTTAATAA	TTTTAATACA	GATTTTAGCT	TTGGCTTTTT	600
TCTTACTTTT	TAGTTTGCAA	ATTATTTTAT	GGTATTCCTA	CAAAGTAGAT	ACAAATTTGC	660
ATTCAGAATG	CACCTTTTGT	TTTTCTGGGT	TTTTTTTTTT	GTTTGTTTGT	TTTTTCAGAA	720
AACTCATGGA	AAAGTACACT	GTTCACCTCA	GCATCTCGAG			760

- (2) INFORMATION FOR SEQ ID NO:1333:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

GAATTCGGCC	AAAGAGGCCT	ANAACTGGGT	AAGGAGCAAA	AAAAGTGACA	GAGGCCAGGC	60
GCGGTGGCTC	ATGCCTACAA	TCCCAGCACT	CTGGCCAAAT	ATTTGATTTT	AAATTCCCAT	120
TGTTACTGAT	TAAAAAAAAA	AAAAATCTGG	ACCAGTTAAC	CTGGAGATTT	AGAGGCTATA	180
GACACAAT'TT	AACATCCATA	CAGGCCTGTG	AACTTCATGC	AGAGAACAAA	CAAACAAACA	240
AAAACTCTAA	TTCAGAGTCT	CTCATTTCAG	CTTAGCCAAC	ACATTTGGAG	ACTTAGGGGC	300
CAGTTCTAGA	AGCTGCTTTT	ACCTCTAGAC	TCGGAGGGC	AGGCCCTGTC	ACCGAAGGGA	360
GGAAAACTCT	TCTTGGCTGT	CAGCCCGGAT	TGAAGCCACT	TCGCTTCCCC	TGGCCCCAGC	420
TTTCCTGCAC	TCTTTTCACC	GTGTCTGACA	CAGGGCAAAC	CACCAACCAC	TCAAATGAGC	480
AAACAATTCC	AGAAAAAAGA	<b>ATCCGAGATA</b>	AAGAATAACC	AACTAGGAGT	CTTTCCATTG	540
TAGCCTAAAC	CGTCGATTGA	ATTCTAGACC	TGCCTCGAG			579

- (2) INFORMATION FOR SEQ ID NO:1334:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 521 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

GAATTCGCGG	CCGCGTCGAC	CAACAAGGGC	AAAGGCCTTG	AGACACAAAC	CAACTGTGTG	60
GGTGTAAAGG	TAAGAAAGGC	CAGTGAGGCC	AGCATGATGA	ACTGGGGGAG	CATGGTGGCT	120
${\tt GATTTGGTCA}$	GGAAGGGAAC	AGAAACCAGA	CCACTTGGGA	TCTTCTAGCC	AGAGTAAAGA	180
GACTGAGTTT	ATTCCTATTG	TAATGGGGAG	CTATTCAGAG	AGGTTAATCA	TGGAAGTGAT	240
GTGACCTGAG	CTACACTCTT	AAAAGATGCC	TCTGGCTGCT	GTGTGGAGAA	TGAACCATGG	300
GGGCAAAAGC	AGAAACAAGA	AGACCACTTA	AGAGGCTCTT	GCAATAATTT	ATGTGAGAAG	360
AGTGATCATC	TTGACTAGGG	TGGTGGTGGT	AGAGGAGGTG	AGTGGTGGTC	AGGACTGAGA	420
GGAGCCAACA	GAATTTGCTG	GCTTGCTTGG	ATGTGGGTGA	TGAGGCAAAC	TGAGAATCCA	480
AGATGGCACC	AAGGCTTATA	CCCTGAGCAA	CTGAACTCGA	G		521

- (2) INFORMATION FOR SEQ ID NO:1335:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 775 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

GAAATTCGCG	GCCGCGTCGA	CGCTCTTGAG	TGAGACCCAA	CAAGCTGCTT	TTCACCAAAT	60
TGCAATGGAG	CCTTTCGAAA	TCAATGTTCC	AAAGCCCAAG	AGGAGAAATG	GGGTGAACTT	120
CTCCCTAGCT	GTGGTGGTCA	TCTACCTGAT	CCTGCTCACC	GCTGGCGCTG	GGCTGCTGGT	180
GGTCCAAGTT	CTGAATCTGC	AGGCGCGGCT	CCGGGTCCTG	GAGATGTATT	TCCTCAATGA	240
CACTCTGGCG	GCTGAGGACA	GCCCGTCCTT	CTCCTTGCTG	CAGTCAGCAC	ACCCTGGAGA	300
ACACCTGGCT	CAGGGTGCAT	CGAGGCTGCA	AGTCCTGCAG	GCCCAACTCA	CCTGGGTCCG	360
CGTCAGCCAT	GAGCACTTGC	TGCAGCGGGT	AGACAACTTC	ACTCAGAACC	CAGGGATGTT	420
CAGAATCAAA	GGTGAACAAG	GCGCCCCAGG	TCTTCAAGGT	CACAAGGGGG	CCATGGGCAT	480
GCCTGGTGCC	CCTGGCCCGC	CGGGACCACC	TGCTGAGAAG	GGAGCCAAGG	GGGCTATGGG	540
ACGAGATGGA	GCAACAGGCC	CCTCGGGACC	CCAAGGCCCA	CCGGGAGTCA	AGGGAGAGGC	600
GGGCCTCCAA	GGACCCCAGG	GTGCTCCAGG	GAAGCAAGGA	GCCACTGGCA	CCCCAGGACC	660
CCAAGGAGAG	AAGGGCAGCA	AAGGCGATGG	GGGTCTCATT	GGCCCAAAAG	GGGAAACTGG	720
AACTAAGGGA	GAGAAAGGAG	ACCTGGGTCT	CCCAGGAAGC	AAACAGAGAC	TCGAG	775

- (2) INFORMATION FOR SEQ ID NO:1336:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 155 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

GTAGATTTAG	ATGTACAGAT	AGAGGTATGA	TTTTTTTAAA	AGGCACCTCA	GTATGGGTAA	60
TGTTATCTTT	CTTGTGTTTC	AGTGCACACA	CATACACACA	CACCATAGAT	GCAAAGTGTG	120
TAGAAAATGT	ATTGAAGGAT	ACCCAGGTAC	TCGAG			155

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 138 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:	
GAATTCGCGG CCGCGTCGAC ATTCATGCAA ATAAATATAT TACTAAAATG CTACCTGTTT CTTTTTCCTC TTTTTCTTCC AGTTTTAGTT TATGAGATTG GGTCTTGCTA TGCTGCCCAT GCTAGGCATG AACTCGAG	60 120 138
(2) INFORMATION FOR SEQ ID NO:1338:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 249 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:	
GAATTCGCGG CCGCGTCGAC CTAAACCGTC AATTCTTCCC ATCTTAGGTT TCTCTCCTCG GAAGCCTTCT CTTTAGAATC GAACATTTTC TCTTCTGGCT TTGTTCGGAT GGTTTCTGGT CTGTTTCTTT CTTGCTCCCT CGTGGCTTTC ACTTCTGTTT TCTTTCCCAG AATGACGGTC CTCTCATTTG ACCGTGTGCT TTCCGAAGCA CCTGCTGCCA CCTTGTCTCG GCGATCCCGG TTACTCGAG	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:1339:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 108 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:	
GAATTCGCGG CCGCGTCGAC AAAACAACAC ATTTTAAAGA TTACGTGCTT CTTGGTACAG GTTTGTGAAT GACAGTTTAT CGTCATGCTG TTAGTGTGCA TCCTCGAG	60 108
(2) INFORMATION FOR SEQ ID NO:1340:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 652 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
536	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

GAATTCGGCC AAAGAGGCCT	AATAGAAGGC	ATTCCATATT	TGTTCAATGA	ATTAACAAAT	60
GTTTTTCATA TTAATTGTTC	TGATTTTTAC	CTCCTTAGGC	CAGCCTTTAT	TATTGCCATA	120
TAAGCCTTCT GGTAGTACCA	AGATGTATTA	TGTTCCACAA	TTAAGACAAA	TTCCTCCATC	180
TCCGGATTCC AAATCAGATA	CCACCGTTGA	AAGCTCCCAT	TCAGGATCCA	ATGATGCCAT	240
TGCTCCAGAC TTCCCAGCTC	AGGTGCTAGG	CACAAGAGAT	GATGACCTCT	CAGCCACTGT	300
TAACATTAAA CATAAAGAAG	GAATCTACAG	TAAGAGGGTA	GTGACTAAGG	CATCCTTGCC	360
AGTGGGAGAA AAACCCTTGC	AGAATGAAAA	TGCAGATGCC	TCAGTTCAAG	TGCTAATCAC	420
TGGGGATGAG AACCTCTCAG	ACAAAAAACA	GCAAGAGATT	CACAGTACAA	GGGCAGTGAC	480
TGAGGCTGCC CAGGCTAAAG	AAAAAGAATC	TTTGCAGAAA	GATACTGCAG	ATTCCAGTGC	540
TGCTGCTGCT GCAGAGCACT	CAGCTCAAGT	AGGAGACCCA	GAAATGAAGA	ACTTGCCAGA	600
CACTAAAGCC ATTACACAGA	AAGAGGAGAT	CCATAGGAAG	AACGACCTCG	AG	652

- (2) INFORMATION FOR SEQ ID NO:1341:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LingTH: 817 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

GAATTCGGCC	AAAGAGGCCT	ACGTGCCATT	TCTCTTCCAC	TATGAGAGGA	CCGATTGTAT	60
TGCACATTTG	TCTGGCTTTC	TGTAGCCTTC	TGCTTTTCAG	CGTTGCCACA	CAATGTCTGG	120
CCTTCCCCAA	AATAGAAAGG	AGGAGGGAGA	TAGCACATGT	TCATGCGGAA	AAAGGGCAGT	180
CCGATAAGAT	GAACACCGAT	GACCTAGAAA	ATAGCTCTGT	TACCTCAAAG	CAGACTCCCC	240
AACTGGTGGT	CTCTGAAGAT	CCAATGATGA	TGTCAGCAGT	ACCATCGGCA	ACATCATTAA	300
ATAAAGCATT	CTCGATTAAC	AAAGAAACCC	AGCCTGGACA	AGCTGGGCTC	ATGCAAACAG	360
AACGCCCTGG	TGTTTCCACA	CCTACTGAGT	CAGGTGTNCC	TCAGCTGAAG	AAGTATTTGG	420
TTCCAGCCAG	CCAGAGAGAA	TATCTCNTGA	AAGTGGANTT	GCCAAGGCCA	TGTTAACCAT	480
TGCTATCACT	GCGACTCCTT	CTCTGACTGT	TGATGAAAAG	GAGGAACTCC	TTACAAGCAC	540
TAACTTTCAG	CCCATTGTAG	AAGAGATCAC	AGAAACCACA	AAAGGTTTTC	TGAAGTATAT	600
GGATAATCAA	TCATTTGCAA	CTGAAAGTCA	GGAAGGAGTT	GGTTTGGGAC	ATTCACCTTC	660
ATCCTATGTG	AATACTAAGG	AAATGCTAAC	CACCAATCCA	AAGACTGAGA	AATTTGAAGC	720
AGACACAGAC	CACAGGACAA	CTTCTTTTCC	TGGTGCTGAG	TCCACAGCAG	GCAGTGAGCC	780
TGGAAGCCTC	ACCCCTGATA	AGGAGAAGCA	CCTCGAG			817

- (2) INFORMATION FOR SEQ ID NO:1342:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 476 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

GAATTCGGCC	AAAGAGGCCT	AGCACCATGG	ACAACCCACA	GGCTCTGCCA	CTCTTCCTAC	60
TCCTGGGGAT	CCTCACCCTC	AGAGCCTCTT	CTGGACTTCA	GCAAACCAAC	TTCTCCTCTG	120
CCTTCTCTTC	AGACTCAAAG	AGCTCTTCCC	AGGGGCTGGG	TGTGGAAGTT	CCCTCCATCA	180
AACCTCCCAG	CTGGAAAGTT	CCAGATCAGT	TCCTGGATTC	AAAAGCCTCT	GCTGGAATCT	240
CTGATTCCAG	CTGGTTTCCT	GAGGCCCTGA	GTTCCAACAT	GTCTGGGTCC	TTCTGGTCAA	300
ATGTTTCTGC	TGAGGGCCAA	GATTTGAGCC	CGGTTTCCCC	CTTCTCTGAA	ACCCCTGGTT	360

> CTGAAGTATT TCCTGATATT TCGGATCCTC AAGTTCCTGC CAAAGACCCC AAGCCTTCCT 420 TCACTGTTAA GACCCCAGCT TCAAACATTT CTACTCAAGT CTCCCATCTC CTCGAG 476 (2) INFORMATION FOR SEQ ID NO:1343: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 726 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343: GAATTCGCGG CCGCGTCGAC CAGGAAATGA AGACATTGCC TGCCATGCTT GGAACTGGGA 60 AATTATTTTG GGTCTTCTTC TTAATCCCAT ATCTGGACAT CTGGAACATC CATGGGAAAG 120 AATCATGTGA TGTACAGCTT TATATAAAGA GACAATCTGA ACACTCCATC TTAGCAGGAG 180 ATCCCTTTGA ACTAGAATGC CCTGTGAAAT ACTGTGCTAA CAGGCCTCAT GTGACTTGGT 240 GCAAGCTCAA TGGAACAACA TGTGTAAAAC TTGAAGATAG ACAAACAAGT TGGAAGGAAG 300 AGAAGAACAT TTCATTTTC ATTCTACATT TTGAACCAGT GCTTCCTAAT GACAATGGGN 360 TCATACCGCT GTTCTGCAAA TTTTCAGTCT AATCTCATTG AAAGCCACTC AACAACTCTT TATGTGACAG GAAAGCAAAA TGAACTCTCT GACACAGCAG GAAGGGAAAT TAACCTGGTT 480 GATGCTCACC TTAAGAGTGA GCAAACAGAA GCAAGCACCA GGCAAAATTC CCAAGTACTG 540 CTATCAGAAA CTGGAATTTA TGATAATGAC CCTGACCTTT GTTTCAGGAT GCAGGAAGGG 600 TCTGAAGTTT ATTCTAATCC ATGCCTGGAA GAAAACAAAC CAGGCATTGT TTATGCTTCC 660 CTGAACCATT CTGTCATTGG ACTGAACTCA AGACTGGCAA GAAATGTAAA AGAAGCACCA 720 CTCGAG 726 (2) INFORMATION FOR SEQ ID NO:1344: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344: GAATTCGGCC AAAGAGGCCT AGGGACAGCA ATCAAGTTCT AATGGTGCTC ACTTTTTAGG 60 TCACCTTCAT CACAGACTGC TCCAAAGGCA GAGCAATGTG GAACGAACCA GCACATTTAC TTAAGATCAA AGTATGATAC ATCTCTTTGA GCGCCTCACT TCACAATAGG GATCCATTCA 180 TTGGCTTCCA GATGATGTTC ACAGTTCATG TAACACTGAT ACTGACTTTG TTCCTTATGT 240 TTAGACAGCT TCTCTGTCTA TACTTCTCAG AAACACCATC AACCAGAACA GAGCCACTTA 300 TTATCCACAA AAGTTGCATC AACCAGCTTA CCTTCTGGGA GGGATGGATG GTACCCAAAT 420

> ACTCAAACTG AATCCTATAG TGTGGAGCAA CCAAACAGAA AACAGTCCAA GGATTCAGGA AATGGTAAAA ACATTTTAAA TCTAAATAGT AGTTATTTTC ATTTTGTTCT GCTCCCACCT 480 CGAG 484

- (2) INFORMATION FOR SEQ ID NO:1345:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 125 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

GAATTCGCGG CCGCGTCGAC ATGAGTTTAA TTTTTTTTT TTTTTTTACA CTTTACATAG 60
AAATAGGATT ATGTGGGCTG GGCACAGGGA CTGACGCCTG TAATCCCAGC ACGTGGAGGC 120
TCGAG 125

- (2) INFORMATION FOR SEQ ID NO:1346:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 760 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

GAATTCGGCC	AAAGAGGCCT	AGACCCAGCG	TACATACTGA	ATGATCTCTA	CATCTCAGAC	60
TACTGTGTGT	GGATTCAGAA	AGTCAAATCC	AAAAGTTGG	CAGCTCTTGC	AGAAGCCTTA	120
AAGGAAGTCT	CCCTTACAAA	GGCCCAGCTG	GGGTTAGAAC	TGGAAGAACT	AGAAGCAGCA	180
GCACTGCTTG	TCCAGGAGGA	AGAAACTGCA	TTAAAAGCAG	CCCATTCAGT	TTCTGGGCAG	240
CAGACACTTT	GCTCCAGCTC	TGAGGCAAGT	GATTCGGAGG	ACTCAGACAG	CAGCGTGTCA	300
TCTGGAAACG	AAGACTCAGG	CTCAGATTCA	GAACAAGATG	AACTCAAAGA	TAGTCCATCT	360 <sup>.</sup>
GAGACAGTCA	GTTCTTTGCA	AGGTCCCTTT	CTTGAAGAAA	GCAGTGCCTT	TCTTATTGTT	420
GATGGTGGAG	TACGCAGAAA	CACAGCCATC	CAGGAGTCTG	ATGCCAGTCA	GGGAAAGCCA	480
CTTGCCTCTT	CCTGGCCTCT	TGGAGTGTCT	GGGCCTCTGA	TAGAGGAGCT	TGGGGAACAA	540
CTGAAGACTA	CAGTTCAGGT	TTCTGAACCC	AAGGGCACCA	CTGCTGTAAA	CCGCAGCAAT	600
ATTCAGGAGA	GAGACGGCTG	TCAGACACCA	AATAATTGAC	TCTTAGGTGG	TTTTATTCAT	660
TGTTGAGAAA	TATGGTAGAT	TGGGTTTCAT	TTACCGAATG	AGAATTCTTC	ATTTTCACTT	720
TGTAATTTTT	CTTAGTATAT	AGTCAGCCCA	CACTCTCGAG			760

- (2) INFORMATION FOR SEQ ID NO:1347:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

GAATTCGCGG	CCGCGTCGAC	CATTTCGAGA	GTCCGTCTTG	TAAATGTTTG	GCACTTTGCT	60
ACTTTATTGC	TTCTTTCTGG	CGACAGTTCC	AGCACTCGCC	GAGACCGGCG	GAGAAAGGCA	120
GCTGAGCCCG	GAGAAGAGCG	AAATATGGGG	ACCCGGGCTA	AAAGCAGACG	TCGTCCTTCC	180
CGCCCGCTAT	TTCTATATTC	AGGCAGTGGA	TACATCAGGG	AATAAATTCA	CATCTTCTCC	240
AGGCGAAAAG	GTCTTCCAGG	TGAAAGTCTC	AGCACCAGAG	GAGCAATTCA	CTAGAGTTGG	300
AGTCCAGGTT	TTAGACCGAA	AAGATGGGTC	CTTCATAGTA	AGATACCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:1348:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 251 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

GAATTCGCGG CCGCGTCGA	C TCTAGGTTTT	CTGATTTTGA	TGGTAATATG	GTATTCTGGG	60
AAATATCTGT CCAAATTAT	C CTGATCTCTG	AACTCCTGCT	GTTGAGGTCA	GTCACTTCAC	120
ACAATACCAT GATGACAGO	T TTATCAAGCC	AGATGCTTAG	TCAGAGCTTT	CCAAGACCCA	180
GCTTTGGTTT TATCAGCAA	A ATCCATCCTT	CCCACCCCC	ATACACACGC	CAGTTTGAGA	240
CTCCTCTCGA G					251

- (2) INFORMATION FOR SEQ ID NO:1349:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 309 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

GAATTCGCGG	CCGCGTCGAC	CTAAACCGTC	GATTGAATTC	TGGACCTCCT	GTGCAAGAAC	60
ATGAACCATC	TGTGGTTCTT	CCTTCTCCTG	GTGGCAGCTC	CCAGATGGGT	CCTGTCCCAG	120
GTGCAGGTGC	AGCAGTCGGG	CCCTAGACAG	GTGAAGCCTT	CGGAGACCCT	GTCCCTCAGT	180
TGTACTGTCT	CTCTCGGCGC	CATGAATGGT	CATTACTGGA	CCTGGATCCG	GCAGACCCCG	240
GGAGGGAGAC	TGGAGTGGAT	TGGATCTGTC	TATTATAATG	GAAACAGAGT	GTATCACCCC	300
TCCCTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:1350:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 553 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

GAATTCGCGG	CCGCGTCGAC	AATTACTACC	ATTGTTAAGT	GTCTCTTTAA	CTAAACTCAT	60
TGTTTAAAAG	TTTTCTCCCT	CTCTGTTTCT	AAATCCAAAT	TTCTGCTCTG	GAATATATGT	120
TAGAAGAGAT	ACATTTGTTG	GAATGTTTGC	ATTTCTTTTA	TGAAATGCAG	TATCTTTTGG	180
GGAATATTAT	GTAAATGAAA	TACCAATTAT	TTTAAAAGAG	CATTTTTGTG	TGACATAGTG	240
CTTTCACAAA	CTAAAACTGG	AATTTCTTTC	TTTAGTCTAT	CTATATCTTT	TGAAAATGTT	300
GACACAGCTA	AGAAGAAGCT	GCCTGTTCAT	ATCTTAGATG	GTCTGACCCT	CAGCTACAAG	360
GTATATGCTG	ATATTCCTTG	TATGAACCGT	GTTTTCTGCT	AACATTAAAA	CATGCAAGTA	420
ATTGGTTACT	TTCTAATTTT	GTTTTTGTTT	CATAGGTCCC	ATGGCCCGTG	GACATTGTTA	480
TAAGTTTGGA	ATGTCAAAAA	ATTTATAATC	AAGTGTTTCT	TCTCTTATTG	CAAATAAAGT	540
GGGCATCCTC	GAG					553

- (2) INFORMATION FOR SEQ ID NO:1351:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 209 base pairs

    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

WO 98/45437 PCT/US98/<u>0</u>6956

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

GAATTCGCGG	CCGCGTCGAC	TTTATTTCAG	TGGATTCTCT	AGGATTTTCT	ATATAAAAGA	60
TGTCATCTGA	TAGAGTAGTT	TACTTCTTCG	TTTCCAACCT	GAATGGCTTT	TATTTCATCT	120
CTTTCCTAAC	TGTCCTGGCT	AGAACCTCCT	TTACCACGTT	GAATGGAAGT	GGCAAGAATG	180
AACATCCTTG	TCTTGTTTCT	GATTTCGAG				209

- (2) INFORMATION FOR SEQ ID NO:1352:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 525 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

GAATTCGCGG	CCGCGTCGAC	AATGGCTTTT	CTTCCTTCCT	GGGTTTGTGT	ACTAGTTGGT	60
TCCTTTTCTG	CTTCCTTAGC	AGGGACTTCC	AATCTCTCAG	AGACAGAGCC	CCCTCTGTGG	120
AAGGAGAGTC	CTGGTCAGCT	CAGTGACTAC	AGGGTGGAGA	ACAGCATGTA	CATTATTAAT	180
CCCTGGGTAT	ACCTTGAGAG	AATGGGGATG	TATAAAATCA	TATTGAATCA	GACAGCCAGG	240
TATTTTGCAA	AATTTGCACC	AGATAATGAA	CAGAATATTT	TATGGGGGTT	GCCTCTGCAG	300
TATGGCTGGC	AATATAGGAC	AGGCAGATTA	GCTGATCCAA	CCCGAAGGAC	AAACTGTGGC	360
TATGAATCTG	GAGATCATAT	GTGCATCTCT	GTGGACAGTT	GGTGGGCTGA	TTTGAATTAT	420
TTTCTGTCTT	CATTACCCTT	TCTTGCTGCG	GTTGATTCTG	GTGTAATGGG	GATATCATCA	480
GACCAAGTCA	GGCTTTTGCC	CCCACCCAAG	AATGAGAGGC	TCGAG		525

- (2) INFORMATION FOR SEQ ID NO:1353:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

GAATTCGGCC	TTCATGGCCT	AGGCTCCTAA	AATAAATAAT	CCACATAATT	GTAAATGAAA	60
CACATCAAGG	ATTTGAGTTA	ATAGCCTCTG	AGCAGCATTA	ATATAGCCAT	TAGACTGGAG	120
TATTTGTTAT	CAAGAGGGCC	AGAGAACCCA	CCGCTAAAGC	CGTAGGGTGG	GAGGAACCCT	180
GGATTGCAGC	TACATGGCTT	ATGTAGGGAG	TTTGTAACAG	CCCCAAGCTG	AAACCAGCTT	240
CTACACCCAT	GACTGTTGAG	TGATTGAATT	CTAGACCTGC	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:1354:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 572 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

GAATTCGCGG	CCGCGTCGAC	CAACAAGAGC	ACTGGCCAAG	TCAGCTTCTT	CTGAGAGAGT	.60
CTCTAGAAGA	CATGATGCTA	CACTCAGCTT	TGGGTCTCTG	CCTCTTACTC	GTCACAGTTT	120
CTTCCAACCT	TGCCATTGCA	ATAAAAAAGG	AAAAGAGGCC	TCCTCAGACA	CTCTCAAGAG	180
GATGGGGAGA	TGACATCACT	TGGGTACAAA	CTTATGAAGA	AGGTCTCTTT	TATGCTCAAA	240
AAAGTAAGAA	${\tt GCCATTAATG}$	GTTATTCATC	ACCTGGAGGA	TTGTCAATAC	TCTCAAGCAC	300
TAAAGAAAGT	ATTTGCCCAA	AATGAAGAAA	TACAAGAAAT	GGCTCAGAAT	AAGTTCATCA	360
TGCTAAACCT	TATGCATGAA	ACCACTGATA	AGAATTTATC	ACCTGATGGG	CAATATGTGC	420
CTAGAATCAT	GTTTGTAGAC	CCTTCTTTAA	CAGTTAGAGC	TGACATAGCT	GGAAGATACT	480
CTAACAGATT	GTACACATAT	GAGCCTCGGG	ATTTACCCCT	ATTGATAGAA	AACATGAAGA	540
AAGCATTAAG	ACTTATTCAG	TCAGAACTCG	AG			572

## (2) INFORMATION FOR SEQ ID NO:1355:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 269 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

GAATTCGCGG	CCGCGTCGAC	TGAAAAGTAG	GTTTTTGAAG	AGATATATTC	GAAATATATT		60
TTTTCACTTG	AAAAAAGTAA	AAATTTTTTT	CAAAAGCAAA	TAATTCAACT	CTAAAATTAT		120
ACTATTTCAA	CATTCTCATT	TATGTGAAAG	CATGTGATAA	ATTGTTGCTG	CGTCAGAGAT		180
ATGAGAAACT	CCTTTGCATT	AGGTGGGCAT	TATTCATAGA	CTTCTACATG	AAAGAGAAGA	•	240
GAAATAAAAG	ATGCACCAGG	ATTCTCGAG					269

- (2) INFORMATION FOR SEQ ID NO:1356:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 713 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

GAATTCGCGG	CCGCGTCGAA	CCCAGCAAAA	TGGGGATCTC	CACAGTCATC	CTTGAAATGT	60
GTCTTTTATG	GGGACAAGTT	CTATCTACAG	GTGGGTGGAT	CCCAAGGACT	ACAGACTACG	120
CTTCACTGAT	TCCCTCGGAG	GTGCCCTTGG	ATACAACTGT	AGCAGAAGGT	TCTCCATTTC	180
CCTCGGAGTT	GACCCTGGAG	TCAACTGTAG	CAGAAGGTTC	TCCGATTTCC	TTGGAGTCAA	240
CCCTGGAGTC	AACTGTAGCA	GAAGGTTCTC	TGATTCCCTC	AGAGTCAACC	CTGGAGTCAA	300
CTGTAGCAGA	AGGATCTGAT	TCTGGTTTGG	CCCTGAGGCT	GGTGAATGGA	GATGGCAGGT	360
GTCAGGGCCG	AGTGGAGATC	CTATACCGAG	GCTCCTGGGG	CACCGTGTGT	GATGACAGCT	420
GGGACACCAA	TGATGCCAAC	GTGGTCTGTA	GGCAGCTGGG	TTGTGGCTGG	GCCATGTCAG	480
CTCCAGGAAA	TGCCTGGTTT	GGCCAGGGCT	CAGGACCCAT	TGCCCTGGAT	GATGTGCGCT	540
GCTCAGGACA	CGAATCCTAC	CTGTGGAGCT	GCCCCCACAA	TGGCTGGCTC	TCCCATAACT	600
GTGGCCATGG	TGAAGATGCT	GGTGTTATCT	GCTCAGCTGC	CCAGCCTCAG	TCAACACTCA	660
GGCCAGAAAG	TTGGCCTGTC	AGGATATCAC	CACCTGTACC	CACTAGACTC	GAG	713

- (2) INFORMATION FOR SEQ ID NO:1357:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 925 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

GAATTCGGCC	AAAGAGGCCT	AGAATAATGC	ATATACTGCC	ATGTCAGATT	CCTACTTACC	60
CAGTTACTAC	AGTCCCTCCA	TTGGCTTCTC	CTATTCTTTG	GGTGAAGCTG	CTTGGTCTAC	120
GGGGGTGAC	ACAGCCATGC	CCTACTTAAC	TTCTTATGGA	CAGCTGAGCA	ACGGAGAGCC	180
CCACTTCCTA	CCAGATGCAA	TGTTTGGGCA	ACCAGGAGCC	CTAGGTAGCA	CTCCATTTCT	240
TGGTCAGCAT	GGTTTTAATT	TCTTTCCCAG	TGGGATTGAC	TTCTCAGCAT	GGGGAAATAA	300
CAGTTCTCAG	GGACAGTCTA	CTCAGAGCTC	TGGATATAGT	AGCAATTATG	CTTATGCACC	360
TAGCTCCTTA	GGTGGAGCCA	TGATTGATGG	ACAGTCAGCT	TTTGCCAATG	AGACCCTCAA	420
TAAGGCTCCT	GGCATGAATA	CTATAGACCA	AGGGATGGCA	NCACTGAAGT	TGGGTAGCAC	480
AGAAGTTGCA	AGCAATGTTC	CAAAAGTTGT	AGGTTCTGCT	GTTGGTAGCG	GGTCCATTAC	540
TAGTAACATC	GTGGCTTCCA	ATAGTTTGCC	TCCAGCCACC	ATTGCTCCTC	CAAAACCAGC	600
ATCTTGGGCT	GATATTGCTA	GCAAGCCTGC	AAAACAGCAA	CCTAAACTGA	AGACCAAGAA	660
TGGCATTGCA	GGGTCAAGTC	TTCCGCCACC	CCCGATAAAG	CATAACATGG	ATATTGGAAC	720
TTGGGATAAC	AAGGGTCCCG	TTGCAAAAGC	CCCCTCACAG	GCTTTGGTTC	AGAATATAGG	780
TCAGCCAACC	CAGGGGTCTC	CTCAGCCTGT	AGGTCAGCAG	GCTAACAATA	GCCCACCAGT	840
GGCTCAGGCA	TCAGTAGGGC	AACAGACACA	GCCATTGCCT	CCACCTCCAC	CACAGCCTGC	900
CCAGCTTTCA	GTCCAGCAAC	TCGAG				925

- (2) INFORMATION FOR SEQ ID NO:1358:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 172 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

GAATTCGCGG	CCGCGTCGAC	AAATAAACCC	AGCAACTTCA	TTCATTTGCC	TTATGTTTAT	60
TGAGGGCCTG	CTAGTGCTGG	GCACTGTTCT	AGGCCCTGGG	AATTTATTAG	TGAGCAAAAC	120
AGCAAAATCT	CTGTCCTCAT	GGAGCTCACA	ATATAGTAGG	GAACGACTCG	AG	172

- (2) INFORMATION FOR SEQ ID NO:1359:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 770 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

GAATTCGGCC	AAAGAGGCCT	AAGTCAGTGA	GGTGGAGTCC	GTTTTTGAGG	TCACGCGGCT	60
AGTAATTGGA	GCCTGGTTTA	GAACCAAGTC	AGTCTCATTC	CAGAATCCAG	AACCAGTGAT	120
TTGTAACTGA	TGCACTTGTC	TCCAAAGGGA	TCCAGCACTG	GGTTTTCTCA	TTTTTAATGC	180
ATCCATTCCT	TAAAGCCTCT	GTTCACAGTC	ACAAGGTGTA	CTTTTTAAAG	GAACACAGCA	240
CACAAATGTG	ACCGCTAGTG	GACAGCAGTG	CCACCCCAGT	TEGATEGEAG	AGCCTGGCAT	300

GCCGACTGGG	ACAGAAGCCC	CAGCACACGG	TGTGATGATG	GCGTCTCCAG	GCTGACCTCC	360
ATGGCCTCAG	GAATCAAAGT	CCTCGGTCTC	TTTCACGCGG	GGTTCAGAAA	GAAAACTCGG	420
CTATCTTACA	TCTCCTCTCC	CCTGTTTATT	TGACTAAAGT	GAAGTTCATG	TGGCTTGAGC	480
CTCGTTTCCT	GGGGAAATCA	GCCTGGCTTA	GGATTCCATT	GTCTTCTGGG	ACTGGGAAGA	540
TGTGGAAGGC	TGACCTCACG	CCCAGCTGAA	GGTCACCTTC	CCAGACTCTG	AGCTCGGCTG	600
CCTTCTGCAT	CGCCACGGCT	GGAGGGCCTG	GCCCAGGCCG	TGGCTGCATG	CTGGCTTTCC	660
ACTGTCTCGG	TGTCCCTGCT	GCCTGTCAGT	AATGTGCCCA	GCACCTTCTG	GTGTCATGTC	720
CCCTCTTGTT	TGTGATTCTT	TTCCTGAGCT	AGTCCATTTT	CTACCTCGAG		770

- (2) INFORMATION FOR SEQ ID NO:1360:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

GAATTCGGCC	AAAGAGGCCT	ACTCAGTGGA	AACCTTTAAA	CCCTAAAATC	CAGGAAAAGA	60
AAATAAATAC	ATTATCATGG	ACCTGAGGGA	TTTTTACCTG	TTGGCTGCTC	TGATTGCCTG	120
TTTAAGGCTG	GATTCCGCAA	TAGCTCAAGA	ACTTATTTAC	ACTATTAGAG	AGGAATTGCC	180
TGAAAATGTG	CCCATAGGAA	ACATACCAAA	GGATCTGAAC	ATTTCTCACA	TCAATGCTGC	240
CACAGGGACC	AGCGCCAGCC	TTGTCTACAG	ACTGGTTTCT	AAAGCTGGGG	ATGCCCCTTT	300
GGTGAAAGTA	TCCAGCAGCA	CTGGGGAAAT	TTTCACAACC	TCCAACAGAA	TAGACAGAGA	360
AAAACTCTGT	GCTGGCGCCT	CATATGCTGA	GGAGAATGAG	TGTTTCTTTG	AACTTGAGGT	420
GGTGATCCTC	CCCAATGATT	TCTTCAGGCT	GATCAAAATA	AAAATAATTG	TCAAGGATAC	480
CAATGATAAT	GCCCCCAATC	TCGAG				505

- (2) INFORMATION FOR SEQ ID NO:1361:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 553 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

GAATTCGGCC	AAAGAGGCCT	AAATTTGTTC	TCTCCAAACC	AGAAGACCTT	AGGTACAGAT	60
GACCCCAGGG	AGCTGGGACA	GCAGGACAGA	NAGGGGAAGG	GACAGGTCCA	TATATAGGTG	120
TGTCATTGCA	GCCACTGCAA	TGAACATAAC	ATGCAAGAAA	TGTACAGAAT	GTGGTCCAGA	180
ATTGCCCACT	GGTGTCCTGT	GCCCTGGTGG	ACCCCACAGA	GGACTGCCCC	AGGCTTTCAC	240
TTTCCTTCCC	CATGGATTGA	GCAAGCTCCC	AGGGCAGGAT	GGGTGGCCAG	GAGGGGCAGA	300
ACGCTGGCGG	GGACGGGGAA	GCCAAGTGCT	CACAGGACCA	TCCACCACAG	CTGCAGCCAC	360
ACTGCAAGAC	GGCGGGGATG	GGACACACGG	TCTAGTTCTT	AGTTCTGCCT	CCTACAGGCA	420
GCCCCTGCTG	TCACTCCAGA	ACTAATTCTC	TGTGTGCCAC	TCACTCGCGT	GTGTGACACA	480
CAACAGATAC	ACATACATAG	ACACATACGT	ACATCTCCTC	CCCCAATCTC	ACCCTCTCAC	540
CACGCCCCTC	GAG		,			553

- (2) INFORMATION FOR SEQ ID NO:1362:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 855 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

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GAATTCGGCC AAAGAAGCCT AGTCAACTTG ATCCAAACCT GTTGGTGAAG CAGCAGACTC
CACCATCTCA GCAGCAGCCA CTCCATCAGC CAGCCATGAA GTCTTTCCTT GACAATGTCA
                                                                      120
TGCCCCACAC TACACCTGAG CTGCAAAAAG GGCCATCACC AATAAATGCT TTCAGCAACT
                                                                      180
TCCCTATAGG CTTGAACTCA AACTTGAATG TAAATATGGA TATGAACAGT ATTAAAGAGC
                                                                      240
CACAGTCCAG ACTAAGGAAG TGGACGACAG TGGACAGCAT TTCTGTGAAC ACATCTTTGG
                                                                      300
ATCAAAACTC CAGCAAACAT GGTGCTATTT CAAGTGGTTT CAGGCTGGAA GAGTCTCCAT
                                                                      360
TTGTNCCCTA TGACTTTATG AACAGCAGTA CTTCACCAGC CAGTCCTCCA GGTTCAATAG
                                                                      420
GAGATGGCTG GCCACGTGCC AAATCGCCTA ACGGCTCTAG CAGTGTTAAT TGGCCACCAG
                                                                      480
AATTTCGTCC CTGGTGAGCC ATGGAAAGGT TATCCAAACA TTGACCCTGA AACTGACCCT
                                                                      540
TACGTCACTC CTGGCAGTGT CATAAACAAT CTTTCAATTA ATACTGTGCG GGAAGTTGAC
                                                                      600
CACCTCAGGG ACAGGAACAG TGGGTCATCC TCATCCTTGA ACACCACGCT GCCTTCAACT
                                                                      660
AGTGCCTGGT CATCCATTCG TGCCTCCAAC TACAACGTTC CCCTCAGCAG TACAGCACAA
                                                                      720
AGCACTTCAG CCAGAAATAG TGATTCCAAA TTGACATGGT CTCCTGGTTC AGTTACAAAC
ACCTCTCTGG CTCATGAGCT GTGGAAGGTC CCTTTGCCAC CTAAAAACAT CACTGCTCCG
                                                                      840
TCCCGCCACC TCGAG
                                                                      855
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- (2) INFORMATION FOR SEQ ID NO:1363:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 646 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

GAATTCGGCC	AAAGAGGCCT	ACAAAAAGTA	CATAGTAAGA	CTAAGATACC	AAGTTGTATA	60
${\tt CTAATATTTT}$	TCAGGCCTTG	GGCCTCAAAT	ATATATATTT	ATATATAATA	CTCCAGTGTG	120
AACAGCAATT	CGATGAAATG	TAAAATGTAT	${\tt CTTTTTTTT}$	TTAAATCACA	CACAAGTATT	180
CATAACCACA	GGGTTCACCA	GAAATCTAAA	GCAAGGAGAC	ACTCACTCAT	ATAGAAATGG	240
AGTTACTCTT	CCACAGATCG	TTCTGATCAA	AGGTTTTGGA	ACAGAAATGA	ATTAATGATT	300
TTTTTGTATA	ATATCCAACA	TGTCCACTAT	CAAATACATT	TAGTATGAAA	AAACAGATGA	360
AGAAAAGGAA	CATACATTAG	GACAAAGTAT	CTGGTTAAAA	TGCTGTTCAT	TTAAATAAAG	420
CCCACTCTCC	TTACTTTAGA	GCTCCTTGGT	GAAATGGAGG	TGAGTTTGAT	GGAGTGCAGT	480
TGATGACCAC	TGAAAAACAC	GAGCCCTTTC	AACAATGTTG	CAACACTGTT	AGTTTTTGGT	540
TTAAACACAC	ACACACACTC	ACAAATGCTA	AGTGTACACT	ACCAAATTCT	GCGGTCAGCT	600
TTTCCAAGAA	CTACTGGGGA	AAGTTTCAAT	GCTGCAAATC	CTCGAG		646

- (2) INFORMATION FOR SEQ ID NO:1364:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 502 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

GAATTCGGCC TTCATGGCCT AATGGCTTAG CTGAAGGAAA TGCTCCAGAA ATTGGACTGT

GTAAACCATC AGTACAATAA TACGCTGTGT ATGTATGTGT ATATAAAATG AGAATTATGG

CATAATTGGA GCATTTGCAT TAATCAACAA ACTCACATTG AGACAAAACT TAGTTTTACA GCTGTCTTGA TTAAAGCCAA GTGTTCCATG TTGCTGTGAA GAATAGCCTC TTTCAAATAC

TTTGGAAAGT AGTTACTTGG AAACTTGTAA AGGTATTACA TTTTTATATT TAAACACCTA

120 180

240

300

TAGAGATCTT CAATTCCTTG AGTCTGAGCT TGTGGGTGGA ATTCTAAATT TGTATCATAA TCTGTCTTTT GTGAAACATT TTGAAAATAT GTATATATAA TATTGTATAT GCAATTGTG TTGTTTCACT TGTAAAGGGA AAAGGCTTAT TTTTCTTTAT ATTTCTGATA ACTTGTTTTG CATATGACCG GCACTTCTCG AG	360 420 480 502
(2) INFORMATION FOR SEQ ID NO:1365:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 197 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:	
GAATTCGGCC TTCATGGCCT ACAGAAGTAC GGGAAGGCGA AGAAAAGAAT AGAGAAGATA GGGAAATTAG AAGATAAAAA CATACTTTTA GAAGAAAAAA GATAAATTTA AACCTGAAAA GTAGGAAGCA GAAGAAAAAA GACAAGCTAG GAAACAAAAA GCTAAGGGCA TCGATTGAAT TCTAGACCTG CCTCGAG	60 120 180 197
(2) INFORMATION FOR SEQ ID NO:1366:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 314 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:	
GAATTCGGCC TTCATGGCCT AGGCCTGGGG TGGGACATTT TGTTTGTGAG AAGCCTGGAC AAGAGGACGA GGTGCACACC ATGTCAGTCA CGGATTTGTG AACTCACAGG AGAGGGTTGG ATAGGGCGTG TGAACGTGAG CCCGCGGGT AGACGATGTG AAGCTGTGGT AACGGGTGGG CTTGTGATGG CACCCGCTGC TCGCAGGAGA GGGTTGGATA GGGCATGTGA ACGTGAGCCT GCAATGTAGA CGATGCGAAG TCGTGGTAAC GGGTGGGCTT GTGACGGCAC CCGCTGCTTG CAGCCTAACT CGAG	60 120 180 240 300 314
(2) INFORMATION FOR SEQ ID NO:1367:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 250 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:	
GAATTCGGCC TTCATGGCCT ACTGGTCCCA TTTTTCTATT GCAGTGGTCA TCATTTTAT TGATGTATAA TAATATTGTA TCATAAATCT TCATAATATG TGCTTCCAAA GTTTTTCTA	60 120
546	

ATTTTCACT AACCTTTGAT TTGGTATTTA ATTTTTAGTT GTCAGAAGTT TTTAATATTT

180

GAAGGTCGAG	240 250
(2) INFORMATION FOR SEQ ID NO:1368:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 261 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:	
GAATTCGGCC TTCATGGCCT AGTGAGAGCA CCACACAAAG GACAGGAAAA ACACCAGCAA TACATCAGCT TTACACAGCA GGCAAGTTTC CTGCTCTCTA CAAGTACAGA TGGAACTTGT CTTGTGAATT AACATCCTGA CTACTTTTGT TGATCATCAC ATTTTTTCCT CATGAGAGAA ATAATAGTGT TTTATAGGCT CCTGAGAATA GGTTTACTAA AGTCATCGAG ATCTGGGTTC AAATGACACT TCATGCTCGA G	60 120 180 240 261
(2) INFORMATION FOR SEQ ID NO:1369:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 408 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:	
GAATTCGGCC TTCATGGCCT AGTTTTTGTT TGTTTGTTTG TTTGTTTTTT GGCAAGAACA GTTAGGAACC AGATCACAGT GAGGTATAGA GTGAATGAGA GTTGAGAATG TAAAGACAAT GGATATAGAT CACTATTTCA GGAAGCTGTT TGTGAGAGGG AGGAGAAAAA TAAAACAGTT ACTGAGCAAT AGGGTGGTTG GTAAGGGGGA GGGATTTTTT TCTGAAAGAT GGGAGAAATT TTAACATACT TAAATTTGAT GGGATAAGCC ATGCACTTAT AGGCATTCAG TCAATATATA	60 120 180 240
TTTCACAAAT GAATGAAGAT AAATTAGGGA GAGGTTAATT GGAGATTTTA GGAGAGAGGG AATAATTGAT CATGTAAAGT CATTGATAAG GTGGGAGCAG AACTCGAG	300 360 408
TTTCACAAAT GAATGAAGAT AAATTAGGGA GAGGTTAATT GGAGATTTTA GGAGAGAGGG	360
TTTCACAAAT GAATGAAGAT AAATTAGGGA GAGGTTAATT GGAGATTTTA GGAGAGAGGGG AATAATTGAT CATGTAAAGT CATTGATAAG GTGGGAGCAG AACTCGAG	360
TTTCACAAAT GAATGAAGAT AAATTAGGGA GAGGTTAATT GGAGATTTTA GGAGAGAGGG AATAATTGAT CATGTAAAGT CATTGATAAG GTGGGAGCAG AACTCGAG  (2) INFORMATION FOR SEQ ID NO:1370:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 369 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	360
TTTCACAAAT GAATGAAGAT AAATTAGGGA GAGGTTAATT GGAGATTTTA GGAGAGAGGG AATAATTGAT CATGTAAAGT CATTGATAAG GTGGGAGCAG AACTCGAG  (2) INFORMATION FOR SEQ ID NO:1370:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 369 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	360
TTTCACAAAT GAATGAAGAT AAATTAGGGA GAGGTTAATT GGAGATTTTA GGAGAGAGGG AATAATTGAT CATGTAAAGT CATTGATAAG GTGGGAGCAG AACTCGAG  (2) INFORMATION FOR SEQ ID NO:1370:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 369 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	60 120 180 240

GGCCCAGGAG AGTCTCGAG	CGCCTGCCAA CGGTACCGCT GTCCGGCATG 1	CACAATAAAT	CTGGAGGAAA	360 369
(2) INFORM	ATION FOR SEQ ID NO:1371:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 443 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		-	
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1	371:		
ACATGGTTGT ATCTCACTAC TTGAATCCTT ATTGTGTGCG ACAACAAGCC ATGTACTTAG AATACTAACT	AAAGAGGCCT ATTTTTTTT TTTTTAACTG ATTGTTGCTAA ACTTTATATA ATGTGTGGTT TATGTAGCAGT ACATTATATG TACATTATATA GATATTGCAA TGGAATTCCT ACTTTATAACTT TTTTAGAAACA GATAGTTTCT GAGAATTACT GAGAAT	CAATTCAGC TAATGTTAG TGTATTTGA TGGTTGTGC GAGCTATGTT	TTGAAAAATA TATTTCTGCT TATGCTAGTT GCTTTCTTTT TGTAATGCAG	60 120 180 240 300 360 420 443
(2) INFORM	ATION FOR SEQ ID NO:1372:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 770 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: CDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1	372:		
TAATTTGGAG GCTACAGCCT AGCTCAGCGG GAGCAACTCA GGAAGCCTCA CTTGACCGCA GAAGGGGCA GCTTCAGGAG GCTTCAGGAG TGCCTCTGCC CACTGTTGCA ACGCTGGGTC	AAAGAGGCCT ACTTCCGGCT GGAGCTGCTG GTGGCCCCTGG AGTCAGTTTC CTACACCATC CCACCAGGAG GGCCTGGAAC CCTCAGCCTG GTGGCAGAGCT TGGGCCCAGA AGCATGCCCT GAGAGAAGAGA	CAGGCCCA CACTTCCTCA CAGGACAGA CTCCTAGGA CCTATTGCAG CGTGTGGCCC CAGGTCACAC CTGCAGGTCC CGGTTCCCGC	CCCAGCACGA ACCCTCAGGA ATGGCAGCAA CCAGTCCCCC GCCCTGGAAA GTGAGAGACGA TGAGTGTTCA TTGAAGACGC ACCCCACTG CAGCCGTGCA	60 120 180 240 300 360 420 480 540 660 720 770
(2) INFORM	ATION FOR SEQ ID NO:1373:			
153	CECUENCE CUADACTEDIOTIO			

- - (A) LENGTH: 597 base pairs

  - (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

PCT/US98/06956 WO 98/45437

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:.

GAATTCGGCC	AAAGAGGCCT	AGTCTCTTTG	AAGATCTCTA	GGAACTTGCT	TTATGAATCT	60
TCATGCTCCT	GTGTTGGATG	CATATACATT	TAGGATAGTT	AGGTGTTCTT	TTTGAATTGA	120
AACTTTTACC	ATTATGTAAT	GCCCTTGTTT	GTCTTTTAAA	ATTTTTGTTG	GTTTAATATC	180
TGTTTTGTCT	AAAATTAGAA	TTTCAGCCTC	TGCTTTTTTT	CTGTTTTCCA	TTTGCTTAAT	240
AAATTTTTCT	TCATTCCCTT	ATTTTTAGCC	TATGGGTGTC	ATTGGATGTG	AGATTCATCT	300
CTTGAACACT	GTACTACTGG	TTCTTGCTTT	TTTACTCAGC	TTGTCACTCT	GTGTCTTTCA	360
ATTGGGCATT	CAAGGCTAGT	GTTGATATGT	GTGAATTTGT	TTCTGTCATC	ATGTTATTAG	420
TTGTTTATTA	TGCTGACTTG	TTTGTGTGGT	TTCNTTATAG	TGTTACTGGT	CTGTGCACTT	480
AAGTGTGTTT	TTTTAGTAGC	AATATTTTCT	TTTCATATGT	AGTGCTTTAT	GCGAGGTATT	540
TTGCAAGGAT	TTTCTGAATN	NTCNGAATTT	TTATGTGGGC	TAAACTAGGG	GCTCGAG	597

- (2) INFORMATION FOR SEQ ID NO:1374:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 459 base pairs (B) TYPE: nucleic acid

    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

GAATTCGGCC	AAAGAGGCCT	AGCCTCCCAG	TGTGAGCCAC	CGCACCCAGC	CTGGATTGTT	60
GAATTCAATG	CTTGGGTCAC	CTCCAGATTC	ATTTTCACAG	TCTTTCATGT	TTTGGTCATA	120
TGACATTGTA	TTTTGCTGCC	ATATGACTGA	TCTTTTTTTG	TTAAATGTGA	GATACTTGTT	180
AAAAAATGTT	TAGCAATGAA	TTGAGGCCTA	GTAGCATGTT	ATCTTGCTGC	AGAAGAGATG	240
GGAGTCTACT	TCTGGGGGAT	GGTCAGGGGT	CCTCCATACA	GGCTGCAATT	GAAGTCGTCG	300
GTGCAGGCTC	AGTCCCTACA	AAGGCCAGGG	TATTTCCTGT	CCACCTTTAT	TCTGATGCAT	360
GACTCTTCTG	GGTCTCAACC	AGAGCCAGTG	GACTTCAGTA	TGGGTCGCTT	TCATTGGCAG	420
ACCCTCAATC	CACTTGTTTT	CCATCTAATC	CCACTCGAG			459

- (2) INFORMATION FOR SEQ ID NO:1375:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 531 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

GAATTCGGCC	AAAGAGGCCT	AATGGATCTC	ATGTGCAAGA	AAATGAAGCA	CCTGTGGTTC	60
TTCCTCCTGC	TGGTGGCGGC	TCCCAGATGG	GTCCTGTCCC	AGCTGCAGCT	GCGGGAGTCG	120
GGCCCAGGAC	TGGTGAAGCC	TTCGGAGACC	CTGTCCCTCA	CCTGCTCTGT	CTCTGGTGGC	180
TCCATCAGCA	GCAATAGTTA	CTCCTGGGGC	TGGATCCGCC	AGCCCCCAGG	GAAGGGGCTG	240
GAATGCATTG	GGAGCATCTC	TTACAGTGGG	AGCACCTACC	TCACCCCGTC	CCTCAAGAGT	300
CGAGTCACCG	TTTCCGTAGA	CCCGTCCAAG	AACCAGTTAT	CCCTGAGGCT	GAGCTCTGTG	360
ACCGCCGCAG	ACACGGCTGT	GTATTATTGT	GCGGGGGGT	CTCCGGGCGA	TTATTCCTAT	420
GAGAATAGTG	ATTACCCCGA	CCCCCCGTAC	TATTTAGACT	CCTGGGGCCG	GGGAACCCTG	480
GTCACCGTCT	CCTCAGCTTC	CACCAAGGGC	CCATCCGTCT	TCCCCCTCGA	G	531

- (2) INFORMATION FOR SEQ ID NO:1376:
  - (i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 661 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:	
GAATTCGGCC AAAGAGGCCT AATGACTCAG AAGAAAGAAG TTACTTTACC ATTTTTGTTT ACACCATTTA AACTGCTTTC TGATTCCAAA CAGTTCAACA TTTTTAGAAA AGCAAGATCT TATATAAAAC ACAGAAAGTT TGATGAAGTG GTCTCCCTTT GCAAGGAGCT AATTCATCTT GCATTGAAAG GATTGTCCTA TTATCACACA TATGACAGAT TCTTTTTGGG CGTCAATGTT GTTATTGGTT TTGTGGGATG GATATCTTAT GCCTCTTTGT TGATCATCAA GTCTCATTCC AACCTTATAA AAGGTGTTAG TAAAGAAGTG AAGAAACCAA GCCATCTCCT GCCTTGTAGT TTTTTGTAGCTA TTGGCATTTT AGTAGCATTT TTTCTGCTGA TTCAAGCCTG TCCCTGGACA GTTATTCAAG ACCTTGTAG ACCTTACCCC TGAGCCATTT TGTTGGGTAC CTGTTAGCCT TTACCCTGG AATTGAAGTA TTAGTTCTCA GTTTTTTCTA CCGCTATATG CTTACCGCT GACCTACTC TGACCCATTT TCACCCGGC GACTTACTG CTTTGCAGCT TGGCCATTT TCACCCGGC GTGGACTCGA G	60 120 180 240 300 360 420 480 540 600 660
(2) INFORMATION FOR SEQ ID NO:1377:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 117 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:	
GAATTCGCGG CCGCGTCGAC AAAAAAGGTA AAGATGTTGC TGTATGCAAA ATGGACCCAA GTTATGTTTA TTCAAGTTGC CTGTAGAAAC TTAGTGCTCT ATAGCCACAA ACTCGAG	60 117
(2) INFORMATION FOR SEQ ID NO:1378:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 118 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:	
GAATTCGCGG CCGCGTCGAC CTTAAATTTA AAACTGGCCT GGTTTGCCTT TTTTATCAAG AGAGCTTAAC AGATAAAAAA TGAAATTAGT CTATTTTCTA CTTGCCAGCA GTCTCGAG	60 118
(2) INFORMATION FOR SEQ ID NO:1379:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 229 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
550	

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:	
GAATTCGCGG CCGCGTCGAC ATTTTATATA ATATTTTAAA TAAGTTTGTG TACAAAACAA AGATTTGACT GCATTTTGAT TGTGACCCCG TTGCATGAAG TCAGGTGTGG AGTTTTCCAC TTGTGGTATC ATGTTGCTGC TGCTCAAGAA GTTTCTGATT TTGGAACATT TTGGATTTTG GATTTTCACA TTGGGGATAC CTAATGTGAG AGAGACTAGG CCACTCGAG	66 120 180 225
(2) INFORMATION FOR SEQ ID NO:1380:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 140 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:	
GAATTCGCGG CCGCGTCGAC GTTGGGGACA TGGTGGGTCT GAGAAAAGTG TTGCCCGCAA CTTTCTATCT GGCATTCCCT GCGGAGGAAA TAGAATGCGC GCTCTCCGAC AGCATTTCCT GTAACATCCG CGAACTCGAG	60 120 140
(2) INFORMATION FOR SEQ ID NO:1381:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 99 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:	
GAATTCGCGG CCGCGTCGAC TCTCAGAAGA GGTTTGTTTA ACTTCTATAA ATACAACCAC TTCATGCGTT GGCATCTCCT TGAGAAAAGG CTTCTCGAG	60 99
(2) INFORMATION FOR SEQ ID NO:1382:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 442 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:	
GAATTCGGCC AAAGAGGCCT AGTTTAAGTG CTGTGGAGTA GTATATTTCA CTGACTGGTT	60
GGAAATGACA GAGATGGACT GGCCCCCAGA TTCCTGCTGT GTTAGAGAAT TCCCAGGATG	120
TTCCAAACAG GCCCACCAGG AAGATCTCAG TGACCTTTAT CAAGAGGGTT GTGGGAAGAA	180
AATGTATTCC TTTTTGAGAG GAACCAAACA ACTGCAGGTG CTGAGGTTTC TGGGAATCTC	240
CATTGGGGTG ACACAAATCC TGGCCATGAT TCTCACCATT ACTCTGCTCT GGGCTCTGTA TTATGATAGA AGGGAGCCTG GGACAGACCA AATGATGTCC TTGAAGAATG ACAACTCTCA	300 360

GCACCTGTCA TGTCCCTCAG TAGAACTGTT GAAACCAAGC CTGTCAAGAA TCTTTGAACA CACATCCATG GCAAACCTCG AG	420 442
(2) INFORMATION FOR SEQ ID NO:1383:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 501 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:	
GAATTCGGCC AAAGAGGCCT ATTCAGGTGT TTTCATTTGG TGATCAGGAC TGAACAGAGA GAACTCACCA TGGAGTTTGG GCTGAGCTGG CTTTTTCTTG TGGCTATTTT AAAAGGTGTC CAGTGTGAGG TGCAGCTGTT GGAGTCTGGG GGAGGTTTAA TACAGCCTGG GGGGTCCCTG AGGCTCTCTT GTGCAGCCTC CGGGTTCATC TTTAGCAACT ATGCCGTGAG TTGGGTCCGC CAGGCTCCAG GGAAGGGGCT GGAGTGGGTC TCAAGTATAA GTGACCATTGG TGACACCAGA TACTACGGAG ACTCCGTGAG GGGCCGATTC ACCATCTCCA GAGACCATTC CAAGAACATG TTGTATTTGG ACATGAACAG CCTGAGAGCC GAGGATACGG CCGTGTATTA TTGTGCGGCA AGGGATTGGT ATCATACTCG TGGCTATTAC TGGTACTACT TTGACTTCTG GGGCCAGGGA TCCTTAGTCA GCGATCTCGA G  (2) INFORMATION FOR SEQ ID NO:1384:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 634 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	60 120 180 240 300 360 420 480 501
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:	
GAATTCGGCC AAAGAGGCCT ACTTCAATAT TCTGTTACGG GTTTTTTTAG TCTTTTTTC TCTTTGCTTT CCTGTGTGG AATTTCTAT TTCTATATAC TCAAGTTCAG AGATTCTTC CTTTTCCATA TCCTGTCTAC TAGTGAGCCC ATCCAAGGCA TTGTTCATTT CTGTTACAGT GTTTTGATCT TTAGTATTC TTTTTCATTC TTCATTACAC TTTCCTCTG CTAACATTGC CCATAAAGTGC TTATATGCTG TATACTTTAT CTGTTGATCA TATTTGTTTT AAATTCCTAA TCTGATAATT CAACATCTCT GACATGTCTG GTTCTGGTTC TGATACTTGT TGTCAAACTG TGGTTTTTTT TCTTTTAGAG TGGCTTTTAA TTTTCTTTTT GTTTTTTTTTT	60 120 180 240 300 360 420 480 540 600
(2) INFORMATION FOR SEQ ID NO:1385:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 700 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:	

GAATTCGGCC	AAAGAGGCCT	ACTCAAGTTC	AAGGAAAATG	AAGACAAAAA	GTGATATGAT	60
GGAAGAAAAC	ATAGATACAA	GTGCCCAAGC	AGTTGCTGAA	ACCAAGCAAG	AAGCAGTTGT	120
TGAAGAAGAC	TACAATGAAA	ATGCTAAAAA	TGGAGAAGCC	AAAATTACAG	AGGCACCAGC	180
TTCTGAAAAA	GAAATTGTGG	AAGTAAAAGA	AGAAAATATT	GAAGATGCCA	CAGAAAAGGG	240
			AGTAAAAAAT			300
AGATGAAGAA	GATCAAAACG	AAGAGAAAGG	GGAAGCTGGA	AAAGAAGACA	AAGATGAAAA	360
					ATGCAAAAGA	420
			AAAAGGAAAT			480
			AAAAGAAACA			540
					AAGAAGATGA	600
			AGGTGGAAAT			
		AGGAAGAAGG		GAGGAAGAAG	CIGGAAAAGA	660
OAAAGAAGA1	111222101210	AGGAAGAAGG	AAAGCICGAG			700
(2) INFORM	ATION FOR SI	EQ ID NO:138	36:			
(i)	SEQUENCE CH	ARACTERISTI	CS:			
		TH: 127 bas				
		: nucleic a	-			
	(C) STRA	NDEDNESS: d	ouble			
		LOGY: linea	-			
(ii)	MOLECULE T	YPE: cDNA				
(xi)	SEQUENCE D	ESCRIPTION:	SEQ ID NO:	1386:		
			TCTTTTCATT ATCCAACTTA		TGTCCTTTGC TTCTGTGGCC	60 120 127
(2) INFORM	TION FOR SE	EQ ID NO:138	37 :			
(i)	(A) LENG' (B) TYPE (C) STRAI	ARACTERISTI IH: 128 base : nucleic ac NDEDNESS: do LOGY: linea:	e pairs cid ouble			
(ii)	MOLECULE T	YPE: cDNA				
(xi)	SEQUENCE D	ESCRIPTION:	SEQ ID NO:	1387:		
					TAGCATTCCA TTCACACAAA	
(2) INFORM	TION FOR SE	EQ ID NO:138	38:	•		
·(i)		ARACTERISTI TH: 816 bas				
	(B) TYPE (C) STRAI	: nucleic a NDEDNESS: d LOGY: linea	cid ouble			
(ii)	(B) TYPE (C) STRAI	: nucleic a NDEDNESS: d LOGY: linea	cid ouble			
	(B) TYPE (C) STRAI (D) TOPO	: nucleic a NDEDNESS: d LOGY: linea YPE: cDNA	cid ouble	1388:		

GAATTCGGCC AAAGAGGCCT AGTTTCTTTT GCTCTACATC TTCACCAGTA TTTGGTGTTA

TCAGTGTTCT	GAATTTTGTC	CATTCTGATA	GGTGTGTAGA	GGTATCTTAT	TTAATTTAA	120
TGTGTTTCTC	TGATGCCATA	TGATGTGTGG	GACATCTTTT	CATATGCTGA	ATTGCCATCT	180
GTATATCTTT	GGTGAGGTGT	CTGTTAAGGT	TGTTGGCCAA	TTTTTTAATT	GGGTTGTTTG	240
TTTTCTTGTG	GAATTTTAAG	AGTTCCTTAC	ACTGTCTCTG	TCTGTCTTGT	CTGTCTGTCT	300
GTCTGTCTGT	NGAGACAGAG	CCTCGCTCTG	TCACCCAGGT	TGCAGTACAG	TGGCACAGTC	360
TTGGCTCCCT	GCAACCTCTG	CCACCTGGGT	TCAAGTGATT	CTCCTGCGTC	AGCCTCCCGA	420
GTAGCTGGGT	TTATACCCGT	GCACCACCAC	ACCTGGCTAA	TTTTTGTATT	TTTAGTAGAC	480
ACGGGGTTTC	ACTANGTTAG	CCAGGCTGGT	CTCGACCTCC	TGACCTCAGG	TGATCCACCC	540
ACCTTGGCCT	CCCAAAGTGC	TGGGANGNGA	GCCACCACAC	CCAGCCTCCT	TACACATTTT	600
AGTTAATAGT	TCTTTATCAG	ATGTGTCTTA	TGTAAATATT	TCCTCCCTAT	CTGTGGCTTG	660
TCTTTTCATA	CTCTTGACAT	TGTCTTTTGC	AAAAGACAAC	AATTTTTAAG	AAACAAGTAG	720
ACAATTTTAA	TGAAGTCTGG	CTTATCAGTT	CTTTTCTTCA	TGGTTGGTAC	CTTTGGTGCC	780
GTATCTAAAA	GTCATCACCA	AACCCAAGAA	CTCGAG			816

- (2) INFORMATION FOR SEQ ID NO:1389:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 163 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

GAATTCGCG	G CCGCGTCGAC	CTAAACCGTC	GATTGAATTC	TAGACGAACT	ATATGTTTAA	60
GCAAAAACA	TAAAAATAAA	CCTCAAAAAA	AGTAATATCA	GAGTTTTAAT	TTCAACCAGC	120
TGGCACAAC	A ATGAAAGTGT	CAGACTTTCT	GAAAGTACTC	GAG		163

- (2) INFORMATION FOR SEQ ID NO:1390:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

GAATTCGGCC	TTCATGGCCT	AAAACCCTCA	TTAAATAAAAT	AGAATCCAGC	ACTGCTACAA	60
TATATTATCT	AAAATGTCTA	ATTCTCAAAA	ATATGAGTGA	TGCAAAGAAA	CAGGAAACAG	120
TGAAACACAG	AGGAAAAAAC	AGTGACTAGA	AACTGACTTA	AGAGTAAGCC	CAGATGTATT	180
TGGGAGCCAG	AGCCTTCAAA	GTAGCTATTA	AATATGTTCG	AAAAAATTAA	GGGAAAATAT	240
GACAATGACT	CAAAAATAAG	GACTCTAAAT	ATAGAAATGG	GAGCTG		286

- (2) INFORMATION FOR SEQ ID NO:1391:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 392 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

GAATTCGGCC TTCATGGCCT ACTTTTAAGG GCTTGGAAGT TTCAAAACCA CAGTCTGCAT

GTGACAGGTG CTCACTGCTG TTGGGTTGGC CGCTGGTTCT AGGCCTCTGC TGGAGTGTGT GATCTGCTTT CTGACGGCAG GGCGTTCACA TGGGTGTGCT TTAATCTTAC GTCTCCGTCC TCTTTTTCCA CTGAGAGTGC TGGTCTCAAG GACAGTGGAG ATGAGAGAAT TGGAATATCG CATAATGTCT CATCTGTTTT ATCTCTTGCT ACAAACATCA CAATCTCAAA ATAACAATGG CAGTACAACT GCCACCTATA TCATTACTGA AAACAGTGAA GATATTTTTT GCCTAAGTCT TCCCATTCTG TGTAGTTATG CAGAGTCTCG AG	120 180 240 360 360
(2) INFORMATION FOR SEQ ID NO:1392:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 286 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:	
GAATTCGGCC TTCATGGCCT AGTAATCTTT CCCCCCAGTT TTTGGATGAA GAAACTAACA CTGAAGGGGC GAGGTGGCCT CCCAGGCTCA GAGGGTGATT CAGAATCCAG GCCTGGTGTT CCTTCCACAG TACCAAAGCG CCACACATTA GTTGTCTTGT AGATTTTCCA CACTTCAGGG AGAATGCCAA AGTATCTTTG CCTTGCACAC ACTACCTGTT CAACACTCAG TGACGAGGGT GTCGTGTGTG CTCAGGCAAC TCCCGCCCTT CTTCCTTTTG CTCGAG	60 120 180 240 286
(2) INFORMATION FOR SEQ ID NO:1393:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 320 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:	
SAATTCGGCC TTCATGGCCT ACTGAGTTCT CAAATCTAAC GTTTTAGGAA TTTTTTATTC TGCAGGAGAG TTGGGGAGCT GTTTAAAAGT TGGTTGGTTT AGCCAGTATA GCTAGATTCC TCAAGGTCAA CACAACGCCA TACTGCTCTA GCTGGGGCTA GATTTCTCAT GATAGTCTAA ACTGTGTGAT GGCCAAGTCC CCACTTTGAA GATGTCCAAA TTCAGCCTCA GACATTTCTC TCAAGAAAG GGGGGCAAA AAAGCCTTTT GTGCCCCTTT CCCAAATTAT TTGCTCATGT TGCAAGACTG AGGTCTCGAG	60 120 180 240 300 320
(2) INFORMATION FOR SEQ ID NO:1394:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 450 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:	
SANTTCGGCC TTCATGGCCT AACGCCATCT ACGACCTGAT CGAGCGCATC GAGGATTTGG GCTGCAGAA CCAGATCCGG GAGCACGTCA TCTCCATCGA GGACTCGTTT GTGAACAGCC	60 120

180

CTAGCGGGAA GTCAC CCCCTGAAGG GGGGC TGATCCGAGA TGAAC TGTTTGTGTT CAGCC	GCCGC TCCGTACCGG GCCCTG GTGCACCGCT GGTTT AAGAAGGAGA GAGGC CCCCTGAGC TGGAG GATGAAATCA GCAAC ACCCCTCGAG	ATCTGACGGG TTGTGGTGGA TCCAGTTTGC	GACCTATGTC TGGCCAGAGT TGCCTGGGTG	CAGGAGGAGT TACCTGCTGC GATGCAGTGG	180 240 300 360 420 450
(2) INFORMATION	FOR SEQ ID NO:13	95:			
(A) (B) (C)	NCE CHARACTERISTI LENGTH: 276 bas TYPE: nucleic a STRANDEDNESS: d TOPOLOGY: linea	e pairs cid ouble			
(ii) MOLE	CULE TYPE: cDNA				
(xi) SEQU	ENCE DESCRIPTION:	SEQ ID NO:	1395:		
CTATTTTGGT GGGAA AAGGCCAGTT TCTGT ACTACCAAGC CCAAA TTCTTCCTCA CTCTC	GGCCT ACCGTCATTC ATCTA GCAGATAGAG GCCTG TCCTCGTTCT ACCTT CAAAAACAAG AAACA ATCTCTATCC	AAGCCAAACA CTCCTCTTTA GACCATGGTA TTCGAG	AGTAGCCCTA CTCTCCAGAA	CAACCTGTAC GAAAAGGAGG	60 120 180 240 276
(2) INFORMATION	FOR SEQ ID NO:139	96 :			
(A) (B) (C)	NCE CHARACTERISTI LENGTH: 241 base TYPE: nucleic a STRANDEDNESS: de TOPOLOGY: linea:	e pairs cid ouble			
(ii) MOLE	CULE TYPE: cDNA				
(xi) SEQU	ENCE DESCRIPTION:	SEQ ID NO:	1396:		
ACTCTTTGAA AACTA GTTAACCGAC ACTCT	GGCCT AGGGGGCGGG AATAG TTTAAAATCT GTATA TCCTGTATAA GCTAG TATACAGTAT	CATCCAACTT AACATTCTAA	CCACCTAACT CTGATGCCCA	TACATGCCTG CGACATACTA	
(2) INFORMATION	FOR SEQ ID NO:139	97:			
(A) (B) (C)	NCE CHARACTERISTI LENGTH: 314 bas TYPE: nucleic a STRANDEDNESS: d TOPOLOGY: linea	e pairs cid ouble			
(ii) MOLE	CULE TYPE: cDNA				
(xi) SEQU	ENCE DESCRIPTION:	SEQ ID NO:	1397:		
TGTGATCGTG GGGGG GGACCCCCTG CGAAG	GGCCT AGAAAATGAA CATGC TGCTGATCGA GACAG TGGAGAAGTA TCTCC TGGAGCACTG	CCTGTGTATC CAGCATGGAG	CTGATCTGCT CCGGACCCAG	GGCAGGCTGT CAGGACGGGA	60 120 180 240

CCGCAACTCT CGAG

CATCGTCTAT GCCTACAAGG GACTTCTCAT GTTGTTCGGT TGTTTCTTAG CTTGGGAGAC

300

314

(2) INFORMATION FOR SEQ ID NO:1398:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 342 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:	
GAATTCGGCC TTCATGGCCT AGTGCACACC AAGAACCAAG TTTCAGCTTG GTTACTGTGT TGAAGACACC TTTGCTATAT TTCAAGTCAT TCCTTCTTTT CTCAATTTTT TTTAATTGAC AAAAATTTTA TATATCGTGT ACAACATCAA TCCATCTTGG CATCTGTATT TGTCAGGGTT GTCTTAGAGG GACAGAACTA ATAGGATATA TATAAGGGGG AGTTTATTAA GTATTAACTT ATATAATCAC AGGGTCCCAC AACAGGCTGT CTGCAAGTTG AAGAGCAAGG AGAGCCAGTC AGAGTGCCGA AACTGAAGAA CCTGGAGTCC GATGTTCTCG AG	60 120 180 240 300 342
-	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 614 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:	
GAATTCGGCC TTCATGGCCT AGGGCCATGT TGGTTAGAAT GGTGCCATAT TTTCTGGGAT AGCACCATGC TGGCTGGGAT GGTGCCATGT TGGCTGGGAT GGCACCTGCC TCAGCCTCCC AAATAGCTGG GATTACAGGC ATCTGCCACC ATGCCTGGCT AATCTTTTGC ATTTTTAGTA GGAGAAGGGGT TCGCCAAAGT GCTGGAATTA CAGGCATGAG CCGCCAAGCC TGGCCTTTTA CTGAGTTTT AATAGGATCG CTCTTGCTGC TATTGAGGAT AGTACATATG GGGTAATGAT GCAAGCAGAG ACCTACTGTA GTACTCTCA GGAGAGAATG GTGGCTTTGCA CAAGGATGGA AGCAATGAAA GTGGTCAGTT TCTATATTTA TTAGGAAACA CCTAGGATGA ATTTTTTGGCT TTGACAACTG AAAGAATAGT TACTATCAAC TGTGATTGGT AACAATGCAC ATGGATCACC CGAG	480
(2) INFORMATION FOR SEQ ID NO:1400:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 244 base pairs  (B) TYPE: nucleic acid '  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:	
GAATTCGGCC TTCATGGCCT AGTTCTATTT AAAAAATAAA CAACTAGACA ATTAACTAGT	60

TGTATTAAAG	ATCACAATTG AATTTTTTT TAATTTTCAG TCTTAACACA TTTTTTAAAA TAATACATTG TAGTAGTAGG ATTATATACT CCTTGGCTGA GAATTCCAAG CTACTGTTTA GTGGAAAACT CTGGAAGTTA AAATATAGAA TATGAAACCT	120 180 240 244
(2) INFORMA	ATION FOR SEQ ID NO:1401:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1401:	
AAGAAGCCAC AAGCACTTAA TCACATAATT TCAAATTGTC	TTCATGGCCT AAAACAAACA AAAAATTATC TGAATGATCC TGTCTCTAAA AGAAATGTTT AAAAACTTCA TCGACTTAGC CTGAGTCATA ACGGTTAAGA ACAGAAGCAG AGGCTAATTC AGTGTCACAT GAGGAAGTAG CTGTCAGATG ACTTTCGTAA TAGCACAGAT TAGAATGGCT ACCCCATTCT CTAGACAAAA CTATTGTGAC TCTTCTAAAA ATGAAGATGA AGAGCTATTT AATGACACAC AACGGGAAAC TCGAG	60 120 180 240 300 325
(2) INFORMA	ATION FOR SEQ ID NO:1402:	•
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 364 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1402:	
TAGTCCCTTT TTCCTTTAGC GTTCAAAAGT TACATCAGCA	TTCATGGCCT AAAAGAAAAG AGAAAGTGTT ATTTTCCTGT TAGTGACATG GTTCTAGTAG GAAAAAAGGT GCCTAGAGGT AGTATATAGA GTAAATATTG CTACTTCCTG CAGCTTCCAA TTTATCCAAG GAAATGTCTA CAACAATTTT CTGTTCTAGT CAATAGCAGG AGAAGTCCAC GTTATTGGGC TGATTTTGCT AGAGAAATGT CACGTGATAC TCAGGCCGCG CTTTCTCTTC CATCACACCA ATGTCAATAA ACCCACTTTG GCTAGGCAGG ATTGAATTCT AGACCTGCCT	60 120 180 240 300 360 364
(2) INFORMA	ATION FOR SEQ ID NO:1403:	
(i)·	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1403:	
TAAGATTGTT	TTCATGGCCT AGTTAGGGAC TAACATTTGT ATCAACAGTT GATAAATGTC TATTATACAG CAGGGTACAA TGGTAGTGCT AATGCCAACA GGGCACCATG TAAAAATTAT CGCTAGGCTT TATACAAGCA ACAACATATG CTGCTGCTCT	60 120 180

TGAATTCTAG ACCTGCCTCG AG	240 262
(2) INFORMATION FOR SEQ ID NO:1404:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:	
GAATTCGGCC TTCATGGCCT AGCAATTTGC TTCAGTTTCC TTATGTTTGC CTTTCTCATC TGTCCTCTTT TCCATTTAT TCCTACTCTG TCTCAGTCCA CTTACAGTTA TATTTCCTAT CTGTGTATTT TATAATATTT GTGCTTTAAT ACTTTTAAAA TATCCTTTAT TTTACTGTTT CTTCTCTTCC CTTGTCATAT TTTAAAGTGT TTTATTTCTC AGCCTTCTAT ATCTTTGCAT TAATTCTGTT CCTCTACAAT AGAGTCCGTT CCAAGCTTTC TGTCTTCCTG TGTCCTTCCA CGGCTCTGGC TCTCTCTGCA TTATTTCCTA TTTATGGAAT ACAAATCTTT TACCCTTGTA TTTTTCTCAC TCCTCTCCAC ACACCCCCGA CTCGAG	60 120 180 240 300 360 396
(2) INFORMATION FOR SEQ ID NO:1405:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 444 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:	
	60
GAATTCGGCC TTCATGGCCT AGACCAAAAT GTCTGCCCAG ATAAAGGATA CATTGTGCAT ACATACACTG GGGAGAGGCA GACAAAAAAA CAATGTAGTT TGAGTGTGTG TGCGTGCTTG CATGCGTGCA TGCAGGCATG TGCATATATA ATGCTAAAAC ATGATAAGTA CTATTAAAAA AACAGGTTAG GGTGATTGAA ACTACTAGGG TATGAATAAG AGTGGGTTGC AATTTAAAGT AGGGTCATTG TGGTTGGCCT TATTGAGGTG ACATTGGAGT CAAGACTTGG AAGAAGAAAG GTTGTTGGCC ACACAGCTAT TGAGGGAAAA ATGTTCCAGA TAGAAGAAAC AGTCAGGGCA ATGCCTTGGG ATGGAATCAT GCATAGAGTA TTCACAGAAT AGCAAGGAAG CTCTAGTTCT AAAGTAAAGT GACTGAGACT CGAG	120 . 180 . 240 . 300 . 360 . 420 .
ACATACACTG GGGAGAGGCA GACAAAAAAA CAATGTAGTT TGAGTGTGT TGCGTGCTTG CATGCGTGCA TGCAGGCATG TGCATATATA ATGCTAAAAC ATGATAAGTA CTATTAAAAA AACAGGTTAG GGTGATTGAA ACTACTAGGG TATGAATAAG AGTGGGTTGC AATTTAAAGT AGGGTCATTG TGGTTGGCCT TATTGAGGTG ACATTGGAGT CAAGACTTGG AAGAAGAAAG GTTGTTGGCC ACACAGCTAT TGAGGGAAAA ATGTTCCAGA TAGAAGAAAC AGTCAGGGCA ATGCCTTGGG ATGGAATCAT GCATAGAGTA TTCACAGAAT AGCAAGGAAG CTCTAGTTCT	120 180 240 300 360 420
ACATACACTG GGGAGAGGCA GACAAAAAAA CAATGTAGTT TGAGTGTGT TGCGTGCTTG CATGCGTGCA TGCAGGCATG TGCATATATA ATGCTAAAAC ATGATAAGTA CTATTAAAAA AACAGGTTAG GGTGATTGAA ACTACTAGGG TATGAATAAG AGTGGGTTGC AATTTAAAGT AGGGTCATTG TGGTTGGCCT TATTGAGGTG ACATTGGAGT CAAGACTTGG AAGAAGAAAG GTTGTTGGCC ACACAGCTAT TGAGGGAAAA ATGTTCCAGA TAGAAGAAAC AGTCAGGGCA ATGCCTTGGG ATGGAATCAT GCATAGAGTA TTCACAGAAT AGCAAGGAAG CTCTAGTTCT AAAGTAAAGT GACTGAGACT CGAG	120 180 240 300 360 420
ACATACACTG GGGAGAGGCA GACAAAAAAA CAATGTAGTT TGAGTGTGT TGCGTGCTTG CATGCGTGCA TGCAGGCATG TGCATATATA ATGCTAAAAC ATGATAAGTA CTATTAAAAA AACAGGTTAG GGTGATTGAA ACTACTAGGG TATGAATAAG AGTGGGTTGC AATTTAAAGT AGGGTCATTG TGGTTGGCCT TATTGAGGTG ACATTGGAGT CAAGACTTGG AAGAAGAAAG GTTGTTGGCC ACACAGCTAT TGAGGGAAAA ATGTTCCAGA TAGAAGAAAC AGTCAGGGCA ATGCCTTGGG ATGGAATCAT GCATAGAGTA TTCACAGAAT AGCAAGGAAG CTCTAGTTCT AAAGTAAAGT GACTGAGACT CGAG  (2) INFORMATION FOR SEQ ID NO:1406:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 363 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240 300 360 420
ACATACACTG GGGAGAGGCA GACAAAAAAA CAATGTAGTT TGAGTGTGT TGCGTGCTTG CATGCGTGCA TGCAGGCATG TGCATATATA ATGCTAAAAC ATGATAAGTA CTATTAAAAA AACAGGTTAG GGTGATTGAA ACTACTAGGG TATGAATAAG AGTGGGTTGC AATTTAAAGT AGGGTCATTG TGGTTGGCCT TATTGAGGTG ACATTGGAGT CAAGACTTGG AAGAAGAAAG GTTGTTGGCC ACACAGCTAT TGAGGGAAAA ATGTTCCAGA TAGAAGAAAC AGTCAGGGCA ATGCCTTGGG ATGGAATCAT GCATAGAGTA TTCACAGAAT AGCAAGGAAG CTCTAGTTCT AAAGTAAAGT GACTGAGACT CGAG  (2) INFORMATION FOR SEQ ID NO:1406:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 363 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	120 180 240 300 360 420

GCCAGCTTCG ATGAGAATAC AACAATGTTA GATATATTCG TTTTGGAAGA TACCTTTCCC CCAGTTATTT TCATTTCACA GCTTCTCCAG CCTCCTTCAG CTTCTGTTCT CCCTCTTTGC TTTTCTGTCT CAATTTTCCT GCCCAGCCCT AAATTCACAG AGTAAATCCA CCAGAACCTC GAG	240 300 360 363
(2) INFORMATION FOR SEQ ID NO:1407:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 229 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:	
GAATTCGGCC TTCATGGCCT AGGCTTCAGG GATAACCACG TTCAGGTGGG TTAGACACAC CTCCTGTGGG AGGGTGATTG CAATTAGCTA TCATAAGGCA GGAGACACAA CAGCAACTTA AATTATCCAC AAGCAGAATC ATGAGCTGTT TGCAAAGGGA GTTTCCATCG CAAGACAGTT TCACTGTATT TAAGCGAGAT CCTGCCCTCG TACACGATCA CCGCTCGAG	60 120 180 229
(2) INFORMATION FOR SEQ ID NO:1408:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 512 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:	
1,	60 120 180 240 300 360 420 480 512
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:1408:  GAATTCGGCC TTCATGGCCT AGGCTTCTAG AACAAGAATG TAGGCAGGCT CCCAAATGGA GAGGTAAACA TGACCGGTT GTTTGAAACT ACTTCATTAA TTTGTAAATC AGAACCAAAA AGCTCTGGCC CTCCCACTTC TCTTAGCTGA CCCTCCTCCC CACTTACGGA TAAACAGACT TTAACTTCCC TAACCCAGAA ACACTTCCAC CAAAAATGTA TGGTTATACC TTATCCTAAA AAGGCACCAT GCAGGCATTT AAGACTGAAC CAGTGAACTC TAAATATGTA GTAGTAGAAA ATATCACTAA TCAAAACTTC CAGCATCAGA TGGTACAAAA CCCCAAGAGG ACTGGTGACA TGTACCCCGG GATGGCAACC CCAGCTTCTG GCAACCCCAC AGCCCAGCGG GAGCTTCAGC TCTGGTCAGG TGCACGGCTG CCAAAGTCTG CACACCTTGG GGACAAGGAA AGGAGACACT	120 180 240 300 360 420 480
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:1408:  GAATTCGGCC TTCATGGCCT AGGCTTCTAG AACAAGAATG TAGGCAGGCT CCCAAATGGA GAGGTAAACA TGACCGCGTT GTTTGAAACT ACTTCATTAA TTTGTAAATC AGAACCAAAA AGCTCTGGCC CTCCCACTTC TCTTAGCTGA CCCTCCTCC CACTTACGGA TAAACAGACT TTAACTTCCC TAACCCAGAA ACACTTCCAC CAAAAATGTA TGGTTATACC TTATCCTAAA AAGGCACCAT GCAGGCATTT AAGACTGAAC CAGTGAACTC TAAATATGTA GTAGTAGAAA ATATCACTAAA TCAAAACTTC CAGCATCAGA TGGTACAAAA CCCCAAGAGG ACTGGTGACA TCTACCCCGG GATGGCAACC CCAGCTTCTG GCAACCCCCAC AGCCCAGCGG GAGCTTCAGC TCTGGTCAGG TGCACGGCTG CCAAAGTCTG CACACCTTGG GGACAAGGAA AGGAGACACT TGCTTCATTG TGCTATTCAT GACCCAGTCG AG	120 180 240 300 360 420 480
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:  GAATTCGGCC TTCATGGCCT AGGCTTCTAG AACAAGAATG TAGGCAGGCT CCCAAATGGA GAGGTAAACA TGACCGCGTT GTTTGAAACT ACTTCATTAA TTTGTAAATC AGAACCAAAA AGCTCTGGCC CTCCCACTTC TCTTAGCTGA CCCTCCTCCC CACTTACGGA TAAACAGACT TTAACTTCCC TAACCCAGAA ACACTTCCAC CAAAAATGTA TGGTTATACC TTATCCTAAAA AAGGCACCAT GCAGGCATTT AAGACTGAAC CAGTGAACTC TAAATATGTA GTAGTAGAAA ATATCACTAA TCAAAACTTC CAGCATCAGA TGGTACAAAA CCCCAAGAGG ACTGGTGACA TGTACCCCGG GATGGCAACC CCAGCTTCTG GCAACCCCAC AGCCCAGCGG GAGCTTCAGC TCTGGTCAGG TGCACGGCTG CCAAAGTCTG CACACCTTGG GGACAAGGAA AGGAGACACT TGCTTCATTG TGCTATTCAT GACCCAGTCG AG  (2) INFORMATION FOR SEQ ID NO:1409:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240 300 360 420 480
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:  GAATTCGGCC TTCATGGCCT AGGCTTCTAG AACAAGAATG TAGGCAGGCT CCCAAATGGA GAGGTAAACA TGACCGCGTT GTTTGAAACT ACTTCATTAA TTTGTAAATC AGAACCAAAA AGCTCTGGCC CTCCCACTTC TCTTAGCTGA CCCTCCTCCC CACTTACGGA TAAACAGACT TTAACTTCCC TAACCCAGAA ACACTTCCAC CAAAAATGTA TGGTTATACC TTATCCTAAA AAGGCACCAT GCAGGCATTT AAGACTGAAC CAGTGAACTC TAAATATGTA GTAGTAGAAA ATATCACTAA TCAAAACTTC CAGCATCAGA TGGTACAAAA CCCCAAGAGG ACTGGTGACA TGTACCCCGG GATGGCAACC CCAGCTTCTG GCAACCCCAC AGCCCAGCGG GAGCTTCAGC TCTGGTCAGG TGCACGGCTG CCAAAGTCTG CACACCTTGG GGACAAGGAA AGGAGACACT TGCTTCATTG TGCTATTCAT GACCCAGTCG AG  (2) INFORMATION FOR SEQ ID NO:1409:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	120 180 240 300 360 420 480

TTTTTGTGCC AGCATGCTCG AG

TGTGGGGTCT AGTGATGTCT CCTCTTTCAG TTCTGATATT GGTAATTTGT GTCTTCTCTC

240

262

(2) INFORM	ATION FOR SEQ ID NO:1410:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 441 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1410:	
GGCCCTGGAT CAGCCTCCAA AACTGGCTGA CACTAAAGGG AATAGAAGCA ATTGCATAAC	TTCATGGCCT AGGGAGGTGG TTTCTCTATC ATTGCATGAG GTAAGAGTCT GCTAAGGCTG CAGTTTCTA CAGAAAGGAG TCATCTCTGT GAGGCAGCAT GACACAGTG1 GCTGACCTGG TTTTGTATAA AGATGAAAAC AGCTGTTCTC GGCCGGCCAC AGAGAGAGCG GCGGGCTCAG CCTTCACAGG ATTGTCCTTC TAGGGGGTTT TAATCATCGC AGAAAGGAAG TGGGGTGAA GGTCAGGAAA CGAATTCACC CCTCAGGCCT CAGCTAGAGG AAGCTAAGAG AAGAATGAG TGTTAAGAAA AAGGCAAAGC TGGAGAGAAT GCAGAGGATT CTGGTTCCTG TCAGACTCGA	60 120 180 240 300 360 420 441
(2) INFORM	ATION FOR SEQ ID NO:1411:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 479 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1411:	
CCTGCTCTCT TTTATATATT GCTACTGCAG TCCAAAAGTA AATAAGCACA GATTTCTGTA	TTCATGGCCT AATTCATTGT CTGGTCCTTT ACAAAAGACA TATGCTGGCT GTGGATGATA GGTCTACAAA GATGTGATTC AACTCATATA TGTCTCCAAA AATTCATATA CTGTTTTGCT TTACATTAAT CTAGCATTGT CTTTTGGCTT TAAGTTACCT TCTAATTCAT CATTAGGTCA ACTTTATCAA CTCACCTAAG AATGTAGGTT TCTCCTGGGT TCTTTTGCCT CTTAAGTTTT GCCATCCCCA ACAGAGACCT GCACCAAAGA ACCTTACTTT TAGACTGTAA GCACCAAAGT GAGAGAGTGA GCCAGGCTCA GTCTTATGAC TGGCAATACA AGTTGAGGGT GACAGAACAC TAGCTATGTA TAGTGTTGTC TAGGTGAGTG CTTCTCGAG	60. 120 180 240 300 360 420 479
(2) INFORM	ATION FOR SEQ ID NO:1412:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 497 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1412:	
	TTCATGGCCT AGCCGATTTA TAAATATGTA TATATAACCT TTCCCTTTTT TTAGTAATAG TCAAAGCCAT ACCCTATTCC TTAGTGAGAA AGCCAGTTTG	60 120
	561	

AAACGAATGT	AGCAATAGAT	GTAAAAACAT	TTAAAGGCGT	TTTAATGTGG	CTTTTTAATG	180
AGCTGGCTTA	TGCCTGTAGT	CCCAGCACAT	TGGGCAGCTG	AGCTGGGAGG	ATCGCTTGAG	240
CCCGGGAGTT	CAAGACTAGC	CAGGGCAACA	TAGTGAGACC	CCATCTCTAT	TTAAAAAAAA	300
ATGTTTTTAA	AGATAAGGAA	CAGACTTAAA	GTGATGATTG	ATTGCTCATA	GAACGTTCAT	360
TTTGGGCTCC	AGAACTAGGA	ATGATGTAGA	ATTTATTGTT	GTGTCATTGT	CTCATTAAAT	420
GCTGTAGTTT	CCTATGTCCT	TGCCTACCTT	CTTTCCTCAG	AGCCTCGCAT	CTGACCCTCA	480
GAGAGTAGCA	GCTCGAG					497

- (2) INFORMATION FOR SEQ ID NO:1413:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 439 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

GAATTCGGCC	TTCATGGCCT	ACAGGAACAA	AAAATGCTAT	GCTATTATCT	CAAAAATGCA	60
TACTCCTTCC	TACTTAAGAA	TAATAAATTT	ATATATTATG	ATATGGTAAA	ATTCACAACT	120
AATTGTATTT	TTCCCTAGAA	TGTTTAAAGC	ATTATCTAAT	ACCAGCTTCA	GTGTCTATAT	180
TACTGTAACT	TCATGAAAGA	CTACTAACAA	TACTGGCTAT	CATTTATTAA	TATTAAGTAG	240
TACTTGCCAG	ATGCCGTTAG	AGGTGCTTTA	AATGCATTCT	CATTTAGTCT	TCGTGTGTAC	300
TACCGTTATC	TTCACTTTTT	AGATAAGGAG	ACTAAAGTAT	AACTAGAGCT	AAGAAACATG	360
AGAAAGACGA	CCTAGCTACT	${\tt GCCTATTTTG}$	TAATTCCCAT	GGACTAAGCT	TGGAGAAGTA	420
AGAACTATTA	CTACTCGAG					439

- (2) INFORMATION FOR SEQ ID NO:1414:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 243 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

GAATTCGGCC TTCAT	GGCCT AGCCACTTCA A	GACGGCAAG TTATTTTAGC	TCCTGTCTAA 60
ATAAGTTAGT GGGCT	CCAGT CCTTAAACCA C	TATTTTCTT TATTAATTCC	TCAAGTACAG 120
ACTTTTGTAT GTAAC	CAGTC TTTTTAAACC T	GTGTATAAT GACTCATTAA	TGAGTTGTAA 180
AATAAATGTA GTGAG	TTATG ACCAATATAA A	AAAATAGAA AAGGCCAGGC	ACAGTCGCTC 240
GAG		•	243

- (2) INFORMATION FOR SEQ ID NO:1415:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 276 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

	TTCATGGCCT AGTCTTCCAA GACAGGAATC AGCAACCTTT TTTTGTTTTT	60
	AATTCATTCT GTATATTTTA AAAAGTTTTA ACCTCTTCTT CCTAGCCCTC	120
	TTATAAATTA AAACGTTTCC CAAAGTGTTT TCTGTGAAAC AATAGTTCTA	180
	TAAGAAAAGC TAAGTACATG GCAAAATCCA AAGTATATGT TTTATTCATT	240
ACATTTGATG	AATTTTTTT GTTTTTTCCT CTCGAG	276
(2) INFORMA	ATION FOR SEQ ID NO:1416:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 341 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1416:	
CAATTCCCCC	TTCATGGCCT AGAGAGCAGG TTTTAGCTTG CATCCAGCTG TTTCTTGAGT	60
	GCTTACCCCC AAAGAGGCAA CTGAATTTCA GCTGCTCTAA TACCCACACC	120
	GTTTAGTCAT AATAAAAAAC AGAATGGATT TGTTAGTTCC ATTGATTGCC	180
	CCTTCTGTGT GGCAGAGATG TGCTTTAGTT CTTCATTGGA ATGTTACTTT	240
	AAACCTCAAA CCTAGGGCAC CACCAATGAC AAAGAGAATG CTAAATAGAT	300
	CCAGGTCTTC AAGCTTTCCA CTCCCCTCGA G	341
		311
(2) INFORMA	ATION FOR SEQ ID NO:1417:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 455 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1417:	
C	A B B C B C C C C B C C C B C C C B C C C B C	60
	AAAGAGGCCT AGCCATTATT ATTAAAAAGT AGGATTGCTA CCCGCCATTA	120
	GTAGGATTGC TACCCGCCAT TATTATTAAA AAGTAGGATT GGTACCCGCC	
	AAAAGTAGGA TTGCTACCCA ACATTATTAT TAAAAAGTAG GATTGCTACC	180
	ATTAAAAAGT AGGATTGCTA CCCTCCATTA TTATTAAAAA GTAGGATTGC	240
	TATTATTAAA AAGTAGGATT GCTACCTGCC ATTATTATTA AAAAGTAGGA	300
	CCATTATTAT TAAAAAGTAG GATTGCTACC CGCCATTATT ATTAAAAAGT	360
	CCCGCCATTA TTATTAAAAA GTAGGACTGC TACCCGCCGT TATTTGCACA	420
GCTACCTTAT	GAAAGTAGTT TCACGCTGTC TCGAG	455
(2) INFORMA	ATION FOR SEQ ID NO:1418:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 573 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(51)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1418:	

					TCCCTTGGCT	12
	TCCCTGTACC					18
					TACCCCTTGC	24
ATGTGTGGCT	GCCCCTCACC	TGGGTGTCCT	CTTCCCTGTC	CCAGCTCTGA	CAÇCCACGCA	30
TGTGGGGCTG	CCCCGTGCCT	AGGTGTCCCC	TCCTCTGCTC	AGGCTCTGTC	CTCCTGCGGT	36
TGGCTTTCCC	ATTCTGGATG	CACCTCACAC	ACAGCCTTGT	CATCTTTGGA	TGAATTTGGC	42
CTCCCCCATC	CACTGCTGGT	GCAGATGCTT	CCTTACGGGG	CCTTGTCTGA	TGGCTTTAGG	48
GCTGAATCAT	GCAGGAAGGA	AGGAGAAGGA	CAAGAAGAAA	AGGGAAGGCT	GGGAAGGGAA	540
GCGGGTGGTA	AAATTGGTTC	ACAAGCCCTC	GAG			57:

- (2) INFORMATION FOR SEQ ID NO:1419:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 188 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

GAATTCGGCC AAAGAGGCCT	ATTTTAAAAA	AAACTATTTA	TAATTTTTTA	TTATTTTTGG	60
TTGTTTTTTG CACAATGAAG	TTTCAGCTTC	TCAACCTTCT	CCCCTACCCA	GGGCTGTGGA	120
CCCAGACTGG CCTTGAGCCA	CAGTCCCTCT	TTCCCTCCTC	ACCCTCTTCC	CCCTCCGGGC	180
ACCTCGAG					188

- (2) INFORMATION FOR SEQ ID NO:1420:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 572 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

GAATTCGGCC AAAGAGGCCT	ACGAGGAAAG	ATCTAATTAT	CATGGACCTG	CGACAGTTTC	60
TTATGTGCCT GTCCCTGTGC	ACAGCCTTTG	CCTTGAGCAA	ACCCACAGAA	AAGAAGGACC	120
GTGTACATCA TGAGCCTCAG	CTCAGTGACA	AGGTTCACAA	TGATGCTCAG	AGTTTTGATT	180
ATGACCATGA TGCCTTCTTG	GGTGCTGAAG	AAGCAAAGAC	CTTTGATCAG	CTGACACCAG	240
AAGAGAGCAA GGAAAGGCTT	GGAAAGATTG	TAAGTAAAAT	AGATGGCGAC	AAGGACGGGT	300
TTGTCACTGT GGATGAGCTC	AAAGACTGGA	TTAAATTTGC	ACAAAAGCGC	TGGATTTACG	360
AGGATGTAGA GCGACAGTGG	AAGGGGCATG	ACCTCAATGA	GGACGGCCTC	GTTTCCTGGG	420
AGGAGTATAA AAATGCCACC	TACGGCTACG	TTTTAGATGA	TCCAGATCCT	GATGATGGAT	480
TTAACTATAA ACAGATGATG	GTTAGAGATG	AGCGGAGGTT	TAAAATGGCA	GACAAGGATG	540
GAGACCTCAT TGCCACCAAG	GAGGGTCTCG	AG			572

- (2) INFORMATION FOR SEQ ID NO:1421:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 498 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

```
GCAAGACGGC TACTGAGGCA GGAGAATCGC TTGAACCCAG GAAGCGGAGG TTGCAATGTG
                                                                      60
CCAAGATCGT GCCACTGCAC ACTCTAGCCT GGGCAACAGA GCAAGACTGT GTCTCAAAAA
                                                                      120
AAAAAAATCT TNGACNAAAC ATAGTTGTTN ACATACTTCT TTAATCCCAG AGTTAGTTTT
                                                                      180
AAAAANNACA TGATTGCTGT TTTTGCATAT TATCTCAGCG GTCTAAAATT AACCTAGCCA
                                                                      240
TGTGCAGGAA TGGGTAAAGT CCCCTTAAAC AAAAATGGGG TTAGTTANGT TAGTTCTTTT
                                                                     300
GCCATTTCAC TGGTCATATA CCTGAAGCGC TTAGCCTGAC ACAATTGAAC GCCAGACGGA
                                                                      360
AGCCGNGATC AGCGGTCCTG ACGGGGGTCA GAGTCAGACC AGGGGTCTTT TACCCAAGTG
                                                                      420
GGGAAGATTG GGAAAGGCCT AGGATCAGAG AGGGAAATGG GTCCCTGGTT GCCCATGGAC
                                                                      480
CTAATGGGGT CTCTCGAG
                                                                      498
```

### (2) INFORMATION FOR SEQ ID NO:1422:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

GAATTCGCGG	CCGCGTCGAC	GAGGAAACCA	GCCAAGGACT	AACTACCACC	ATGAGATTCG	60
		TTTGGCATTG				120
CTGGCAGCTC	AGAGGAGAAG	CTTTACAGCC	TGCACCCAGA	TCCTATAGCC	ACATGGCTGG	180
TGCCTGACCC	ATCTCAGAAG	CAGAATCTCC	TTGCGCCACA	GAATGCTGTG	TCCTCTGAAG	240
AAAAGGATGA	CTTTAAGCAA	GAAACTCTTC	CAAGCAATTC	CAATGAAAGC	CATGACCACA	. 300
TGGACGACGA	TGATGACGAT	GATGATGACG	ATGGAGACCA	TGCAGAGAGC	GAGGATTCTG	360
TGGACTCGGA	TGAATCTGAC	GAATCTCACC	ATTCGGATGA	GTCTGATGAG	ACCGTCACTG	420
CTAGTACACA	AGCAGACACT	TTCACTCCAA	TCGTCCCTAC	AGTCGATGTC	CCCAACGGCC	480
GAGGTGATAG	CTTGGCTTAT	GGACTGAGGT	CAAAGTCTAG	GAGTTTCCAG	GTTTCTGATG	540
AACAGTATCC	TGATGCCACA	GATGAGGACC	TCACCTCTCA	CATGAAGAGC	GGTGAGTCTA	600
AGGAGTCCCT	CGATGTCATC	CCTGTTGCCC	AGCTTCTGAG	CATGCCCTCT	GATCAGGACA	660
ACAACGGAAA	GGGCAGCCAT	GAGTCAAGTC	AGCTGGATGA	ACCAAGTCTG	GAAACACACA	720
GACTTGAGCA	TTCCAAAGAG	AGCCAGGAGA	GTGCCGATCA	GTCGGATGTG	ATCGATAGTC	780
AAGCAAGTTC	CAAAGCCAGC	CTGGAACATC	AGAGCCACGG	CCTCGAG		827

- (2) INFORMATION FOR SEQ ID NO:1423:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 348 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (C) STRANDEDNESS: doubl
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

GAATTCGCGG	CCGCGTCGAC	GGGAGAGGAA	GGGTTGGGCA	GGATGGAATA	TTAAATTGTA	60
ACATGATAAA	CATGCAAGAC	TGTTATCCAA	TCTAGATAAT	TTATATACAT	TTTGATGACT	120
TAGGAAAACA	AAGCAATCAT	TTGTGACAAG	CCTAAAAAGC	TTGACATATT	TAACATACTT	180
AGGAACTTTT	TTTGTGCGGT	GGGAATTCTC	TAATTGTATC	ATGTGGGCCT	TTTGAAAGTA	240
ACAAACAGAA	${\tt GGCCAGTCTG}$	TTGCAAGTTT	GCTGCTGAAC	ATCACATTCC	ACCCTAAGAA	300
AACACAAGGT	GGATTGCATC	GAGGGTGGAT	ACCTTACCTT	AGCACAGA		348

(2) INFORMATION FOR SEQ ID NO:1424:

(A) LENGTH: 152 base pairs

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:	
GAATTCGCGG CCGCGTCGAC TTGGAGAATG TGGCCTCTGA TCACTAACCA GGGTTTTCTC	60
TTTACACTGG CTTGTTTACT TATTTCTTCA CCAAAGCCAG GGAACGTCCC TTTAGCTACT GCAGCATTTC TAACAGATGC GACAAATCAC AG	120 152
GLAGUATTIC TAACAGATGC GACAAATCAC AG	152
(2) INFORMATION FOR SEQ ID NO:1425:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 206 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:	
GAATTCGCGG CCGCGTCGAC CTAAACCGTC GATTGAATTA GACCTGCCTC GAGATGCGCC ACTTTCTGCT CACCCACCTT AGAGCCTTTG CATATGCAGT TGCTTCCTCA GAGTATTGCC	60 120
ATCCCCAGCA CGACCCCCAG CTCATTCTTC AGGCCACTAA CGTAAATGTT ACTTTCTCAA	180
AAACACCCTC TCCATCCCGG CACCCA	206
(2) INFORMATION FOR SEQ ID NO:1426:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 353 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:	
GAATTCGCGG CCGCGTCGAC GTGGGTACTT CATCCTCCTC ATCACTGGTT GGCACTGAGA	60
GCTTCTTAAG ACGCTCCATG AGCTCTTTCT CTTCTCCATC ATCATCCACA TCCTTCTTCC	120
GCCTGCCTTT TCGGGTATCT CGCTTTTTTT TTTGCTGCTG TTGCTGTTGC TGCTGCTGCT GCTCCTTCTC CTTGAGCACT TTCTCTTCTT CCCCAGCCTG TTTATCTTCT ACTGCCAGCT	180 240
CTTCAAAGAA CGTTTTTTTG ATCTTCTNGT CCTTCTTCCC TTTCTTCACC ACTTTGTCTG	300
ATGGGCTCGT GCTCTCTCCG TCCCCGATCC ACTCGGGCTC CGGCGGACTC GAG	35
(2) INFORMATION FOR SEQ ID NO:1427:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 343 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(C) STRANDEDNESS: GOUDIE (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

GAATTCGCGG	CCGCGTCGAC	AGATATTTGG	TTATCTTGAC	TTTTTAAAAT	AACATATTTC	60
TACAGGATTT	TGAGTCTGAG	AAGAGAAAGG	TAATATGCAA	GACACTTCGA	TTTGTTGCAC	120
ATTATTATGG	AGCATCATTA	ATGGTTTGTA	CATTTCTTGT	CCTTTGGGCT	TGAATGGACA	180
GTACCAAATT	TGGGGAAATC	AGCAACTTGA	TGCACAGCTA	CGAGGAATAA	ATGCTTTTGC	240
TAATGCACAT	GGTCCCGTTG	CTTTCCCACT	GCTGAAGACC	TCTCCTTACA	GAGTGTTTGA	300
TAATGCATCT	GTTGAACATG	CACTGCTAGA	TGGTCCTCTC	GAG		343

- (2) INFORMATION FOR SEQ ID NO:1428:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 542 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

GAATTCGCGG	CCGCGTCGAC	GAGGGGAAGA	TGTCACGCAA	GATAGAAGGC	TTTTTGTTAT	60
TACTTCTCTT	TGGCTATGAA	GCCACATTGG	GATTATCGTC	TACCGAGGAT	GAAGGCGAGG	120
ACCCCTGGTA	CCAAAAAGCA	TGCAAGTGCG	ATTGCCAAGG	AGGACCCAAT	GCTCTGTGGT	180
CTGCAGGTGC	CACCTCCTTG	GACTGTATAC	CAGAATGCCC	ATATCACAAG	CCTCTGGGTT ·	240
TCGAGTCAGG	GGAGGTCACA	CCGGACCAGA	TCACCTGCTC	TAACCCGGAG	CAGTATGTGG	300
GCTGGTATTC	TTCGTGGACT	GCAAACAAGG	CCCGGCTCAA	CAGTCAAGGC	TTTGGGTGTG	360
CCTGGCTCTC	CAAGTTCCAG	GACAGTAGCC	AGTGGTTACA	GATAGATCTG	AAGGAGATCA	420
AAGTGATTTC	AGGGATCCTC	ACCCAGGGGC	GCTGTGACAT	CGATGAGTGG	ATGACCAAGT	480
ACAGCGTGCA	GTACAGGACC	GATGAGCGCC	TGAACTGGAT	TTACTACAAG	GACACTCTCG	540
AG						542

- (2) INFORMATION FOR SEQ ID NO:1429:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 465 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

GAATTCGCGG	CCGCGTCGAC	TTAAGAGTCT	GCTTCGGAGA	CCGTAAGGAT	ATTGATGACC	60
ATGAGATCCC	TGCTCAGAAC	CCCCTTCCTG	TGTGGCCTGC	TCTGGGCCTT	TTGTGCCCCA	120
GGCGCCAGGG	CTGAGGAGCC	TGCAGCCAGC	TTCTCCCAAC	CCGGCAGCAT	GGGCCTGGAT	180
AAGAACACAG	TGCACGACCA	AGAGCATATC	ATGGAGCATC	TAGAAGGTGT	CATCAACAAA	240
CCAGAGGCGG	AGATGTCGCC	ACAAGAATTG	CAGCTCCATT	ACTTCAAAAT	GCATGATTAT	300
GATGGCAATA	ATTTGCTTGA	TGGCTTAGAA	CTCTCCACAG	CCATCACTCA	TGTCCATAAG	360
GAGGAAGGGA	GTGAACAGGC	ACCACTAATG	AGTGAAGATG	AACTGATTAA	CATAATAGAT	420
GGTGTTTTGA	GAGATGATGA	CAAGAACAAT	GATGGCATAC	TCGAG		465

- (2) INFORMATION FOR SEQ ID NO:1430:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 373 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

GAATTCGCGG	CCGCGTCGAC	GCTGTTCATG	AGGAGACTTA	ACCACAATTC	AAAGTGTAGC	60
AGTTGTGTAT	TTTAGCATTA	TAATATTTGA	TTGAGGCCCT	GAGGTGTTAA	TATCTCAATC	120
TCAGAGTTAG	ATGTTCATGT	CCTTTTTGAA	TTTTTTAAAC	ATTTTTCATA	ATTTTTTTT	180
TAAGTTAGGG	AGCACATTGA	GTGAAGTTCT	CTGTGTAGAA	CAATACCTTC	TGCTCTGCTT	240
CTCCCAGCTT	TCACTGAGGG	CTGGAAAAGG	ACAGGCCTGT	CCAGCTGTAC	TGTCCCACTG	300
TGTATGGGGA	AGCTCAGGCT	CTGGTGGAAG	CAGGGGGCAT	GGATGTCAAA	CAACTGATGT	360
GCAAACACTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:1431:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 632 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

GAATTCGGCC TT	CATGGCCT ACTACT	GATG AGAACATTA	T CTGCATATGC	CAAAAAATTT	60
TAAGCAAATG AA	AGCTACCA ATTTA	AGTT ACGGAATCT	A CCATTTTAAA	GTTAATTGCT	120
TGTCAAGCTA TA	ACCACAAA AATAAT	GAAT TGATGAGAA	A TACAATGAAG	AGGCAATGTC	180
CATCTCAAAA TA	CTGCTTTT ACAAA	GCAG AATAAAAGC	G AAAAGAAATG	AAAATGTTAC	240
ACTACATTAA TO	CTGGAATA AAAGAA	GCCG AAATAAATG	A GAGATGAGTT	GGGATCAAGT	300
GGATTGAGGA GG	CTGTGCTG TGTGC	CAATG TTTCGTTTG	C CTCAGACAGG	TATCTCTTCG	360
TTATCAGAAG AG	TTGCTTCA TTTCAT	CTGG GAGCAGAAA	A CAGCAGGCAG	CTGTTAACAG	420
ATAAGTTTAA CT	TGCATCTG CAGTAT	TTGCA TGTTAGGGA	T AAGTGCTTAT	TTTTAAGAGC	480
TGTGGAGTTC TT	AAATATCA ACCATO	GCAC TTTCTCCTG	A CCCCTTCCCT	AGGGGATTTC	540
AGGATTGAGA AA	TTTTTCCA TCGAGO	CTTT TTAAAATTG	T AGGACTTGTT	CCTGTGGGCT	600
TCAGTGATGG GA	TAGTACAC TTTTC	ACTCG AG			632

- (2) INFORMATION FOR SEQ ID NO:1432:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 298 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

GAATTCGGCC	TTCATGGCCT	ACTAATTTCC	AAGAGCTAAA	CTTTATACCG	CCTGCAATAT	60
TTCCATTTAC	TACCAGTTTT	TTTCTGACCT	AGTCAGATAT	AAGAAGCCCC	CTTACTGGAT	120
ACAAGACAGT	TAATTATCAG	ATCCAGTCTG	ATCCTAGATC	CAGTCTGATC	CTAGACCCAG	180
TCCAGTTTCT	GTTGTGACTT	CCAAACCCAG	TTTGGATCAG	AAATTTGCTC	AAAGAAACTA	240
GGAGAGCTCA	AAACACAAAT	ATGTGGAGCT	TCTGAATCTG	AGAGAGAACG	AACTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:1433:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433: GCGTGGTTTC ACCTTGTTGG CCAGGCTAGT CTTGAACTCC TGACCTCAGG TGATCCACCC ACCTCGGCCT TCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCATCTG ACTGGTGCAC 120 TTTACTTGA CCTGTCATAA ATCCCTTGGT TTGTTATTAC TAGTTTTTAC TTTAGACAGC 180 AATTATCTTT CAAGGAAAAA TTTAAAAGGA AAAAATGTCT TATATTTACC CTCATGTTTA 240 CCATTCCCAG TGCTCTTTAT TTCTTTATGT CAATCCGGAT TTCAATTTGT TATCATACTG 300 TTTCTGCCTG AATAACAGTT TAACAGCAAC TCGAG (2) INFORMATION FOR CEQ ID NO:1434: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 316 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434: GAATTCGGCC TTCATGGCCT AATGCTCTGT GTCACTGTCT CCCGGTGCTC AGCACAGACA 60 AGTTCAAGAC AGATTTTTAT GATCAATGCA ACGACGTGGG GCTCATGGCC TACCTCGGCA 120 CCATCACCAA AACGTGCAAC ACCATGAACC AGTTTGTGAA CAAGTTCAAT GTCCTCTACG ACCGACAAGG CATCGGCAGG AGAATGCGCG GGCTCTTTTT CTGATGAGGG TACTTGAAGG 240 GCTGATGGAC AGGGGTCAGG CAACTATCCC AAAGGGGAGG GCACTACACT TCCTTGAGAG 300 AAACCACTGT CTCGAG 316 (2) INFORMATION FOR SEQ ID NO:1435: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 383 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435: GAATTCTAGA CCTCCCACCC TGTAGAACAT TCTCCTCACT TAGGAGATAG TCATATTTTC AGGCTGCCTT TGAAACTGTG GGTACACAAA CAGCAGAGCG ATCTATTTCA GCAGTTGAAG 120 TTGTATTTGA GCCATTATTT CTTCCACTCT CTTTTTGGTT GAGTTTCTAG GAAGGAAAGG 180 GCTGAACTCC ATGACTGCTC ATATTACAGT GCTAAGTCCT CACAGCCATC CACTGTTTAT 240 ACACAAGAAG AAACTAGGCC CACCAAGAGT AAGCGCCTGC CTGAGGTCCG TGAGTGAGTA 300 AGGGCCAAAG GTGAGGTTGG GATCTGGCCC TTTCTCTTTT CTGGCCACCA CAGGGCACTA 360 CCTCCCATAC CCACACACTC GAG (2) INFORMATION FOR SEQ ID NO:1436: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 303 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

GGAGAACTGC	TAAGGTCCAC	AACGTCGACA	ATTGAAAGCT	TTGCTGCACA	AGAAAAACAA	60
ATGGAAGTTT	GTGAAGTATG	TGGAGCCTTT	TTAATAGTAG	GAGATGCCCA	GTCCCGGGTA	120
GATGACCATT	TGATGGGAAA	ACAACACATG	GGCTATGCCA	AAATTAAAGC	TACTGTAGAA	180
GAATTAAAAG	AAAAGTTAAG	GAAAAGAACC	GAAGAACCTG	ATCGTGATGA	GCGTCTAAAA	240
AAGGAGAAGC	AAGAAAGAGA	AGAAAGAGAA	AAAGAACGGG	AGAGAGAAAG	GAAAGAACTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:1437:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 228 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

GAATTCGGCC	TTCATGGCCT	AGACTTTTAC	ACATTTTTAT	TAGCTACCTG	GAATTATTTT	60
TGTAACACGT	TAAGTGTAAA	TAAACAAATA	ATGCTTTGCT	TTTTGTTTTC	TGGAATTATT	120
GTTGTATTTC	TTTGCCAAAT	GCATATATCT	TCAGGTCTTT	TTTTTATAAC	CATATGCATA	180
CCAAGGCACC	ATTCCATTGA	CTTTCCAACT	TCTGTCCCAA	CCCTCGAG		228

- (2) INFORMATION FOR SEQ ID NO:1438:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 498 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

GTGAATTCCA GTCCCCACCC	AGAAACCCGC	AGCATGATTG	TCTGCCTCCT	TTTCATGATG	60
ATTTTATTGG CAAAGGAAGT	TCAACTGGTA	GACCAAACAG	ATTCACCTTT	ACTTAGTCTC	120
CTTGGACAGA CAAGCTCACT	TTCATGGCAT	CTTGTGGATA	TTGTGTCGTA	CCAGAGTGTG	180
CTAAGTTATT TCAGCAGCCA	TTACCCGCCG	TCCATCATCC	TGGCAAAAGA	ATCTTATGCT	240
GAATTAATCA TGAAGCTCCT	AAAAGTGTCT	GCGGGCCTTT	CTATTCCTAC	TGACAGCCAG	300
AAGCATCTTG ATGCAGTTCC	AAAATGCCAA	GCTTTTACTC	ATCAGATGGT	TCAATTCCTC	360
AGCACCCTGG AACAAAATGG	AAAAATCACC	TTAGCAGTCC	TAGAACAGGA	AATGTCTAAG	420
CTCTTAGACG ATATCATTGT	CTTTAACCCG	CCCGACATGG	ACAGCCAGAC	CCGCCACATG	480
GCCCTCAGCG GTCTCGAG					498

- (2) INFORMATION FOR SEQ ID NO:1439:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 314 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

GAATTCGGCC	TTCATGGCCT	AGCAGGGAGA	GGGGTTCTGT	GCTCCTGAGA	TTAGTTCAGA	60
TGGTCTAACC	ATTGTTCTAT	ATGTGCATTT	TAGTTAATAT	TGTGTATTAA	AGGATAAGTC	120
TTAATGCTCA	AAGTATGTTA	AAAATAGATG	TAGTAAATCA	GTCCCTTTGT	GAATGTCCTT	180
TTGTTAGTTT	TTAGGAAGGC	CTGTCCTCTG	GGAGTGACCT	TTATTAGTCC	ACCCCTTGGA	240
GCTAGACATC	CTGTACTTAG	TCACGGGGAT	GGTGGAAGAG	GGAGAAGAGG	AAGGGTGAAG	300
GGAAGTGGCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:1440:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 424 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

CCAGCCGTCT GCAGCTCCGG	CCGCCACTTG	CGCCTCTCCA	GCCTCCGCAG	GCCCAACCGC	60
CGCCAGCACC ATGGCCAGCA	CCATTTCCGC	CTACAAGGAG	AAGATGAAGG	AGCTGTCGGT	120
GCTGTCGCTC ATCTGCTCCT	GCTTCTACAC	ACAGCCGCAC	CCCAATACCG	TCTACCAGTA	180
CGGGGACATG GAGGTGAAGC	AGCTGGACAA	GCGGGCCTCA	GGCCAGAGCT	TCGAGGTCAT	240
CCTCAAGTCC CCTTCTGACC	TGTCCCCAGA	GAGCCCTATG	CTCTCCTCCC	CACCCAAGAA	300
GAAGGACACC TCCCTGGAGG	AGCTGCAAAA	GCGGCTGGAG	GCAGCCGAGG	AGCGGAGGAA	360
GACGCAGGAG GCGCAGGTGC	TGAAGCAGCT	GGCGGAGCGG	CGCGAGCACG	AGCGCGGGCT	420
CGAG					424

- (2) INFORMATION FOR SEQ ID NO:1441:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 346 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

GAATTCGGCC	TTCATGGCCT	ATAGGCCATG	AAGGCCGGCC	TTCATGGCCT	AGTCAGGCTT	60
AAGTTTAATA	AATAGCAAAT	TGCATACAGA	TATTTACAAT	GATCGAAAGA	CAAACAGAGG	120
TCCTATCCGT	GCAGTCCCAA	CAATAAAGAC	AGGCATTGGC	ATAAAGTJTT	TATAAATTCT	180
TGGGTACAGC	TGTTCTGAAA	GTAAAGTTCA	CTTTCAATCC	TAAAAAAAGT	CCGCTATTCC	240
TCCCTGGCTG	CTCTGGACTG	TCCTCATCCT	CTTTAGCTGC	TGTTGCGCCT	TCCGCCACCG	300
ACGAGCTAAA	CTCAGGCTGC	AACAACAGCA	GCGGCAGCAT	CTCGAG		346

- (2) INFORMATION FOR SEQ ID NO:1442:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 591 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

GAATTCGGCC	TTCATGGCCT	AGGCTTCCCT	GTTCCCTCAG	CCCCAGTCGA	GAGGAAAGAG	60
AATCGGGCCA	CTGCCAGAAA	GAGAGTCAAG	CAAACCTGGA	AGGGCAAATC	TGAGAGTGGG	120
AAGGCCAAAG	GCCGAGGCCC	AGATTTAGTA	TTCACTAGCA	GCGCCTTCGG	GTAGCAGGAT	180
GATTCCTTTT	CCTGCCTGTC	TGCTGCTGGC	TCTCTTCCCT	AAGGTACAGG	TTGGCAGGAC	240
CACCTCCGCC	TACTTCTCCA	CCATCCCTAG	CATGCCAGCC	CGTTCCCAGA	TCAACCTGCC	300
AGTGGAGTCA	GGCAGTGCAC	TCCTGGAGCC	AAGAGGGAAG	GGCAGGGTAG	AGAGGGTATG	360
TCCAGTAGCC	TGGAGCTCCA	TGGTGGCTTC	ATGCCTCCCT	TCTCCCAGCT	CAGGTGGCCC	420
TGAGGGCTCC	CTCGGAACAG	TGCCTCAAAT	CCTGACCCAA	GGGCCAGCAT	GGGGAAGAGA	480
TGGTTGCAGG	CAAAATGCAC	TTTATAGAGA	TTTTCTATTG	CTGGGAAGGT	GTGTTTCTCC	540
CACAATTTGT	TTGTGAATAT	TCACTTGTTT	TATAAATGTC	TGACCTGTCC	G	591

- (2) INFORMATION FOR SEQ ID NO:1443:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 526 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

GAATTCGGCC	TTCATGGCCT	AGATTGAATT	ACCTGCCTCG	AGCTCCTGTC	CTTAGGTGAT	60
				TGAGCCACCT		120
GCTTTTAAAG	TTCTGCCAGC	ATAGCCCCGG	GATGGGGTGG	GGGTAGACAG	GGCCTTAGGA	180
CTTTCATTTT	TAAAATGCTC	ACTCCACAGT	GAAGAAACAG	GTGATGACTA	TCCTGAATAT	240
TTGGGAAGCT	GTGTCCTAGA	ATTTTTGGCC	TCAGTTCCAG	AACCCACAGC	TTCTTTACAA	300
CATGCTTCAA	GCCTGGGACT	GAGCTGCCAG	TAAATAAACC	CCTAGTAACC	TTAATATGGG	360
TTAATAAGAT	TAGGTGCCCG	CTCTGCACGC	TCCCCTGCCC	CTCCTCGTCC	GGGCACCTGT	420
TATGCTAGGC	CAGCATGTTT	GCAGCTTAGC	CAGGGAAAAT	CGTGGACCAA	GACAGGGCTT	480
TTCATCCACG	ACTGGCTAAA	AAGATGGCTC	TCAATAATAT	CTCGAG		526

- (2) INFORMATION FOR SEQ ID NO:1444:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 279 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

GATTGAATTC	TAGACCTACC	TCTCTTTTTT	TGTGGTCTCT	CCTTCATTCT	CTGTTCATTT	60
CTCCGTGAGA	TTTTCTGATT	AGTAGTTACC	TTCAGCATGC	CAGTTGACTT	GCAAACCTAC	120
AATCCAACCT	TTCTTCTACT	TTGTCATCTG	ACAACAGCCT	GGTTTGTAGC	TGATTCCAGG	180
ACTTCTTCAC	TTGGGTGGCC	ACTCTCATTA	CCACAGAGTT	CACTAGTCAT	GGTGAACACA	240
CCAGTCTTTT	ACACCTCCCT	CACTCCCAAA	CCACTCGAG			279

(2) INFORMATION FOR SEQ ID NO:1445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 644 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

GAATTCGGTC	TTCATGGCCT	AGGGGAAGAA	AGGCACCTTT	CTCACAGGGT	GGTGAGAGAG	60
AGGAAGGGGG	ACGGGGAAAG	CCCTTTATAA	AAGCATCAGA	TCGGCTGGGC	ACAGTGGCTC	120
ACGCGTGTAA	TCCCAGCACT	TTGGGAGGCC	GAGGCGGGTG	GATCGCGGGG	TCGGGGGTTT	180
GAGGCCGGCC	TGGCCAATAT	GGTGAGACCC	CGTCTCTGCT	GAAGATACAA	AAATTGGCTG	240
GGCATGGTGG	CGGGCACCTG	TGGTCCCGGC	TGCTTGGGAG	GCTGAGGCGG	GAGAATCGCT	300
TGAGCCCGGG	AGGCAGAGGT	TGCAGTGAGC	TGAGATCGCG	CTACTGCACT	CCAGCCTGGG	360
CAACAGAGCG	AGACTCCATC	TCAAAAATAA	AAGAAAGGCA	TAAATATTAC	ATTACCCTCT	420
GAATACTGTG	GTTGTATACT	TGAGTTTTTA	TGTGTGTATA	TATATGTGTA	TAGGAGAGTA	480
TAAAATAAAAT	GAAATTAGGA	TTTTGCAAGT	TATAATCATA	TAAAATTGAT	TACCCTAAAT	540
ATATCATTAG	GATATTATGT	TATTTACATC	TCTTATGCTA	ATTCTAATTT	TCTTTTATTG	600
TAGTATAGTA	GAATTGAGAT	TTGNNAATGG	AATTGGTCCT	CGAG		644

- (2) INFORMATION FOR SEQ ID NO:1446:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 756 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

GAATTCGGCC '	TTCATGGCCT	ACCTCACCCG	GCCCGGACAC	GGACAGGATT	GACAGATTGA	60
TAGCTCTTTC '	TCGATTCCGT	GGGTGGTGGT	GCATGGCCGT	TCTTAGTTGG	TGGAGCGATT	120
TGTCTGGTTA	ATTCCGATAA	CGAACGAGAC	TCTGGCATGC	TAACTAGTTA	CGCGACCCCC	180
GAGCGGTCGG	CGTCCCCAA	CTTCTTAGAG	GGACAAGTGG	CGTTCAGCCA	CCCGAGATTG	240
AGCAATAACA	GGTCTGTGAT	GCCCTTAGAT	GTCCGGGGCT	GCACGCGCGC	TACACTGACT	300
GGCTCAGCGT	GTGCCTACCC	TACGCCGGCA	GGCGCGGGTA	ACCCGTTGAA	CCCCATTCGT	360
GATGGGGATC	GGGGACTGCA	ATTATTCCCC	ATGAACGAGG	AATTCCCAGT	AAGTGCGGGT	420
CATAAGCTTG	CGTTGATTAA	GTCCCTGCCC	TTTGTACACA	CCAACCCGTC	ACTGACTTTT	480
ACCGCAGCTG	GAACTGTGCT	CCAGGGCCTT	TCCATCTTTT	CCCCCACACT	CCCTTTGACC	540
CTGTGTTGCC	CTCAGAGGCC	AAATTCTTGG	GCTCAGGGAC	TGGCTTTCGG	CCTATTGGTG	600
GTGGAGCTGG	GGTTCTGGCA	AGGAATTTCA	GGCAGCGCTT	GGAGGCAATG	TTCCCCGAGA	660
GCAGTTCACG	GTGGTGATGT	TGACTTATGA	GCGGGAGGAA	GTGCTTATGA	ACTCTTTAGA	720
GAGGCTGAAT	GGCCTCCCTT	ACCTGGAACT	CTCGAG			756

- (2) INFORMATION FOR SEQ ID NO:1447:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 359 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

ACAGGCTACT TGTACAGAGA AAAAATTAAT ACTCAAAGGA AATCTTCATT TTTTAGATACTTTTGGAA TTTGAATTTT CATCAGTGCA AATATAAATT TCTCATCCT GCTCTGAC TAATTGGTAC CATATTTTCC CTTTGTGTCT TGTGACTCTG CCACATCCCA TCTCATCC GCCTCTGAGT CAAGAACCCA GTGAACTGAC TTTCTAGTTC TAGAAAGTTC GCTGCAACCCAGGAAAGCT TGAGAAAGGT ATTGTGGAAG AAGCAAAGGT AGACCCCCAT TCACTCGA	TTG 120 GGC 180 TTG 240 GGC 300
(2) INFORMATION FOR SEQ ID NO:1448:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 146 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:	
GAATTCGGCC TTCATGGCCT AGGGAAAATA AGTTAATTCT AAATCAAATC	
(2) INFORMATION FOR SEQ ID NO:1449:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 308 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:	
GAATTCGGCC TTCATGGCCT ACTTTCAAA AGCAGCTTTG CTCTACTGAT TTGGGTAA GCTTAGTTGC AGTTGGNTTG GGAGGAAAATG GGAGCAGAAA ATTTGAGAGA GTGAGTGT ACAACTCTTT CAAGGAATTT CGCTATAAAT GGGAGTAGAG ATCTGAAGAC TGAATAAT GCAAACTCAA AAGTGGGAAG ACGTAATTCT CTTATTATTT CATTTTTCTT AGTGAAAA GAGGTGAAGT TCTCTGAGTA ATAGGAGGGT CAAACAGGNG TTAGAAGTTC ACAAAGAA GTCTCCGAG	TAG 120 TTA 180 TAA 240
(2) INFORMATION FOR SEQ ID NO:1450:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 545 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:	
GAATTCGGCC AAAGAGGCCT AGCATGTTGT GGCTGTTCCA ATCGCTCCTG TTTGTCT GCTTTGGCCC AGGGAATGTA GTTTCACAAA GCAGCTTAAC CCCATTGATG GTGAACG TTCTGGGGGA GTCAGTAACT CTTCCCCTGG AGTTTCCTGC AGGAGAGAAG GTCAACT TCACTTGGCT TTTCAATGAA ACATCTCTTG CCTTCATAGT ACCCATGAA ACCAAAAC CAGAAATCCA CGTGACTAAT CCGAAACAGG GAAGGGACT GAACTTCACC CAGTCCT	GGA 120 TCA 180 GTC 240
COURTELLES COLOROLANT COURTAINES UMMICUMEL UMMELLICALE CAULEEL	

CCCTGCAACT CAGCAACCTG AAGATGGAAG ACACAGGCTC TTACAGAGCC CAGATATCCA CAAAGACCTC TGCAAAGCTG TCCAGTTACA CTCTGAGGAT ATTAAGACAA CTGAGGAACA TACAAGTTAC CAATCACAGT CAGCTATTTC AGAATATGAC CTGTGAGCTC CATCTGACTT GCTCTGTGGA GGATGCAGAT GACAATGTCT CATTCAGATG GGAGGCCTTG GGAAACACAC TCGAG	360 420 480 540 545
(2) INFORMATION FOR SEQ ID NO:1451:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 331 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:	
GAATTCGGCC AAAGAGGCCT ACAGTAAGCA GATGAACTTG CTTGCTGTTC TCGAAGTGAG GACTGAAGGG AACGAAAACT GGGGTGGGTT TTTGCGCTTC AAAAAGGGGA AGCGATGTAG CCTCGTTTTT GGACTGATAA TAATGACCTT GGTAATGGCT TCTTACATCC TTTCTGGGGC CCACCAAGAG CTTCTGATCT CATCACCTTT CCATTACGGA GGCTTCCCCA GCAACCCCAG CTTGATGGAC AGCGAAAACC CAAGTGACAC AAAGGAGCAT CACCACCAAT CCTCTGTAAA TAATATTTCA TACATGAAGG GAACCCTCGA G	60 120 180 240 300 331
(2) INFORMATION FOR SEQ ID NO:1452:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 263 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:	
GAATTCGGCC AAAGAGGGAA GGGAAAATTT CAAGTCAGAT AGAATTCTAT ATATACCATT TCTTTGGAAC CTTCAGCCCT CAAGATTCCA ACATCATGAC CTCAGTTTCA ACACAGTTGT CCTTAGTCCT CATGTCACTG CTTTTGGTGC TGCCTGTTGT GGAAGCAGTA GAAGCGTATA TGCACGAAAA AGAAATGGAC AGATGTGACT TTGAAAGGCC TACTGAGTCA AACCTCACCC TGAAAACCTT TGCAGCACTC GAG	60 120 180 240 263
(2) INFORMATION FOR SEQ ID NO:1453:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 558 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	*
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:	
GAATTCGGCC AAAGAGGCCT AATTTTAAAG CCCTGCTAAC TTCAATGTCT AGGTCACCCA TTTGTTTATT TTTATGGTCT TTTTTCATCC TGATTTTTGG TCATTTGGTC CCGTCTTATG GCATACCTGG TAATATTTTA TTGAATCCTT AGTACTGTAC ATGAAAAATT GTAGAGGCCC CAGTAGTTTT CTTTCTCTGA AGAGGAGTCA CCCTTTCCTT CACTAGACAG TTATGTTGGG	60 120 180 240

GGTTATATAC	CTTACTCCAA	TCAAAGATTG	AGCTGAGTCA	GAACTCTAAG	GGAGTTAAGT	300
TTTTGTGTCC	TCTGGGGACC	AGGGGTTCCA	ACTAAGACTG	TGATATTCAC	CAGGATCCAA	360
TTTCCCGATG	CCTCTTGAAC	TCTTATTCTT	ATCTTTTTAA	CACATCAAGG	CAGCTGGTTT	420
GCATTTTTCT	TTCTGTTCAG	CTTTTTAGCT	TCATCCTTTG	CAGCTTTAGA	AATTGACAGT	480
TGTCTTACAG	GGAAAAGTAG	CTGTGTAACA	AGCTCATGTC	TCTGCCTCTC	TTCCACTGAT	540
ATCTTAGCCC	CGCAGGAG					558

- (2) INFORMATION FOR SEQ ID NO:1454:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

GAATTCGGCC	AAAGAGGCCT	ACCTAAACCG	TCGATTGAAT	TCTAGAAATA	CAATGATTTT	60
AAAAAAGATT	TCCAAAGGCT	TTTTCTTTTT	TTCTTTTTTC	TNGAGACAGG	GTCTCACTCT	120
GTCGCCCAGG	CTGGAGTGCA	GTGACACAAT	CTCGGCTCAC	GGCAAGCTCC	GCACTGCCCC	180
CTCAGGTTCA	CGCCATTCCT	CCGCCTCAGC	CTCCCGAGCA	GCCGGGACCA	CAGGCACGCG	240
CCACCACGCC	CAGCCAACTT	TTACATTTTT	AGTAGAGACG	GGGCTTCACC	ATGTTGGCCA	300
GGATGGTCTC	GGTCTCTTCT	GCCTCGAG				328

- (2) INFORMATION FOR SEQ ID NO:1455:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

GAATTCGGCC	AAAGAGGCCT	ACTTGATGTC	TGTGACCCAC	ACNTATTCGC	ACACTCCCTC	60
CCCTTTTGAA	AATCCCTAAT	AAAAACTTGC	TGGTTTTTGC	GGCTAGTGGG	GCATCATGGA	120
ACCTACTGAC	ATGTGATGTC	TCCCCCGGAT	GCCCGGCTTT	AAAATTTCTC	TCTTTTGTAC	180
TCTGTCCCTT	AATTTCTCAA	GCTGGCCGAT	GCTTAGGGAA	AATAGAAAAG	AACCTAGGTG	240
AATATTGGGG	CAGGCTCCCT	GATGAAATGA	TATATATTCT	TAAAATAAAC	TTTTCATCTT	300
TGCATATACG	TTTATATGCC	GAGTTTTCTC	CAACCTTGTC	TTACAGCACT	TTGTATACTA	360
CATTCTAGCC	ATACTAAACT	CTTGCAGTTC	CTGAGACATG	TGCTGTATCC	TATTTCTTCT	420
GGTCCTTTTC	TCATTGATTA	ACTACCTGGA	GCATACTTTT	AATTCAGTGT	CAGCGCTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:1456:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

GAATTCGGCC AAAGAGGCCT ACTTCACCTT CAAGTCCCCT TTCTCAAGAA TCCTCTGTTC

TTTGCCCTCT AAAGTCTTGG TACATCTAGG ACCCAGGCAT CTTGCTTTCC AGCCACAAAG

60

120

AGACAGATGA AGATGCAGAA AGGAAATGTT CTCCTTATGT TTGGTCTACT ATTGCATTTA GAAGCTGCAA CAAATTCCAA TGAGACTAGC ACCTCTGCCA ACACTGGATC CAGTGTGATC TCCAGTGGAG CCAGCACAGC CACCAACTCT GGGTCCAGTG TGACCTCCAG TGGGGTCAGC ACAGCCACCA TCTCAGGGTC CAGCGTGACC TCCAATGGGG TCAGCATAGT CACCAACTCT GAGTTCCATA CAACCTCCAG TGGGATCAGC ACG	180 240 300 360 393
(2) INFORMATION FOR SEQ ID NO:1457:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 266 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:	•
GAATTCGGCC AAAGAGGCCT AGTGTGTGT TGTGTGTGT TGTGTGTGT TTATCTCCTT CAACTCTGAC CACCTGGAAG TCAGCCTAAT CTCTGCCCTC GTGTTGATCT TTAATTCAAC ATTTAATTAC CTATCTTGGT ATCCATATGA ATTTGATTGT TTTTTTTGGCT TTTTTTTGAAC TCATAAAAGG TATCCAAGTT CCTGGAGGGC ATAGTGCCCA TCTCCTCCCA TCCACCAGTG GACATTCTTT TCCAAAAGAC ACATGG	60 120 180 240 266
(2) INFORMATION FOR SEQ ID NO:1458:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:	:
GAATTCGGCC AAAGAGGCCT AGGTTGTAGT TACTTTCAGA GTAGATACAG GGTTTTAGAT CATTACAGTT TAAGTTTTCT GACCAATTAA AAAAACATAG AGAACAAAAG CATATTTGAC CAAGCAACAA GCTTATAATT AATTTTTATT AGTTGATTGA TTAATGATGT ATTGCCTTTT GCCCATATAT ACCCTGTGTA TCTATACTTG GAAGTGTTTA AGGTTGCCAT TGGTTGAAAA CATAAGTGTC TCTGGCCATC AAAGTGATCT TGTTTACAGC AGTGCTCTCG AG	60 120 180 240 292
(2) INFORMATION FOR SEQ ID NO:1459:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 289 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:	
GAATTCGGCC AAAGAGGCCT AGTTTTATGA GAGGGTTTCC ATTAAGAAGT TAATTGAAAT TCTTTATTTA TGTAAAATGA AATTTCCAAT TAAATTATTT CACACAGCAT TTTTTCCCCT TAATTTCATT AGTTTTTTA TTTCTTGGCC GACCCAGGCC AGGAGCTTAG GGAAAATGAT	60 120 180
577	

GAGGCCTCTT TTACGCTGTA GTCCTGCAAA TGCTGTGTTT TATTCCCCCT CCCCTGCTCA

GCACTCACCC ACGACTGACA CATGGGGTAC ACACACACA ATACTCGAG	289
(2) INFORMATION FOR SEQ ID NO:1460:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:	
GAATTCGGCC AAAGAGGCCT ACACCTGCGT TGGAACATCT GATCCAGTGA TAGCACGTCA CTAGGTGCCT TAATTAATAA AGCCAAAATA TCTTTCCACT AGCAAACTAA TCGTATTCAC TTTTACTCTC CCATTTTTAA TTAATCTTTC CTATTTCATT TCACCCTCTC ATCTCTTTCC TCTATTGGAT TATCTCAGGT ATCTAATCCA ATTCACTACT GTTTAATGAA TGTAATTGCA ACCAGTCTGC AATTCCTAAG GTTTTGTTTC TTTGCTTTTT TCTTTTGTAG TCCATCTCTT TGCTACACTC AAGCAGGTCT AGAATTCGAG	60 120 180 240 300 330
(2) INFORMATION FOR SEQ ID NO:1461:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 383 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:	
GAATTCGGCC AAAGAGGCCT AGGGACAGTG ATTATAGGAC TCCACACATG CAACTGAATC TAGCATTACT GACTTTAAAT TTTTTGAGCC TATCTAAAGG CCAGATGCTA TCAGCAGCTG AACGGCATCT ACCAAAACCA GCTGCAAAGA TAGAAGCGGA ACAACTGGTT TGGTGGAGAG ATTCGATAAC AACGAGTTGG GAAATAGGTA AAATAATAAC ATGGGGTAGA GGTTATGCTT GTGTTTCTCC AGGCCAAAAC CAGCAGCTGA TTTGGATACC ATCAAGATAC CTGAAAACCT ATCATCAGCC AGATGCCAAG GAAGAGATTT TGGGAGGAAC CCGAGGACCC CATGTTATTA	60 120 180 240 300 360 383
(2) INFORMATION FOR SEQ ID NO:1462:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 375 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:	
GAATTCGGCC AAAGAGGCCT ACGATGACGT CACCGTCACC ACCGGCGTGA AGCGAGACAG TGGTGAGGGC TTCTGGACTG GATGGAGGAC CTGAAGACAT GAGGTGGAGG CACAGGTAGA AGAGAAGATT CTCACCATCG CTGATTCACA CAAAAGCATT TCTCCAAGTG GTTGCAGATG ACATGATTCC CCAAAGTGTT AGAGCTGAAG TGTGTTTCCT TGTGTATATA TACTGTGGTT CCTTTATCCC TTCATCTGTG GATAGACAGG TGCAACCGTG TGGTTCCCCA CGATATGATT	60 120 180 240 300

TCATTGTGGT TTTCTGTCTG AAGAGTATCC CAGTATGTAC CTGTGGAGCA GCTTCTTAT CCCTTCTTAC TCGAG	360 375
(2) INFORMATION FOR SEQ ID NO:1463:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 174 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:	
GAATTTGGGC GGAGACACAA ATTCAAATCA TATCAACCTG GTAAAGAATT TGGATTTTAT TTTGAGTGTG TTAGTGAGTA TTGCATGGCT TTGAGCAGAG AAAGGATGAT TTATATGTTT AAAAGAGTGC TTTGCCTCTT ATATGTGGAA GAGATGTAG GAGGAGGACT CGAG	60 120 174
(2) INFORMATION FOR SEQ ID NO:1464:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 122 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:	
GAATTCGGCC AAAGAGGCCT AGTTGCGGTT TAAATTTCCA AATGTATGGC ATTTGCTTGT TTTTTAAGTT GATTTCTAGT TTTATCACAT TGTGGTCAGA GAATGCTGAG AAAGAGCTCG AG	60 120 122
(2) INFORMATION FOR SEQ ID NO:1465:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 315 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:	
GAATTCGGCC AAAGAGGCCT ACTTGAGCTT TTTTCATGTG TATATATTTA TGCTTCTTTT CTAAAAAAAA TTGAGATGGA AATTCACATA ACAGAATTAA CTAAAGCATA CATTTCATTG GTATTTACTA CATTCACAAT GTTGTGCAAT CATTACCTCT CTCCAGITCT AAACATTTCA TCACCCCAAA AGGAACCCCT AAGCGGTCAC TCCCCACTCC ACTGTCTCCC ACAGCCCCTG GCAACCAGCA GTCTGCTTTG TGTCTCAATG GATTTACCTA CTCTTGATAG CTCTACAAAT GGAACAATAC TCGAG	60 120 180 240 300 315
(2) INFORMATION FOR SEQ ID NO:1466:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 175 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	

WO 98/45437 PCT/US98/06<u>9</u>56

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

GAATTCGGCC	AAAGAGGCCT	AGGTAAGAGA	AACGACCAAT	TCTACCAGTT	ATTCTACAAT	60
GTGGGTTTTC	ACTGCTCTGT	TCACATGCCT	TATTCAGACT	TCTTGTGGTG	GTCAATTGCT	120
AGATGGTCTG	TTGGAATTAT	CTGCTGTCAT	ACATCCAAAA	AGGTCTCACA	GAGAG	175

- (2) INFORMATION FOR SEQ ID NO:1467:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

GAATTCGGCC	AAAGAGGCCT	AGAAGGACAC	CTCCATCCAT	TCCACGCAGT	TGCTCAAAGC	60
AGAAATTTTC	AGTGCAAGTC	TTGATGCTGC	GCCGTCCCCC	ACTCCCTACA	TCAGAACGCA	120
TCCCTCATCT	GGACTCCAGC	GGTGGCTTCT	TGATGCTGCG	CGGTCCCCCA	CTCCCTACAT	180
CAGAATGCAT	CCCGCATCCA	GACTCCAGCG	GTGGTGCTCT	ACCTGCACGC	TGTTGCCAAG	240
TCCAAGCTAC	CATACTCCTG	CCTGAGCTAT	GACAACAGCC	TCCTCACTGA	TCTCCCCTTT	300
CTTCCCTTTG	CCTCCTCCAG	CTCATTTTTC	ACAGTGTAGA	ATGACTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:1468:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 419 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

GAATTCGGCC	AAAGAGGCCT	ACTATACTAA	AATTCTGTGC	AAAAAGATGC	TTGAAATTAT	. 60
TGTAGAGACT	GAATCTTTGC	TGCTTGTTAT	AAATATTGCA	GGGCATAAAC	CTTCCATTCA	120
TAGGTTCATC	AGCTTTTATG	ATTGGGAGTG	ACAGGGAGGC	AGCATTGCAG	TCCTTAGTCC	180
TAGGTGTGGT	CTAGAATTTA	CCCTGTATTT	AAGTCACTTT	GGAATAGAAG	TTTTTTTTCT	240
CGGACAGGAT	ACACTATATA	TTTTTAAATC	TCCTCCCATA	GTCGTAGTGC	AGAGATATAA	300
ATAGAAGTAC	AGGTAAGAGA	TGTCTTCTGC	CTTTCAAACC	CTTCCTAAGT	TTGTGTGCTG	360
CTTTAACTTT	ATTCACATAG	AGCAGTCTGT	TTTATTACTC	AGGATATGGG	CCACTCGAG	419

- (2) INFORMATION FOR SEQ ID NO:1469:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 612 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

GAATTCGGCC	AAAGAGCGAT	GGGGACAAAG	GCGCAAGTCG	AGAGGAAACT	GTTGTGCCTC	. 60
TTCATATTGG	CGATCCTGTT	GTGCTCCCTG	GCATTGGGCA	GTGTTACAGT	GCÁCTCTTCT	120
GAACCTGAAG	TCAGAATTCC	TGAGAATAAT	CCTGTGAAGT	TGTCCTGTGC	CTACTCGGGC	180
TTTTCTTCTC	CCCGTGTGGA	GTGGAAGTTT	GACCAAGGAG	ACACCACCAG	ACTCGTTTGC	240
TATAATAACA	AGATCACAGC	TTCCTATGAG	GACCGGGTGA	CCTTCTTGCC	AACTGGTATC	300
ACCTTCAAGT	CCGTGACACG	GGAAGACACT	GGGACATACA	CTTGTATGGT	CTCTGAGGAA	360
GGCGGCAACA	GCTATGGGGA	GGTCAAGGTC	AAGCTCATCG	TGCTTGTGCC	TCCATCCAAG	420
CCTACAGTTA	ACATCCCCTC	CTCTGCCACC	ATTGGGAACC	GGGCAGTGCT	GACATGCTCA	480
GAACAAGATG	GTTCCCCACC	TTCTGAATAC	ACCTGGTTCA	AAGATGGGAT	AGTGATGCCT	540
ACGAATCCCA	AAAGCACCCG	TGCCTTCAGC	AACTCTTCCT	ATGTCCTGAA	TCCCACAACA	600
GGCGCACTCG	AG					612

- (2) INFORMATION FOR SEQ ID NO:1470:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 220 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

GAAAAGCCAA	GACTTTAACT	TTCATTACAT	ATCTAATAGT	TGATATCACC	AGTTACCATT	60
TTGAATTTTG	TATAGTACTA	GGTTAGAACA	TTGCTTAATC	CTTTTAAAAA	AAATGCATTT	120
ACGTAGAACT	CGAGCAGGAT	GTTTGGCCCC	GATGTTTTTT	CTTCATACTC	TTCTGTCGCC	180
TCCTCCCATT	TCTGCACAGT	TCTCACCCAC	TACTCTCGAG			220

- (2) INFORMATION FOR SEQ ID NO:1471:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 349 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

GAATTCGGCC	AAAGAGGCCT	- AGGGCATCAT	GCAGACACAT	CTGTTAAAGC	AGGAAAAAAA	60
AAACCATGTG	GAAGATTAAG	CTAGGCAGAG	TGCCTGAAAA	GCCCTCTGCA	ATAAGTTGAG	120
CTGGAAAAAC	CTCCATATCT	AAAGATGCTT	TAATCATCTC	AAGAACACCA	ACAACATTTT	180
CTATTATAAT	ATAACTATGA	TAGATGTGAA	TCTACCTCTT	GGATTAAGGC	AATAATTTTA	240
TAGCTATCAA	ATTTTCACAG	ACACCATTTT	CACTACTCTG	AGTTGCATCT	CTAACAAGCT	300
TCTTTAGCCT	CTGCCTACAG	ATTTCAGTGA	CAAAGCCATT	CAGCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:1472:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

GAATTCGGCC	AAAGAGGCCT	ACAACAAACC	ATTCTTCAGC	ACCTTTGCAA	AAACATCTAT	60
GTTTGTTTTG	TACCTTTTGG	GCTTTATTAT	TTGGAAGCCA	TGGAGACAAC	AGTGTACAAG	120
AGGACTTCGC	GGAAAGCATG	CTGCTTTTTT	TGCAGATGCT	GAAGGTTACT	TTGCTGCTTG	180
CACAACAGAT	ACAACTATGA	ATAGTTCTTT	GAGTGAACCT	CTGTATGTGC	CTGTGAAATT	240
CCATGATCTT	CCAAGTGAAA	AACCTGAGAG	CACAAACATT	GATACTGAAA	AAACCCCCGC	300
GGTACTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:1473:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 297 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

TCTGGGGCAC AGGAGCTGCC CCTCTTGGTC TGAGATTTGG CCATGGGGTG ATTAGGACAG GTATAGTGGC ACAGAGTGTA AAAACCCCAT AATGGTGTGG ATTCTGGATT GCTTAGTTTG CATTTGACAA GTGCATGCCT GGGAGGAGGA CTCCTCTTAG TAAAGAGGAT GGGAGGCAAG AAGAGAGGCC AGAGGCCAAG ACAAGGTAAC TTAGGCATAG CATCAGGTTG TCTCGAG	GAATTCGGCC	TTCATGGCCT	ACAACTTTAA	GATTAGCTAC	TTTGAATAAT	CTCAGTAGGT	60
CATTTGACAA GTGCATGCCT GGGAGGAGGA CTCCTCTTAG TAAAGAGGAT GGGAGGCAAG	TCTGGGGCAC	AGGAGCTGCC	CCTCTTGGTC	TGAGATTTGG	CCATGGGGTG	ATTAGGACAG	120
	GTATAGTGGC	ACAGAGTGTA	AAAACCCCAT	AATGGTGTGG	ATTCTGGATT	GCTTAGTTTG	180
AAGAGAGGCC AGAGGCCAAG ACAAGGTAAC TTAGGCATAG CATCAGGTTG TCTCGAG	CATTTGACAA	GTGCATGCCT	GGGAGGAGGA	CTCCTCTTAG	TAAAGAGGAT	GGGAGGCAAG	240
	AAGAGAGGCC	AGAGGCCAAG	ACAAGGTAAC	TTAGGCATAG	CATCAGGTTG	TCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:1474:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 510 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

GAATTCGGCC	TTCATGGCCT	AAAAAAGTAT	GCAACACTCA	GTTTATTTAA	TACTTACAAG	60
GGGAAATCAT	TAGAAACACA	GAAAACCACA	GTTGCAGCTC	GACATGGATT	ACAGAGTCTT	120
GGAAAAGTCG	GTATTTCACG	GCGTATGCCT	CCACCTGCTA	ACCTCCCAAG	TCTTAAAGCA	180
GAAAACAAAG	GCAATGATCC	TAATGTAAAC	ATTGTACCTA	AAGATGGCAC	AGGGTGGGCA	240
TCAAAACAAG	AGTAACATGA	AGAAGAAAA	ACACCAGAAG	TGCCACCAGC	ACAGCCAAAA	300
CCTGGGGTTG	CAGCTCCCCC	AGAAGTAGCA	CCTGCTCCCA	AATCATGGGC	CAGTAACAAG	360
CAAGGTGGGC	AAGGAGATGG	AATCCAAGTG	AATAGTCAGT	TTCAGCAAGA	ATTTCCCAGC	420
CTGCAGGCAG	CTGGGGATCA	GGAAAAAAAA	GAAAAGGAAA	CAAATGATGA	CAACTATGGA	480
CCTGGACCCA	GTTTACGTCC	ACCACTCGAG				510

- (2) INFORMATION FOR SEQ ID NO:1475:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 400 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

GAATTCGGCC	TTCATGGCCT	AATCCATTCA	TTTGATGGAC	ATTTTCTAAG	TAÇCTGTGAG	60
CCAGGTGCTG	CCATTTCAAA	GTCTCTTCTT	ACCACGCTCC	TCAGTGGCTA	GACATTTTCA	120
CGTGGCCAGA	AAGTCCCGAC	TCTTGCTGGG	CGTCCCTGGA	CAAGTTGCCT	TCCTCCTCTG	180
AGCTTGGCGC	TCCCCATCTG	TATAGTGGAG	ACCCTTGGCC	CCCCTCTGTA	CGGAAGGGCC	240
GATGCGAAGC	TGCAGTTAAA	AAAGGCTCAC	ATGCTCCTAG	CCTTGTGCAG	TCAGGAGGGG	300
AGACCAGGAC	AGTTGGAAAT	TATGATTGCA	AATGGCTTTG	CATTTTAGAT	CATTCGTGTG	360
TGTGGATCAG	AGAAACGCAC	AAGTTCCCTG	GCATCTCGAG			400

- (2) INFORMATION FOR SEQ ID NO:1476:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 465 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

GAATTCGGCC	TTCATGGCCT	ACCACATTTT	GTCAGCAGAG	AGCCTTTTAA	ACTTGGATTC	60
CAACTTCCTG	TTGTCTAAAC	GGAACCCTCC	GAACGTAGGA	CTTATAGGGG	AAGCTGCTGT	120
GCATGTCAAA	AAAACTACTA	ATCAGAATGA	GCTTTGTCAT	CCAGAGCCAG	AACTGCTGCA	180
GAAATTTTTA	TAATTTTGCA	ACTTCTTTTT	TTACAAGGAA	CTTTTGTGCT	ACTACACATC	240
AGGACTTTTG	AAGCATCCAA	TAAATCCATT	TAATAAGTAT	GAGCATGTGT	CTGAGTGGAC	300
AAGAAAGTGA	AACCATCCAT	GCTACATTGG	ATAATTTTTC	CTCCCCCAGA	CTGGACAGGG	360
AATCTCAGCT	TTCAAAACAG	AGTAACCTGG	CTCCACTTAC	AAAGCTGCAC	AGGCATTAAA	420
GATCGTGCTG	CCTTTGTTAG	GCAGATTTGG	AGGGGAGAGC	TCGAG		465

- (2) INFORMATION FOR SEQ ID NO:1477:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 377 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

GAATTCGGCC	AAAGAGGCCT	ACATGTAGCT	ATCCTAAGAC	GTATTTTATT	TTGAGCCACT	60
TTCTCAGAGG	GAATTGGGTG	GGTGTGGTCG	TAAGAACACC	TAGAAAATAG	GGGTGAAACC	120
TTTATGGGGC	CAGGGGAGCC	ATGGCAGAGG	GTGGAGTGGG	GGATAGAAGC	CTTCAGACTC	180
CTCCGCCCCA	GCCACTCTGC	ACCTGGGGCC	TTTCAGCTGT	TAAAATGAAA	AGCCAATTAT	240
CTTCTGTAAA	TGAGGGAAAA	AAAGAAGGAA	TAAAAGTGTC	TATTATGTAT	GCTGATATGC	300
ATAACACTTC	AAATAAAAGG	ATATATAAGC	ACTTGACAAA	TTGAGGGAGA	AGGAGGGGAG	360
AGTGCTGGGC	GCTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:1478:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

GAATTCGGCC AAAGAGGCCT	AGAGATTCAG	TTTATTCTAT	ACTCAGACTT	TGGTATCCCC	60
TTAGATGCCC ATGTCAAAAA	TGAGAAAGTT	GGTGACATGG	TATGGCATTT	TATTGCTTTT	120
TGTTTGTTTT CCATTGCTAC	TTTCACTCAA	ATTCCAAGGA	AATCACAGAA	GAAGGGCTTT	180
TGGTGACCTA AAAGTAGAAA	TGAAAGCAAC	AAAATGCATT	CTGTCCAGCA	GTACACTGAA	240
GACAAAAAT GTAGTTGAAA	AGTCTCAGGG	AGCGCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:1479:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 491 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

GAATTCGGCC AA	AGAGGCCT A	ATTTGCTTT	GCCCAGTAGT	TGGAAAGTGA	ACTCGACTCG	60
TGATGGTTCT CC	TGTCACTT T	GGTTGATAG	CAGCCGCTCT	GGTAGAGGTT	AGGACTTCAG	120
CTGATGGACA AG	CTGGTAAT G	AAGAAATGG	TGCAAATAGA	TTTACCAATA	AAGAGATATA	180
GAGAGTATGA GC	TGGTGACT C	CAGTCAGCA	CAAATCTAGA	AGGACGCTAT	CTCTCCCATA	240
CTCTTTCTGC GA	GTCACAAA A	AGAGGTCAG	CGAGGGACGT	GTCTTCCAAC	CCTGAGCAGT	300
TGTTCTTTAA CA	TCACGGCA T	TTGGAAAAG	ATTTTCATCT	GCGACTAAAG	CCCAACACTC	360
AACTAGTAGC TC	CTGGGGCT G	TTGTGGAGT	GGCATGAGAC	ATCTCTGGTG	CCTGGGAATA	420
TAACCGATCC CA	TTAACAAC C	ATCAACCAG	GAAGTGCTAC	GTATAGAATC	CGGAAAACAG	480
AGCCACTCGA G						491

- (2) INFORMATION FOR SEQ ID NO:1480:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 523 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

GAATTCGGCC AAAG	SAGGCCT AATTCATTC	A GTCGTCATGA	GTTGAGTGCT	TACTACATGC	60
AAGGCACTCT GCTA	GTTATA TTCTAATAA	r gcagagataa	TTAGACATGG	TTCCCGCCCT	. 120
CAAGAAGCTC ACAA	AAAGTAT TCAGGAAAT	A ATGCAGACTA	GTGATTTTGC	TATAAAATTA	180
TTTTTGAAGG AAGC	CAGACAC AGCAGTATT	r acctgtaggt	GGAGCAAGTA	ATAAGCCATG	240
CTGTGCAATA TATA	ACATAAA GCTTCTGCT	T CTCATGGGAA	TTTAGTTACA	GTGCTTGGAA	300
TGAGAAGGGG AAGG	BAAAGAA TTAACAAAT	G CCAAGATTTC	TGGAGCAGAT	TGTACAGCTG	360
TGACTTTGGA AAAC	CAGAAAG TAAGACCCT	C AGAAAACCAA	TGAAGTCTAA	GAGAAATAAA	420
ATTTAGTGGA CAGG	STATGAA AAGTGTAAT	T GCGCCTAACT	ACCAGATGGA	GACCTTCAGA	480
ATGGGCTATC CTTA	AGAGTCT AGTACATCA	A GAGACCCCTC	GAG		523

- (2) INFORMATION FOR SEQ ID NO:1481:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 104 base pairs
    - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:	
GAATTCGGCC AAAGAGGCCT AAAAAAAAAA AAAAAAGAAG ATATAAGCTA CTAGTATCAA AAATGAAAGA GGGGCTGTTT CTACTGATCC TGCAGACACT CGAG	60 104
(2) INFORMATION FOR SEQ ID NO:1482:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 337 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TC:OLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:	
GAATTCGGCC AAAGAGGCCT AAACTGAACT AAGAGATGCA CCTGAGAAAA CCTTGGCTTG CATGGGTTTG GCAATACATC AGGTGTTAAC TAAGGACCTT GAAAGGCATG CAGCTGAGTT ACAAGCCCAG GAAGGATTGT CTAATGATGG AGAAACAATG GTAAATGTGC CACATATTCA TGCAAGGTGA GGAATTGAT GTATTAAAAAT GAGGAAATCA GTAAAAAGGA CATGAGTTCC TTAGCAATGTAC ACACTGAACA ACTCGAG  (2) INFORMATION FOR SEQ ID NO:1483:	120 180 240
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 168 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	-
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:	
CGATTGAATT CTAGACCTGC CTCGAGAGCG CGCTGTTGAA TACCCAGTAT GATGGTCCTT AGCCTTCTTA GACCTTTCCT GTACCACTAC CTCTATGCCT TTTGCCAAGT CCAAGTGTTC ACCAGAAATG GAACTGATGC CAGAAAGACT ACAGCAACAA TACTCGAG	
(2) INFORMATION FOR SEQ ID NO:1484:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 478 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:	
GAATTCGGCC AAAGAGGCCT AGCAACCGCG CCTGGCTGCC TTTTCATTTT TAAAAACGTC	60

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AGTGTCGCTC CCACACAACA TGCAAACCCT CCTGCCGAGC TGCGACCTTC GCCTGTCACG 120
GAACCTGGTG CTGAGTGTGG TGAGAGTGAA TCCTGCAGCA CGTGGCGCAC TGTCGGCCTC 180
TTTCATGTTT AGCTTTTGAT TGTGCTTATT GTCCATTTGT ATTTCTTCTT CTAAGTGTCT 240
GTTCAAGACT TTTCCGTCTT GGCTGGAGGT GGGAGGTGCC TGCTCCTGTG TTTTCTGGCA 300
TCTTTCTCTG CTGTCTTTGT GTGTCTGCAC TCAGGGAGTT TCCCTGGGGT GTGTGCCTAG 360
AGAGGTGCTG GTTGTACATT TCAACGTAGG GACAGATTCC CAGCGTGTCT TTAAAAGGAGC 420
TGTGCCGCTG TGTGCTCACT TGACTCGCCG GCGTTCTTGT TTCTCCAGGC CTCTCGAG 478
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- (2) INFORMATION FOR SEQ ID NO:1485:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

GAATTCGGCC	AAAGAGGCCT	ACACACTGCA	AGAACAGAGC	CAAGAACCTA	CCATGTACCC	60
TTTACTTGGA	TTTATCATTA	CTGTTTTGCA	CATTTGCTTT	ATCATTCTTG	TTATATTTAC	120
ATATAGTTCC	TTCCCCTTGG	ATTATTTGAG	AACAAACTGC	AGAACTCACA	CCTCTTTCCC	180
CGAAGAACTA	GGCATTAGCA	CATTACAAGA	ATACGATGAT	AGAGATCAGA	AGTTAAATGC	240
TGATGAGATA	TTCCTGTCTA	ATCCACGAAC	CTTATTTCAT	TGTCATCAGT	TGTCCCAACA	300
GCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:1486:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

GAATTCGGCC AA	AGATTGCT GTCC	TTCAAC GTGTTC	TTA TGAAGTTATT	AGTAATACTT	60
TTGTTTTCTG GA	CTTATAAC TGGT	TTTAGA AGTGACT	CTT CCTCTAGTTT	GCCACCTAAG	120
TTACTACTAG TA	TCCTTTGA TGGC	TTCAGA GCTGATT	TATC TGAAGAACTA	TGAATTTCCT	180
CATCTCCAGA AT	TTTATCAA AGAA	GGTGTT TTGGTAG	SAGC ATGTTAAAAA	TGTTTTTATC	240
ACAAAAACAT TT	CCAAACCA CTAC	AGTATT GTGACAC	GCT TGTATGAAGA	AAGCCATGGC	300
ATTGTGGCTA AT	TCCATGTA TGAT	GCAGTC ACAAAG	AAAC ACTTTTCTGA	CTCTAATGAC	360
AAGGATCCTT TT	TGGTGGAA TGAG	GCAGTA CCTATT	TGGG TGACCAATCA	GCTTCAGGAA	420
AACAGATCAA GT	GCTGCTGC TATG	TGGCCT GGTACTO	SATG TACCCATTCA	GGATACCATC	480
TCTTCCTATT TT	ATGAATTA CAAC	TCCTCA GTGTCAT	TTTG AGGAAAGACT	TTATAATAAA	540
ACTATGTGGC TA	AACAATTC GAAC	CCACCA GTCCTC	SAG		579

- (2) INFORMATION FOR SEQ ID NO:1487:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

GAATTCGGCC	AAAGAGGCCT	AGATTGAATT	CTAGACCTGC	CTCGAGAGTC	ACÇCTTAGTT	60
TGCCATTGTG	CCAGCTAGTG	ATATTGCTGA	TGTTTTTTGT	${\tt GGGTGTTCTT}$	TTAGCAAAAC	120
GTGAATGAAT	GCATGTTTAC	AGGGATGCTC	TGGACTGGAG	GATGGTGAAA	TCCATCGTGG	180
TTGTCCCTCT	CCCTGAATGT	CCTTTTGTAG	CCAGGGCATC	TTTCCAATAT	GAATTATTAA	240
GCCTTAACTT	ACATTTTTGC	ATAACTTATA	ACTCTCCATT	ATATATTTGG	TTACATTTCT	300
TAGATGTTTT	CAACATTCTT	TATTAAAGTT	ATTTTATCAG	CATCCGCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:1488:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 422 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

GAATTCGGCC	AAAGAGGCCT	ACAAATGGGC	AGAAGTGAAA	CAGTCTTGTG	AGATACCTGT	60
TTTTTAAAAC	TCCATTTTAG	AAAAGGAATT	AACTAGGACT	TTATATCTCT	TCGTTCAATA	120
TAATTTTAAA	GAAGAATTGT	TGAAAAGTAG	ATATGTTTTG	CCATTTGCTG	AGAATATTTT	180
GTACGTTAGC	TTGTCTCTTA	CAAAAACTAA	ATGTGTTCCT	ACTTCTGATA	ATGTATGTCA	240
ATTTAAAATT	TGGAATGGCC	AAGATAAGTT	GCTCTGCATC	TGTCCTTCAT	ATGGCTCCTG	300
AGCACAGCTC	AGTGACTGGC	CCTTGCAGTG	CTTCTACCGT	TGTAATGGGT	AAAACCAGGG	360
GAAACTGCCT	TGCTCTTGAG	CTTGAGCAGG	TTAATCAAAA	GGATAGAGCT	TCCACTCTCG	420
AG						422

- (2) INFORMATION FOR SEQ ID NO:1489:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 293 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

GAATTCGGCC	AAAGAGGCCT	AGAGAAAGAG	AGAAAGAAAG	GAGGGAAGGA	AAGGAAGGAA	60
GGAAGGAAAG	AAGGAAAGAA	GGAAAGAGAG	GAGACTGAAG	GGCCAAGGAG	GGCATACAAT	120
GGAAGATGAG	AGCTGTGCTC	CCGGGAGGCT	TGTACTCATC	AAGAAAGAAA	GGAGAAAGAG	. 180
GGGGAAGAAA	AGAAAAAAA	AGAATAAAGA	AAGGAGAGAT	GAAGGAATAA	AGGAAAAAA	240
GTAGAAAGGA	AAGAAGGAGA	AGGGAGAGAA	GAAAGTAGGA	AGGAGAACTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:1490:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 250 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

GAATTCGGCC	AAAGAGGCCT	AGTGCAACTA	CAGATAAGTA	AACTTCGACT	GGGTTTAGTA	60
ACACCTGTCT	TTAATATTTG	TCAGTGTACC	TACATTGATA	ACATTGACCT	TTGGAAAAAT	120
TGGACTTGTA	TTGTGTTATT	TCTCTAGCAT	ATTAGTCCTA	AAAAAGTGTG	AGTAATAGGA	180
GATGGAGAGG	TGTTTGTGGA	TTGTCATTCT	GTGGTTCCTA	CAGCATTCAA	GTTGCGTCCG	240
TACGCTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:1491:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 435 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

GAATTCGGCC	TTCATGGCCT	AATTCTTAGA	AATAAAGCCA	CTATCATGCA	GGTTATTTAC	60
AAGTAAAAAC	ATGGAGTCAG	CCCAGTAGAG	AAACGTTCAA	ATAGTGTGGC	TCCTGCTCTG	120
CCACGTTCTG	TTTATGACTT	TGGATATTTT	ATTTATCCTT	TCTGGGGTAG	TTTTTCAACT	180
TTAAGGTCCT	AATAAACTTT	TAGATTTTAT	GACCTGTCCT	CTTTAGCCCT	GTAAGATTTA	240
AATATTATAA	AGAACCTGAT	TTCAAAGACA	CTGGTAAACT	TGGACAACTA	AACAAGTCCA	300
AGTATGGTAC	TTATTTGTGT	GTGTGCATAT	ATTAACCTTA	TGCATATGCT	GTTTTCACAC	360
CTATTTAAAC	TGTTTTTGAA	AAACGTATAT	ATCAGTTTTT	GGAAAACAGA	AGAAGATTTT	420
AAACGGCTAC	TCGAG					435

- (2) INFORMATION FOR SEQ ID NO:1492:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 360 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

GCGATTGAAT	ACATGTTCAA	TAAGGACAAT	GGACAGGCAC	CTTTTACCAT	CACTCCTGTG	60
TTTTCAGATT	TTCCAGTCCA	TGGGATGGAG	CCCATGAACA	ATGCCACCAA	AGGCTGTGAC	120
GAGTCTGTGG	ATGAGGTCAC	AGCACCATGT	AGCTGCCAAG	ACTGCTCTAT	TGTCTGTGGC	180
CCCAAGCCCC	AGCCCCCACC	TCCTCCTGCT	CCCTGGACGA	TCCTTGGCTT	GGACGCCATG	240
TATGTCATCA	TGTGGATCAC	CTACATGGCG	TTTTTGCTTG	TGTTTTTTGG	AGCATTTTTT	300
GCAGTGTGGT	GCTACAGAAA	ACGGTATTTT	GTCTCCGAGT	ACACTCCCAT	CGATCTCGAG	360

- (2) INFORMATION FOR SEQ ID NO:1493:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 271 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

GAATTCGGCC TTCATGGCCT AAGCAGACAA TATAGTAGTA ATTTAAATTT TTGTTTCCTG	60
ACTITCTGTA GTCCCTAAAC AAACAACAAA AAATCCTAGT AATCTTAAAC TTTTACATTA	120
ATAGAGATCC AAGAGAAAAT AAGCCATTTT TCACCATTGT GGACCCAAAT AAATCATAGA	180
CATGGTATTA AGAAGCCCTT TTCAGTCTGG TTGCAGTATT ATTTTCCTAC CTTTCTTTTT	240
CCTGTTCCCT GCTGTATGCC CACAGCTCGA G	271
(2) INFORMATION FOR SEQ ID NO:1494:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 310 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO.1494:	
GAATTCGGCC TTCATGGCCT AATGGGTCAG AAATTTGGGC CTGGCTAAGT GGATCCTCCA	60
CCCCAGGGTC TCTCACAAGG CTGCAATCAA AGGGCTGACT AGGACTTGGA ATCTCATTTG	120
AAAGTTAGAT TGGGGAAGGA TCTGCTTCCA AGCTCACTCA GTAGTTACTG GCAGGATTAG	180
GTTTCTCCAA GGTCGTTGGA CTAAGGGTCT CAGTTCCTCA CTGACAGTTG GCCTGAGGCT	240
GCCTTCAGTT TCTTGCCATG TGGGCCTCCC CAGCATAACT GTTTACTTCA TCAAAACAAA	300
CAAACTCGAG	310
(2) INFORMATION FOR SEQ ID NO:1495:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 138 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:	
THE RESERVE ASSESSMENT ASSESSMENT ASSESSMENT OF THE RESERVE ASSESSMENT	60
GAATTCGGCC AAAGAGGCCT ACGTCGATTG AATTCTAGAC CTGCCTCAGC TCTAATTATG	120
GTTCATGTTA GATTGTCTGC CCTTCCTCTT CCTCTTCTCT TTTGGGGAAA GATAATAGCA	138
CTTAATAACG CCCTCGAG	130
(2) INFORMATION FOR SEQ ID NO:1496:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 102 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:	
GAATTCGGCC AAAGAGGCCT ACAAAATTGT TCCTTTTACG TACGACAGAC TTCTGAAATG	60
GTAGTAGTAG TAGTGCCCTT TTTTTTCTC TTTTTAGCCC AG	102
GINGING INDIDECCII IIIIIIICIC IIIIIMOCCC NG	
(2) INFORMATION FOR SEQ ID NO:1497:	

(i) SEQUENCE CHARACTERISTICS:

No. of the second second

<ul><li>(A) LENGTH: 483 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:	
ANCGGTANCA TGAAAACATT TTTAGAGAGA ATTACCAGGC ATTTTTGGTA GAATGAGTGT TTAATGGAAC AGTCCAGAGA ACTCATCAAA GATGTTTATT AAAACGCGCA GACCTGCTCC AATTAAGGGC CCAGTCAGTG GTGTTAACAG TGAAGGGACT GTTCCAGAGG CGTGCTGCAC GGGACGCCCA CCCCAAATAC AAATGGTTTG CCAGTAGCTC ACAAATGAAC CCCATTGCCT TGCACTTAAG CTTCCTGAAG CACATACATA TCCTGCTTTG TGCTTTCCGC CCTATAGTAA ACGCAAACCA ATGGAGATGT GAAGCAATCT AATAGCAACA AGGCAAACCT CTACTTCCTC TAAAGAGGGAT TGCATCCTCT TGCTATCTTT GCCGATGCTC TCCTACAGAC CCATCCGCTC	60 20 80 40 00 60 20 80
(2) INFORMATION FOR SEQ ID NO:1498:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 144 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:	
GTGTGTGTGT GTGTGTGTG GTGTAAAGAA CTCTTACATT TCAGTGAGAA AATATTTTCA 1	60 20 44
(2) INFORMATION FOR SEQ ID NO:1499:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 418 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:	
CCTTGGGATG GGGATAGAAA TCTTTTCNTT CTTCNTTCTT GGGGGTTTGA GACAGAGTCT CGCTCTGTCA CCCAGGCCGG AGTGCAGTGG CGCAATCTCC GCTCACTGCA AACTCCACCT CCTGGGTTCA AGTGATCCTC CTGCCTCAGC CTCCCAAGTA GCTTGGATTA TGGGTGCCCA CCACCATGCC TGGCTAATTT TTGTATGTTT GATAGAAACG GTGTTTCACC CTGTTGACCA	60 120 180 240 360 416
(2) INFORMATION FOR SEQ ID NO:1500:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 337 base pairs	

PCT/US98/06956 WO 98/45437

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

GAATTCGGCC	AAAGAGGCCT	ACAAAGACCA	AGGTATCACA	TTCTGCCATT	AGCTGCTACC	60
TCTCCCTTCC	CCATTTTCAG	ACAGATTGAG	CCCACTTTTT	GTGTCCTCCT	CTGCTCTTAA	120
GCTGTTTCTC	ATCGTGGGTG	CTCAGCAACT	TGTCTGCTCT	CACTCTAGTT	TCTATTTGCT	180
TCCCTGAAAT	TAGCCTTTAA	CTATGCCCAG	ACAAGCCAGA	GCCTTGCCTA	AACTTCTAAT	240
TCCTCTGTGC	TTCTTAGTGT	ATCCTTTCTG	CCTGCTTGCC	TGCCTGCCTT	CCTGCCTGCT	300
TGCCTGCCTT	ACTGACCCTT	TGCCCCACGC	TCTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:1501:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

GAATTCGGCC AAAGAGGCCT AAACCGTCGA TTGAATTCTA GACCAGCCTC ATCTCCTGTT 60 105 CCTCTCTCCC TCCCAACTAT GTTGGCCTCC CTGCTGCTCC TCGAG

- (2) INFORMATION FOR SEQ ID NO:1502:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 701 base pairs (B) TYPE: nucleic acid

    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

GAATTCGGCC	AAAGAGGCCT	ACTGTGAACC	TAAAACTCCT	ATAAAGAAAA	GTAAAGTCTT	60
AAAAACAAAC	AAATACACAG	CAACAATCTT	ATTTTCCCCA	GCCTGTCTTA	TGTTAGGGTG	120
CAGATGTGAT	TTCTGTGTGG	CTAATCAGAT	GCCCTTGTGT	GAGAGACTGA	TTTGAACAGA	180
GGCAGGGGCA	TCCATCTTTC	TAGTGTCAGT	CACAGCAGAA	GCAGTGAGGT	CCTGGTGTCT	240
GTCGCTGCAG	TGGTGGCTTT	TGATACAGGA	GTTCCCTGAT	GGCAGTAGCT	TCTTTGTGGG	300
TTCAGTTCTG	TTGTGTGGTT	CTGCAAGTTC	AGCTTAGAGT	CTGTTTCTTC	AGCTGTTTCA	360
ATGACCCTCT	GAGCTGTCTA	CCATGAAAAA	TTCTATCCTG	CTTACACTAA	TTAGAGCCAA	420
TCCTGTTATT	TACAAATGAA	TATCCTGACC	AGTAATGAAG	GTCTAGACTT	AACTGTAATA	480
TTTTATGACT	TAAATTGTTG	GCATATGTGA	AAACTTTTTG	TTTATTCTAA	ACTTTTTTGT	540
TGTTGTTGTA	AAATAAAACA	TTTATGAAAA	GCGCACCAAA	AAGGATAACA	AATGAGAGTA	600
ATGCAACATA	CAGGCACCAG	CAACTCAGGC	CAGGGAGATG	ATATATGAGC	ATCCCCAATC	660
TCCCCTTTAC	ACTCCCTCAA	ATAACTCAAT	CAAGACTCGA	G		701

- (2) INFORMATION FOR SEQ ID NO:1503:
  - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 257 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503: GAATTCGGCC TTCATGGCCT AGGAACTAGG TGACTTTGGG GCTCATCTCA CAAGTTTCCT 60 TACACTTAGG GATCAGTCTT TTGCTTCCTG TTGTCCTCTG CCTGAAAGTA GTTGCCAAGT 120 TGTACTGTTT TATATATCCA CCACAGCATG AGTTAAACCA AAGTCTGGAT CAGCAGACTG 180 CCAGATTTT TTTTAACAAA TTTATTAATC AATACATTT GTCCATGTCT ACAGTTGTTT 240 ATGGGGGAGA ACTCGAG 257 (2) INFORMATION FOR SEQ ID NO:1504: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 277 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504: GAATTCGGCC TTCATGGCCT AGGGGACCTT GGGAGAATGT AATCCCTGCC CCTAGTCTCA 60 GTTTCTGCAT CCACGGAAGA GGGGTGAAGA TGGTCCCTAC CCCTCCAGAA TGTTCTTTTT 120 TTTTTTTTT AAAAAAAAA AAAAAAAA AAAGTACGTT ATGTTTTCAG ATAAGAACAC 180 TTCTTCATGG ATGACTTGAA ATAATTGCCA TGGTCCCTAA GTTTTCCTCT CTGTAGATGA 240 ATGATATAGC TCAGTATCTA AGCAGTGGAT CCTCGAG 277 (2) INFORMATION FOR SEQ ID NO:1505: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 341 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505: 60 GAATTCGGCC TTCATGGCCT AGACCTGCCT CGAGCCTCCC AAGCTGCTGG TATTACAGGC GTGAACCACT GCACCTGGCC TAATACGATA TTCTTACAAT TTAAAAAATG AAAGCAGAGG 180 AATGGTGGCA GGGAAGCTGA CATTTTAAGA GTTCACTTCC TTGTAGTTAT CACAGTTAAT 240 TCTTACTGTT AGAATAAGTG GTAACTTGCC AAGGTCACAT TGCTAGATGT CAGAGCAGAA 300 GTTAGTGTTT ATTGAACACC TATTGTGTTC TGGCCCTCGA G 341

- (2) INFORMATION FOR SEQ ID NO:1506:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 270 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

GAATTCGGCC	TTCATGGCCT	AGGCATTTTG	TCTCTAGAAT	TACCCACCCG	TTCCTGCGCT		60
CTACGGTTCT	CCATGCCCCC	TCCAGTTTGG	GGGTCTAAAC	CGAACAGGAG	AGGTGCAGGG		120
GACCAGGAGG	TGTCCTGGCA	CAAAGGTTCG	GGGGTCTCCC	TGGCAAGGGG	TCCCAGGGCC		180
TGGAGCCCGA	GGCCCAGCCA	AAAGCACACA	GCATCAAAAC	ATGTTTTTAG	TGGGAAGCTC	•	240
CAGGCCCTGC	CCCTCCCCGG	GGGCCTCGAG					270

- (2) INFORMATION FOR SEQ ID NO:1507:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 462 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

GAATTCGGCC	TTCATGGCCT	AGAGCAGGAA	GATTGTGTGA	GTGCTGGGGT	TTGGGGGTGC	60
CCAAGTTGGG	AACCAGTGGA	GGGAGAGAGA	GGTAGGAGGT	AGATGGATGG	AGATCAAAGG	120
CCAGGCCTGT	GGCCAAGGGG	GCTGCTAACC	CTTCAACCCT	GTGTTAGCCT	GTACACTCAC	180
CAGGCCAGGC	TCAGCAGGCG	GGCTGTTCAC	CTCCTGGCAG	CAAATGGTCC	AGAATGTGCC	240
CTCGCTGCAG	CCCAGCTGGC	TCCAGAAGGG	GGACCACAGA	GGCTGGAGCT	ATGCATGCAC	300
AGTGCTTTCT	CCCAACCTTG	CTTCTGAGAA	AAGTGTCCCT	GCGAGGGCCC	TGGAGGAGGG	360
AGCTAGGGAC	CAGCAGAAGG	GCCTAGGTTT	CTGTAGCATC	ATTTTTAGCC	CTGGCTGAAT	420
CTGGGAAGCA	CCTGGTGGCT	TTAACATTCC	CGTTAGCTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:1508:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 694 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

GAATTCGGCC TTCA	TGGCCT AGTCACAATC	CACTTAAAGA	AGTTTGGTTA	TATTTCAGTG	60
AAAATTTTCT TCCA	GAGTAG GTTTTTTTC	GTGGGTTGGG	GGGTAACTTT	ACTACAATTA	120
GTAAGTATGG TGCA	GAATTT CATGCAAATG	AGGAGTGCCA	${\tt GCAGTGTGAT}$	AATTTAAACA	180
TATTTAAACA AAAA	CAAAAA AAATGAATGC	ACAAACTTGC	TGCTGCTTAG	ATCACTGCAG	240
CTTCTAGGAC CCGG	TTTCTT TTACTGATTT	AAAAACAAAA	САААААААА	TAAAAAAGTT	300
GTGCCTGAAA TGAA	TCTTGT TTTTTTTAT	AAGTAGCCGC	CTGGTTACTG	TGTCCTGTAA	360
AATACAGACA CTTG	ACCCTT GGTGTAGCTT	CTGTTCAACT	TTATATCACG	GGAATGGATG	420
GGTCTGATTT CTTG	GCCCTC TTCTTGAATT	GGCCATATAC	AGGGTCCCTG	GCCAGTGGAC	480
TGAAGGCTTT GTCT	AAGATG ACAAGGGTCA	GCTCAGGGGA	TGTGGGGGAG	GGCGGTTTTA	540
TCTTCCCCCT TGTC	GTTTGA GGTTTTGATC	TCTGGGTAAA	GAGGCCGTTT	ATCTTTGTAA	600
ACACGAAACA TTTT	TGCTTT CTCAAGTTTT	CTGTTAATGG	CGAAAGAATG	GAAGCGAATA	660
AAGTTTTACT GATT	TTTGAG ACACTAGACT	CGAG			694

- (2) INFORMATION FOR SEQ ID NO:1509:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

GAATTCGGCC	TTCATGGCCT	AATGAGGTTC	TATCTAGAGG	TGATGGGAGA	CAGTGACAGA	60
TCATCAGGCA	TTAGATTCTC	ATAAGGACTG	CGCAACCTAG	ATCCCTTGAA	TGAACAGTTC	120
ACAATAGGGT	TCACTCTCCA	ATGAGAATCT	AATGCTGCCG	CTGATCTGAC	AGGTGCCAGA	180
GCTCAGGCGG	TAATACGAGA	GGCTGGAGAT	ACAGATAAAG	CTTCAGTTGC	TTGCCCGCCA	240
CTTACCTCCT	CTTGTGCGGC	CCAGTTCCTA	ACAGGCCACA	GACCGCTACC	AGTCCATGGC	300
CTGGAAGTTG	GGGACCCCTC	TACTGGGATA	TTTATAATTG	CATATGTGGT	TACCTAATAT	360
TTCCATGATA	CAACACTGGT	CTAGATTCTA	GGCCATTCTC	CTTCAAAAAG	AACCCTGCTT	420
CCTTACAGTT	TTACTGTTTA	GCAGCAATGT	TTTCTACCCC	TTCTTAAAAT	TTTCAGCCAC	480
CACACTCGAG						490

- (2) INFORMATION FOR SEQ ID NO:1510:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 313 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

GAATTCGGCC	TTCATGGCCT	ACTCTCTCAT	TCCTACCCTC	CTCCCCTCCA	CTCACGCTCC	60
TCCCAATCCC	CAAGGTCCTC	TCATTCCCAC	CTTCCTCCCT	TCCTCTCCTC	ACGCTCCTCC	120
CTATCCCCGA	GCTCCTCTCT	CATCCCTACC	CTCCTCCCCT	CCACTCACGC	TCCTCCCAAT	180
CCCCAAGGTC	CTCTCATTCC	CACCTTCCTC	CCTTCCTCTC	CTCACGCTCC	TCCCTATCCC	240
CGAGCTCCTC	TCTCACTCCC	TCCCTCCTCT	CATGCTCCTC	CCCCCTCTCC	TCATGCTCCT	300
CCCCATCCTC	GAG					313

- (2) INFORMATION FOR SEQ ID NO:1511:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 354 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

GCCGGGTGGG	CCGGAGGTGG'	CGCGGCCGCA	CGGCTTTGTT	CCGGAAAGCC	CTTAGGTGGA	60
GAGCGATGTG	GGGCGCGCA	GGGGGATCGC	GTAGAGGAAC	CTTCGCGCAC	CGCCTCTCCG	120
GGTCTGGGAA	TCTGCTGAAC	TCCTTGCCTC	TCTTGGGGTC	CCTCGAACGC	CCCAGCTAAG	180
AAGGGCGGGG	GCCTTGCCAG	GGCGCGAGCA	ACATGACGTT	CAAGGTCTTC	CTGTGGCTTC	240
TGTAAAGAAA	TGTTCACGTG	GGAGCCTGTC	CACATGGGCT	GTACTAAGGA	TCTGGCACGA	300
GGAAGAAATA	TCACTGCAGA	ACCTGAAGCC	CTCCGTTGGA	AGGGTCACCT	CGAG	354

(2) INFORMATION FOR SEQ ID NO:1512:

PCT/US98/06956 WO 98/45437

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 407 base pairs

  - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

GAATTCGGCC	AAAGAGGCCT	AGAGCAGCTT	GGCTAAAAGT	AAGGGTGTCG	TGCTGATGGC	60
CCTGTGCGCA	CTGACCCGCG	CTCTGCGCTC	TCTGAACCTG	GCGCCCCGA	CCGTCGCCGC	120
CCCTGCCCCG	AGTCTGTTCC	CCGCCGCCCA	GATGATGAAC	AATGGCCTCC	TCCAACAGCC	180
CTCTGCCTTG	ATGTTGCTCC	CCTGCCGCCC	AGTTCTTACT	TCTGTGGCCC	TTAATGCCAA	240
CTTTGTGTCC	TGGAAGAGTC	GTACCAAGTA	CACCATTACA	CCAGTGAAGA	TGAGGAAGTC	300
TGGGGGCCGA	GACCACACAG	GTGGGAACAA	GGACAGGGGG	ATTTAAGCAG	TCAAAAGGAA	360
AAACATGTTA	AGACCCTAGA	CTTGTATATT	GACACACAGA	ACTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:1513:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 422 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

GAATTCGGCC	AAAGAGGCCT	ACATTCATAC	AATTACAGAA	TTCAAATATT	GCAAAAGGAT	60
GTGTGTCTTT	CTCCCCGAGC	TCCCCTGTTC	CCCTTCATTG	AAAACCACCA	CGGTGCCATC	120
TCTTGTGTAT	GCAGGGCTAT	GCACCTGCAG	GCACGTGTGT	ATGCACTCCC	CGCTTGTGTT	180
TACACAAGCT	GTGGGGTGTT	ACGCATGCCT	GCTTTTTTCA	CTTAATAATA	CAGCTTGGAG	240
AGATTTTTGT	ATCACATTAT	AAATCCCACT	CGCTCTTTTT	GATGGCCACA	TAATAACTAC	300
TGCATAATAT	GGATACGCCT	TATTTGATTT	AACTAGTTCC	CTAATGATGG	ACTTTTAAGT	360
TGTTTCCTTT	TTTTTTTTTT	TTTGCTACTG	CAAACGATGC	TATCTAGGCC	TCTTTGGCCG	420
AA						422

- (2) INFORMATION FOR SEQ ID NO:1514:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 485 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

GAATTCGGCC	AAAGAGGCCT	ATGGAAATTC	AAGACCTGAT	GTTTGAGGAG	ATGAGGGAAA	60
CTCTTAAAAA	TGACCTAAAA	GCAGTTTTAG	GAGGAAAAGC	TACAATACCT	GAGGTAAAGA	120
ATTCAGAGAA	CTCCAGTAGT	AGGACAGAGT	TTCAGCAAAT	AATCAATTTA	GCATTACAAA	180
AAACAGGGAT	GGTAGGGAAA	ATAGAAGGAG	AAAACTCTAA	AATAGGTGAT	GATAATGAAA	240
ATTTAACCTT	TAAATTAGAA	GTAAATGAGC	TGAGTGGTAA	ATTAGACAAC	ACTAACGAAT	300
ACAATAGTAA	TGATGGTAAG	AAATTACCCC	AGGGTGAATC	ACGAAGTTAC	GAAGTCATGG	360
GAAGTATGGA	AGAAACCTTA	TGCAATATAG	ATGACAGAGA	TGGAAATCGC	AATGTCCATT	420
TAGAATTTAC	AGAAAGAGAG	AGTAGGAAGG	ATGGAGAGGA	TGAATTTGTC	AAAGAAAAAC	480

TCGAG	485
(2) INFORMATION FOR SEQ ID NO:1515:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 400 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:	
GAATTCGGCC AAAGAGGCCT AGGCACAGAA GGGTGGTGAG TGTGATCAAA TCTAGTCTCA CTCCCACTTT TTAGTCTCAC TCCTACTTTT GTCCACCACC CAGGCACGGA GAGAAAGGAA TGTTTAGCAC AAGACACAGC GGAGCTCGGG ATTGGCTAAA CTCCCATAGT ATTTATGGTG GCCGCCGGC GGGGCCCCAG CCCAGCTTGC AGGCCACCTC TAGCTTTCTT CCTACCCCAT TCCCGGCTTC CCTCCTCCTC CCCTGCAGCC TGGTTAGGTG GATACCTGCC CTGACATGTG AGGCAAGCTA AGGCCTGGAG GGTCAGATGG GAGACCAGGT CCCAAGGGAG CAAGACCTCG CGAAGCGCAG CAGCCCCGGC CCTAGGCCTC TTTGGCCGAA	60 120 180 240 300 360 400
(2) INFORMATION FOR SEQ ID NO:1516:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 145 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:	
GAATTCGCGG CCGCGTCGAC GTCGACGCGG CCGCGAATTC GGCCAAAGAG GCCTACCCAT GTCAATCAAG ATGGGTGATT ATGAAATGCC AGACTTCTAA AATAAATGTT TTGGAATTCA ATGGGTAAAT AAATGCTGGC TCGAG	60 120 145
(2) INFORMATION FOR SEQ ID NO:1517:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 277 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:	
GCTGGACCTC CTGTGCAAGA ACATGAAACA GCTGTGGTTC TTCCTTCTCC TGGTGGCAGC TCCCAGATCG GTTCTGTCCC AGGTGCAGCT GCGGGAGTCG GGCCCAGGAC TGGTGAAGCC TTCGGAGACC CTGTCCCTCA CCTGCACTGT CTCTGGTACT TCCGTCAGAA GTGTTAGTTA CGACTGGAGT TGGCTCCGGC AGTCCCCGGG GAAGGGACTG GAGTGGCTTG GAGAGATTGA	60 120 180 240

- (2) INFORMATION FOR SEQ ID NO:1518:
  - (i) SEQUENCE CHARACTERISTICS:

TTACAGGGGG AGAGGCAATT ACAACCCGTC CCTCGAG

277

- (A) LENGTH: 161 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

GAATTCGGCC	AAAGAGGCCT	ACTCATGCAC	CTAATTGGAT	CCTATCTTTG	TGTTGTTAGC	60
TGGTTATTAT	GCAGACTTTA	TTATGTGGTT	GTTTTATAGT	GTCCATAACC	TATGTACTTA	120
AGTTTGTTTT	TGTGGTGGCG	CTTCCAATTA	GGGCTCTCGA	G		161

- (2) INFORMATION FOR SEQ ID NO:1519:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 561 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

GAATTCGGCC	TTCATGGCCT	AATATAAAAC	AATGTTTTTC	AAGGCATTAT	ATAATAGGCT	60
AAGGACAGTG	ACCTCCAAGA	GACAGCAAAC	AAGGTAATAC	CTGTGACTGC	TCCAGCTTAC	120
TGCCTTGAGA	GAATTAATAG	TAGGTTTGTG	GTACAGGGAG	GGAGAATCCA	GTCAGAGCCC	180
AGCGGACTTG	CTGAATTAAG	GAAATGGAGC	TGAGAGTCCA	GAGAGACCAA	CATGGCTAAA	240
GTTGTCATGA	CAGAGCACTC	AGAACTAGAG	AGCTGCACAG	CAACATAACC	TAAGAGCTCT	300
GAAGATAATC	TCCCTCAAAT	ACTCAGCTGA	GTACTGATCA	ACATATATGT	GTGAGGAAGC	360
TATCTGAGGC	TGACAAAGAA	CTGCCTGAAG	AGATTAGAGG	GAACAGTACT	TGGCACTCAC	420
ACAGAATTGG	AAACTGTACC	TGTTCCCACC	AGCCAAACTG	GAAAAACCTC	AGGATTCATG	480
GGGTACTCAG	AAAGGACTTG	CATCAGGTAT	GGGGAATAAT	TAGCCCTAGA	CAGAGCACTG	540
CTCTAATCCC	ATCCACTCGA	G				561

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEO ID NO:1, SEO ID NO:2, SEO ID NO:3, SEO ID NO:4, SEO ID NO:5, SEO ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96. SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEO ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEO ID NO:137, SEO ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,

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NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID

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NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, SEQ ID NO:1500, SEQ ID NO:1501, SEQ ID NO:1502, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID NO:1505, SEQ ID NO:1506, SEQ ID NO:1507, SEQ ID NO:1508, SEQ ID NO:1509, SEQ ID NO:1510, SEQ ID NO:1511, SEQ ID NO:1512, SEQ ID NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;

or a complement of said sequence.

2. An isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

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NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;
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or a complement of said sequence.

3. An isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:1

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NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID

NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID

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NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495. SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, SEQ ID NO:1500, SEQ ID NO:1501, SEQ ID NO:1502, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID NO:1505, SEQ ID NO:1506, SEQ ID NO:1507, SEQ ID NO:1508, SEQ ID NO:1509, SEQ ID NO:1510, SEQ ID NO:1511, SEQ ID NO:1512, SEQ ID NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;

or a complement of said sequence.

4. An isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

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or to a complement of said sequence.

- 5. An isolated protein encoded by an isolated polynucleotide of claim 1.
- 6. An isolated protein encoded by an isolated polynucleotide of claim 2.
- 7. An isolated protein encoded by an isolated polynucleotide of claim 3.
- 8. An isolated protein encoded by an isolated polynucleotide of claim 4.

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